

PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
PS Claim 4; SEQ ID NO 6620; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 12 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3260 GATATTTTATTCCTT 3275
Db 16 GATATTTTATTCCT 1
RESULT 2081
ADN48306
ID ADN48306 standard; DNA; 20 BP.
XX
AC ADN48306;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human Jun N-terminal kinase 1 (JNK1) oligonucleotide #17.
XX
KW Human; Jun N-terminal kinase; JNK; Jun N-terminal kinase 1; JNK1;
KW hyperproliferative disease; cell cycle progression;
KW protein phosphorylation; tumour growth; cancer; apoptosis;
KW prostate cancer; inflammation; fibrosis; fibrotic disease; scarring;
KW peritoneal adhesion; lung fibrosis; conjunctival scarring; cytostatic;
KW antiinflammatory; vulvurey; ss.
XX
OS Homo sapiens.
XX
PN US2004029823-A1.
XX
PD 12-FEB-2004.
XX
PF 15-JAN-2003; 2003US-00345444.
XX
PR 13-AUG-1997; 97US-00910629.
PR 07-AUG-1998; 98US-00130616.
PR 07-APR-1999; 99US-00287796.
PR 15-SEP-1999; 99US-00396902.
PR 31-JAN-2001; 2001US-00774809.
XX
PA (MCKA/) MCKAY R.
PA (DEAN/) DEAN N M.
PA (MONI/) MONIA B P.
PA (NERO/) NERO P S.
PA (GAAR/) GAARDE W A.
XX
PI Mckay R., Dean NM, Monia BP, Nero PS, Gaarde WA;
XX WPI; 2004-168941/16.
XX
DR New oligonucleotides, which specifically hybridizes with Jun N-terminal
PT

PT kinase protein, useful in diagnosing or treating inflammation, fibrosis
XX or a fibrotic or hyperproliferative disease or condition.
PS Example 3; SEQ ID NO 17; 71pp; English.
XX
CC The invention relates to an oligonucleotide comprising 8-30 nucleotides
CC connected by covalent linkages, where the oligonucleotide has a sequence
CC specifically hybridizable with a nucleic acid encoding a Jun N-terminal
CC kinase (JNK) protein and modulates the expression of the JNK protein. The
CC invention also relates to a pharmaceutical composition comprising the
CC oligonucleotide(s) or its bioequivalent and a pharmaceutical carrier, a
CC method of treating an animal having, suspected of having or prone to
CC having a hyperproliferative disease, a method of modulating the
CC expression of a JNK protein in cells or tissues, a method of modulating
CC cell cycle progression, phosphorylation of a protein phosphorylated by a
CC JNK protein and expression of a cellular protein that promotes one or
CC more metastatic events in cultured cells or the cells of an animal, a
CC method of inhibiting the growth of a tumour in an animal, a method of
CC inducing apoptosis in a cell, a method of treating a human having a
CC disease or condition characterised by a reduction in apoptosis and a
CC method of treating an animal having a disease or condition associated
CC with a JNK protein. The oligonucleotide and composition are useful in
CC diagnosing or treating a disease or condition characterised by a
CC reduction in apoptosis (e.g. prostate cancer), a disease or condition
CC associated with a JNK protein (e.g. inflammation, fibrosis), a fibrotic
CC disease or condition (e.g. scarring, peritoneal adhesions, lung fibrosis,
CC conjunctival scarring) or a hyperproliferative disease or condition (e.g.
CC cancer), or in inhibiting the growth of a tumour. This sequence
CC represents a human JNK1 oligonucleotide of the invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1060 GCGTCATCAGCTCCA 1075
Db 5 GCATCCATGAGCTCCA 20
RESULT 2082
ADN89289
ID ADN89289 standard; DNA; 20 BP.
XX
AC ADN89289;
XX
DT 01-JUL-2004 (first entry)
XX
DE P16DF PCR primer #1.
XX
KW P16DF; primer; ss; nucleic acid label; hybridization assay;
KW primer extension; terminal transferase addition; ligation; end labelling;
KW PCR; nick translation labelling; reverse transcription;
KW Southern blotting; Northern blotting; enzyme linked immunosorbant assay;
KW ELISA; arrays; SKYS; cloning; transcription; abortive transcription;
KW sequencing.
XX
OS Synthetic.
XX
PN US2004054162-A1.
XX
PD 18-MAR-2004.
XX
PF 29-APR-2003; 2003US-00425037.
XX
PR 30-OCT-2001; 2001US-00984664.
PR 29-OCT-2002; 2002WO-US034419.
XX
PA (HANN/) HANNA M M.
XX
PI Hanna MM;
XX

DR WPI; 2004-281628/26.
XX Labeling nucleic acid which is used in hybridization assays, primer
PT extension, terminal transferase additions, involves incorporating 8-S-
PT substituted purine or 5-S-substituted pyrimidine analog into nucleic
PT acid.
XX
PS Disclosure; SEQ ID NO 1; 104pp; English.
XX
CC The invention relates to a method of labelling a nucleic acid which
CC involves incorporating at least one nucleotide analogue into a nucleic
CC acid, where the analogue comprises an 8-S-substituted purine or 5-S-
CC substituted pyrimidine analogue. The method is useful for labelling a
CC nucleic acid. The method is useful for detecting a second nucleic acid of
CC interest. The method is useful for labelling a nucleic acid which is used
CC in hybridization assays, primer extension, terminal transferase
CC additions, ligation, end labelling, PCR, nick translation labelling,
CC reverse transcription, Southern blotting, Northern blotting, enzyme
CC linked immunosorbant assay (ELISA), arrays, SKVE, cloning, therapeutic
CC abortive transcription, sequencing, diagnostic techniques, therapeutic
CC applications, and treatment and prevention of diseases and conditions.
CC The labelled nucleic acids are useful in assessing methylation state of
CC specific genes, detecting presence of known genetic mutations, detecting
CC mRNA expression levels, detecting presence of pathogenic organisms, and
CC detecting and amplifying proteins. The present sequence represents a
CC PL6DF PCR primer.
XX
SQ Sequence 20 BP; 1 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1209 TGGGAGGGCTGCTTC 1224
Db 5 TGGCGAGGGCTGCTTC 20
RESULT 2083
ADM14899/c
ID ADM14899 standard; DNA; 20 BP.
XX
AC ADM14899;
XX
XX 01-JUL-2004 (first entry)
DE Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1086.
XX
KW chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nontropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c

FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
XX
PN WO2004028458-A2.
XX
PD 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030374.
XX
XX 25-SEP-2002; 2002US-0413549P.
XX (PHAA) PHARMACIA CORP.
PI Gierse JK;
XX
XX WPI; 2004-305094/28.
XX
XX New antisense compound, having a sequence targeted to a nucleic acid
XX encoding mPGES-1, useful for preparing a composition for treating e.g.,
XX inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
XX ischemia.
XX
XX Claim 4; SEQ ID NO 1086; 132pp; English.
XX
XX The present sequence represents a chimeric antisense oligonucleotide
XX targeted to human microsomal prostaglandin E2 synthase (mPGES-1). The
XX human mPGES-1 gene is located on chromosome 9, more specifically to
XX 9q34.3. The present invention also describes: (1) antisense compounds,
XX having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
XX mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
XX inhibits its expression; (2) a method of inhibiting the expression of
XX mPGES-1 in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with mPGES-1. mPGES-1 chimeric
XX antisense oligonucleotides and antisense compounds have cytostatic,
XX antidiabetic, immunomodulator, cardiant, neuroprotective,
XX antiinflammatory, neuroprotective, nontropic, antiarthritic, vasotropic,
XX ophthalmological, immunomodulatory, and cardiovascular activities, and can
XX be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
XX can be used for preparing a composition for treating a disease or
XX condition associated with mPGES-1 e.g., inflammation, Alzheimer's
XX disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
XX ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2316 TCTGTGTGTGTGTGTG 2331
Db 16 TCCGTGTGTGTGTGTG 1
RESULT 2084
ADN72001/c
ID ADN72001 standard; DNA; 20 BP.
XX
XX ADN72001;
XX
XX 12-AUG-2004 (first entry)
DE Human glucose transporter-4 antisense oligonucleotide #42.
XX
XX ss; human; antisense therapy; glucose transporter-4;
XX hyperproliferative disorder; probe.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= Other

PD 10-JUN-2004.
XX
PF 10-DEC-2002; 2002US-00317279.
XX
XX 10-DEC-2002; 2002US-00317279.
PR 10-DEC-2002; 2002US-00317279.
XX
XX (ISIS-) ISIS PHARM INC.
PA Chiang M, Dobie KW;
XX
XX WPI; 2004-440383/41.
DR
XX New compounds, particularly oligonucleotides targeted to a nucleic acid
PT encoding DRI-associated protein 1, useful for treating diseases
PT associated with DRI-associated protein 1, e.g. developmental disorders.
XX
XX Example 15; SEQ ID NO 22; 33pp; English.
PS
XX The present sequence is directed to antisense oligonucleotides targeted
CC to DRI-associated protein 1 [also known as DRAP1 and negative cofactor 2
CC alpha (NC2-alpha)] and which modulates to the expression of DRI-
CC associated protein 1. The invention is useful for treating a disease or
CC condition associated with DRI-associated protein 1 such as a
CC developmental disorder. The present sequence is human DRI-associated
CC protein 1 antisense oligonucleotide. This sequence is used in the
CC exemplification of the invention.
XX
XX Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

QY 1545 CTTCAAGGACCTGGTG 1560
DB 16 CTTGAAGGACCTGGTG 1

RESULT 2087
ADP82172
ID ADP82172 standard; DNA; 20 BP.
XX
XX ADP82172;
XX
XX 26-AUG-2004 (first entry)
DT
XX Human DRI-associated protein 1 target oligonucleotide #4.
DE
XX DRI-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha;
XX developmental disorder; therapy; human; ss.
XX
XX Homo sapiens.
XX
XX US2004110703-A1.
PN
XX 10-JUN-2004.
PD
XX 10-DEC-2002; 2002US-00317279.
PF
XX 10-DEC-2002; 2002US-00317279.
PR
XX (ISIS-) ISIS PHARM INC.
PA Chiang M, Dobie KW;
XX
XX WPI; 2004-440383/41.
DR
XX New compounds, particularly oligonucleotides targeted to a nucleic acid
PT encoding DRI-associated protein 1, useful for treating diseases
PT associated with DRI-associated protein 1, e.g. developmental disorders.
XX
XX Example 15; SEQ ID NO 51; 33pp; English.
PS
XX

CC The present sequence is directed to antisense oligonucleotides targeted
CC to DRI-associated protein 1 [also known as DRAP1 and negative cofactor 2
CC alpha (NC2-alpha)] and which modulates to the expression of DRI-
CC associated protein 1. The invention is useful for treating a disease or
CC condition associated with DRI-associated protein 1 such as a
CC developmental disorder. The present sequence is human DRI-associated
CC protein 1 target oligonucleotide. This sequence is used in the
CC exemplification of the invention.
XX
XX Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

QY 1545 CTTCAAGGACCTGGTG 1560
DB 5 CTTGAAGGACCTGGTG 20

RESULT 2088
ADO39459
ID ADO39459 standard; DNA; 20 BP.
XX
XX ADO39459;
AC
XX 26-AUG-2004 (first entry)
DT
XX Novel human CD25 antibody-related PCR primer SeqID42.
DE
XX monoclonal antibody; CD25; IL-2 binding; immunosuppressive;
XX antiinflammatory; cytostatic; gene therapy; transplant rejection;
KW graft-versus-host disease; autoimmune; inflammatory disease;
KW inflammatory skin disorder; hyperproliferative skin disorder;
KW lymphoid neoplasm; PCR; primer; ss; human.
XX
XX Homo sapiens.
OS
XX WO2004045512-A2.
PN
XX 03-JUN-2004.
PD
XX 14-NOV-2003; 2003WO-US036126.
PF
XX 15-NOV-2002; 2002US-0426690P.
PR
XX (GENM-) GENMAB AS.
PA
XX Schuurman J, Havenith CEG, Parren P, Van De Winkel JGJ;
PI Williams DL, Petersen J, Baadsgaard ODMS;
PI
XX WPI; 2004-420514/39.
DR
XX New human monoclonal antibody that binds to human CD25 and inhibits IL-2
PT binding to CD25, useful in treating or preventing e.g., autoimmune or
PT inflammatory disease or hyperproliferative skin disorder or lymphoid
PT neoplasm.
XX
XX Example 2; SEQ ID NO 42; 114pp; English.
PS
XX This invention relates to a novel isolated human monoclonal antibody
XX which binds to human CD25 and inhibits IL-2 binding to CD25. The
XX invention may be useful for the development of compounds with an
XX immunosuppressive, antiinflammatory or cytostatic activity whilst the
XX disclosed sequences may be useful for gene therapy. The monoclonal
XX antibody is useful in treating or preventing a disorder involving cells
XX expressing CD25, for example transplant rejection, graft-versus-host
XX disease, autoimmune or inflammatory disease, inflammatory or
XX hyperproliferative skin disorder or lymphoid neoplasm. The present
XX sequence is that of a PCR primer which was used for amplification of a
XX region of sequence encoding part of a novel human CD25 antibody and which
XX was used in the exemplification of the invention.
XX

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SQ Sequence 20 BP; 3 A; 3 C; 8 G; 4 T; 0 U; 2 Other;
Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGTGAGGC 872
      :||| |||||:|||||
Db 1 SAGGTGCAGCTGKTGGAGTC 20

RESULT 2089
ADP49595
ID ADP49595 standard; DNA; 20 BP.
XX
AC ADP49595;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human BAF53 antisense oligonucleotide ISIS280388.
XX
KW Human; ss; antisense; chromatin; BAF complex; BRG1/brm-associated factor;
KW BAF53; BRG1-associated factor 53kDa; cancer; tumour;
KW actin-related protein; hyperproliferative disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone and all cytidines are 5
FT -methylcytidines"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl residue"
XX
PN US2004110147-A1.
XX
PD 10-JUN-2004.
XX
PF 09-DEC-2002; 2002US-00316243.
XX
PR 09-DEC-2002; 2002US-00316243.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW, Jain R;
XX
DR WPI; 2004-440336/41.
XX
PT New oligonucleotide compound that inhibits expression of BAF53, useful
PT for preparing a composition for treating hyperproliferative disorder,
PT e.g. cancer.
XX
PS Example 15; SEQ ID NO 82; 72pp; English.
XX
CC The invention relates to a compound, having a sequence comprising 8-80 bp
CC targeted to a nucleic acid encoding BAF53 (a member of the BAF complex
CC (BRG1/brm-associated factor), BRG1-associated factor 53kDa which is an
CC actin-related protein), specifically hybridises with the nucleic acid
CC encoding BAF53 comprising 28001-bp sequence (derived from human
CC chromosome 3) and inhibits expression of BAF53, i.e. an antisense
CC oligonucleotide. Also included are inhibiting the expression of BAF53 in
CC cells or tissues, screening for a modulator of BAF53, a diagnostic method
CC for identifying a disease state, a kit or assay device comprising the
CC compound and treating an animal having a disease or condition associated
CC with BAF53. The oligonucleotide compound is useful for preparing a
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CC composition for treating hyperproliferative disorder), e.g. cancer or a
CC tumour. The present sequence is an antisense oligonucleotide targeting
CC human BAF53.
XX
SQ Sequence 20 BP; 7 A; 8 C; 1 G; 4 T; 0 U; 0 Other;
Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3069 CCACACCCCAACACTT 3084
      ||||| ||||| |||||
Db 4 CCACATCCCAACACTT 19

RESULT 2090
ADP49668/C
ID ADP49668 standard; cDNA; 20 BP.
XX
AC ADP49668;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human BAF53 antisense oligonucleotide target region #58.
XX
KW Human; ss; antisense; chromatin; BAF complex; BRG1/brm-associated factor;
KW BAF53; BRG1-associated factor 53kDa; cancer; tumour;
KW actin-related protein; hyperproliferative disorder; chromosome 3.
XX
OS Homo sapiens.
XX
PN US2004110147-A1.
XX
PD 10-JUN-2004.
XX
PF 09-DEC-2002; 2002US-00316243.
XX
PR 09-DEC-2002; 2002US-00316243.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dobie KW, Jain R;
XX
DR WPI; 2004-440336/41.
XX
PT New oligonucleotide compound that inhibits expression of BAF53, useful
PT for preparing a composition for treating hyperproliferative disorder,
PT e.g. cancer.
XX
PS Example 15; SEQ ID NO 155; 72pp; English.
XX
CC The invention relates to a compound, having a sequence comprising 8-80 bp
CC targeted to a nucleic acid encoding BAF53 (a member of the BAF complex
CC (BRG1/brm-associated factor), BRG1-associated factor 53kDa which is an
CC actin-related protein), specifically hybridises with the nucleic acid
CC encoding BAF53 comprising 28001-bp sequence (derived from human
CC chromosome 3) and inhibits expression of BAF53, i.e. an antisense
CC oligonucleotide. Also included are inhibiting the expression of BAF53 in
CC cells or tissues, screening for a modulator of BAF53, a diagnostic method
CC for identifying a disease state, a kit or assay device comprising the
CC compound and treating an animal having a disease or condition associated
CC with BAF53. The oligonucleotide compound is useful for preparing a
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Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3069 CCACACCCCAACACTT 3084
      ||||| ||||| |||||
Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3069 CCACACCCCAACACTT 3084
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Db      17  CACATCCCAACACTT 2
||||| ||||| ||||| |||||
RESULT 2091
ADQ09480/c
ID      ADQ09480 standard; DNA; 20 BP.
XX
AC      ADQ09480;
XX
XX
DT      09-SEP-2004 (first entry)
XX
DE      Murine Angiopoietin-2 DNA antisense oligonucleotide #16.
XX
KW      Mouse; Angiopoietin-2; ss; antisense oligonucleotide;
KW      phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KW      5-methylcytosine; hyperproliferative disorder; cancer; cytostatic.
XX
OS      Mus musculus.
FH      Key      Location/Qualifiers
FT      modified_base 1..20      /tag= b
FT      /mod_base= OTHER
FT      /note= "OTHER= Phosphorothioate backbone. All cytidines
FT      are 5-methylcytidines"
FT      modified_base 1..5      /tag= a
FT      /mod_base= OTHER
FT      /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16..20     /tag= c
FT      /mod_base= OTHER
FT      /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
XX
US2004115640-A1.
XX
PN      17-JUN-2004.
XX
XX
PF      11-DEC-2002; 2002US-00317803.
XX
XX
PR      11-DEC-2002; 2002US-00317803.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Myers K, Dobie KW;
XX
XX      WPI; 2004-449380/42.
XX
XX      New oligonucleotide compound that inhibits expression of Angiopoietin-2,
XX      useful for preparing a composition for treating hyperproliferative
XX      disorder, e.g., cancer.
XX
PS      Example 16; SEQ ID NO 116; 102pp; English.
XX
XX      The invention relates to a compound targeted to a nucleic acid molecule
XX      encoding the human Angiopoietin-2 polypeptide. The compound is an
XX      antisense oligonucleotide that specifically hybridises with the nucleic
XX      acid and inhibits expression of the polypeptide. The antisense
XX      oligonucleotide comprises at least one modified internucleoside linkage
XX      i.e. a phosphorothioate linkage, at least one modified sugar moiety,
XX      preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified
XX      nucleobase comprising a 5-methylcytosine. The antisense compounds are
XX      useful for modulating the expression of the human Angiopoietin-2
XX      polypeptide and in preparation of a composition for treating
XX      hyperproliferative disorders, e.g. cancer. This sequence represents an
XX      antisense oligonucleotide targeted to DNA encoding the murine
XX      Angiopoietin-2 polypeptide of the invention.
XX
SQ      Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
Query Match      0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      53 GGCTGCAGGTGCTGAA 68
Db      18 GGCTGCAGGTGCTGGA 3

RESULT 2092
AD081060
ID      AD081060 standard; DNA; 25 BP.
XX
AC      AD081060;
XX
XX
DT      29-JUL-2004 (first entry)
XX
DE      Cow prion protein microsatellite locus primer #72.
XX
KW      gene typing; polymorphic microsatellite loci; PML;
KW      disease predisposition; microsatellite marker; prion disease;
KW      cystic fibrosis; malignant hyperthermia syndrome; metabolic disease;
KW      milk protein; hormone; transcription factor; pT7-blue-vector; cow;
KW      microsatellite; PCR; primer; ss.
XX
OS      Bos taurus.
XX
PN      DE10236711-A1.
XX
PD      26-FEB-2004.
XX
XX
PF      09-AUG-2002; 2002DE-01036711.
XX
PR      09-AUG-2002; 2002DE-01036711.
XX
XX      (UYHO-) UNIV HOHENHEIM.
PA      Geldermann H, Preuss S, Han Y;
XX
PI      WPI; 2004-215730/21.
XX
XX
PT      Typing genes that contain polymorphic microsatellite loci, useful for
PT      identifying predisposition to disease, by amplification and determining
PT      length of amplicons.
XX
XX
PS      Example 3; Page 28; 64pp; German.
XX
XX      The invention describes a method of typing (M1) a gene (I) that has one
XX      or more polymorphic microsatellite loci (PML). The method comprises: PCR
XX      amplification of at least one DNA region of (I) that includes PML, using
XX      as template a DNA sample containing at least one segment of (I); and
XX      determining the length of the resulting amplicon(s). Also described are:
XX      a method of determining (M2) microsatellite markers (MW) for
XX      predisposition to a disease, associated with a gene that includes one or
XX      more PML; and prediagnosis (M3) of diseases associated with gene that
XX      include PML. The method is used to identify microsatellite markers, in a
XX      disease-related gene, that are associated with a predisposition to
XX      diseases and for prediagnosis of such diseases, especially prion diseases
XX      but also cystic fibrosis, malignant hyperthermia syndrome in pigs and
XX      metabolic diseases; also to type genes that encode milk proteins,
XX      hormones or transcription factors. The method is simpler, quicker and
XX      particularly less expensive than known methods based on sequencing. This
XX      sequence represents a primer used to genotype a region of the cow prion
XX      protein (PrP) comprising a polymorphic microsatellite locus.
XX
SQ      Sequence 25 BP; 0 A; 3 C; 0 G; 22 T; 0 U; 0 Other;
Query Match      0.4%; Score 14.4; DB 1; Length 25;
Best Local Similarity 75.0%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY      3262 TATTTTATTGCTTGCTCTTTT 3285
Db      2 TTTTATTTTATTTTTCCTTTT 25
```

```

XX FH Key Location/Qualifiers
XX FT modified_base 1..26
XX FT /tag= a
XX FT /note= "phosphodiester oligonucleotide"
XX
XX PN WO9720924-A1.
XX PD 12-JUN-1997.
XX
XX PF 04-DEC-1996; 96WO-EP005388.
XX
XX PR 04-DEC-1995; 95IT-MI002539.
XX
XX PA (SAIC-) SAICOM SRL.
XX
XX PI Scaggiante B, Quadrifoglio F;
XX WPI; 1997-319771/29.
XX
XX PT New phosphodiesteric oligonucleotide(s) - which exert a specific and
XX PT selective cytotoxic effect on tumour cells, for treating both solid and
XX PT liquid tumours.
XX
XX PS Claim 10; Page 5; 38pp; English.
XX
XX CC Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
XX CC generic formula, in the 3'-5' or 5'-3' direction: (Gata')a'-(Gbtb')b'-'-
XX CC (Gctc')c'-(Gdtd')d'-(Gete')e'-(Gftf')f'-(Ggtg')g'-'N', where: N and
XX CC N' = T or G, equal or different from each other; x = 0-8, equal or
XX CC different from each other; a, b, c, d, e, f, and g = 0-10, equal or
XX CC different from each other; a', b', c', d', e', f', and g' = 0-30, equal
XX CC or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
XX CC 16, equal or different from each other; The oligonucleotides are believed
XX CC to selectively bind and sequester some proteins which are essential to
XX CC the viability and growth of tumoural cell line. They have specific and
XX CC selective cytotoxic activity against tumour cells, and can be used for
XX CC treating tumours of the liquid type, in particular of lymphoblastic
XX CC origin, and of solid type, in particular lymphomas. The present
XX CC phosphodiester oligonucleotide, at a concentration of 15 micromolar,
XX CC reduced growth of CCRP-CEM tumoural cells by 76%, which is detectable 48
XX CC hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
XX SQ Sequence 26 BP; 0 A; 0 C; 2 G; 24 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 26;
XX Best Local Similarity 75.0%; Pred. No. 2.3e+03;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 3262 TATTTTATTTGCTTTGTCCTTTT 3285
XX Db ||||| ||||| ||||| |||||
XX 3 TTTTGTGTTTTTTTGTGTTTTTT 26
XX
XX RESULT 2095
XX AAA13806
XX ID AAA13806 standard; DNA; 26 BP.
XX
XX AC AAA13806;
XX
XX DT 27-JUL-2000 (first entry)
XX
XX DE Yeast DOG2 stress responsive gene PCR primer SEQ ID NO:5.
XX
XX KW Yeast; stress responsive gene; promoter; brewing; beer; wine; sake;
XX KW bread; oxidative stress; osmotic pressure; stress; glucose starvation;
XX KW PCR primer; ss.
XX
XX OS Saccharomyces cerevisiae.
XX
XX PN JP2000078977-A.
XX
XX PD 21-MAR-2000.
XX
XX
XX RESULT 2093
XX AAC96591/c
XX ID AAC96591 standard; DNA; 25 BP.
XX
XX AC AAC96591;
XX
XX DT 26-FEB-2001 (first entry)
XX
XX DE HLA DRB345 gene PCR primer #62.
XX
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW Gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200065088-A2.
XX
XX PD 02-NOV-2000.
XX
XX PF 20-APR-2000; 2000WO-EP003636.
XX
XX PR 26-APR-1999; 99EP-00303215.
XX
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX PI Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX PT Identifying extendible primers for use in identification, or
XX PT classification of a nucleic acid of an organism, allele or gene such as
XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX PT specific length.
XX
XX PS Claim 14; Page 54; 66pp; English.
XX
XX CC The present invention provides a method for identifying a set of
XX CC extendible primers which can be used in the identification, typing and
XX CC classification of genes. This can then be used to predict protein
XX CC sequence and structure, in organ donation to match the organ with the
XX CC receiver, and to identify bacteria in a sample. The method can be used to
XX CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
XX CC particular
XX
XX SQ Sequence 25 BP; 2 A; 4 C; 3 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 25;
XX Best Local Similarity 75.0%; Pred. No. 2.3e+03;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 1362 GAAGATGATCGGAAACACAAA 1385
XX Db ||||| ||||| ||||| |||||
XX 24 GAACCTGATCAGAAAAA 1
XX
XX RESULT 2094
XX AAT93819
XX ID AAT93819 standard; DNA; 26 BP.
XX
XX AC AAT93819;
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 24-FEB-1998 (first entry)
XX
XX DE Antitumoural phosphodiester oligonucleotide 9 with cytotoxic activity.
XX
XX KW Phosphodiester; selective binding; cell viability; growth;
XX KW lymphoma cell line; cytotoxic activity; tumour cell; lymphoma;
XX KW lymphoblastic tumour; ss.
XX
XX OS Synthetic.

```

XX 04-SEP-1998; 98JP-00251390.
 XX 04-SEP-1998; 98JP-00251390.
 XX (TAIF) MARUHA CORP.
 XX WPI; 2000-285929/25.
 XX A stress-responsive gene promoter.
 XX Example 3; Page 10; 12pp; Japanese.
 XX The present invention describes a stress responsive gene promoter isolated from *Saccharomyces cerevisiae* (yeast). Also described in the present invention are: (1) a promoter containing a DNA hybridising with the above DNA under a stringent condition and having stress-responsive promoter activity; (2) a gene expression cassette containing the above cassette; (3) an expression vector containing the above gene expression cassette; (4) a recombinant vector in which a gene encoding an optional polypeptide is recombined to the above expression vector; (5) a transformant containing the above recombinant vector; and (6) a method for the preparation of the above polypeptide in which the above transformant is cultured and the polypeptide is collected from the resultant culture. *Saccharomyces cerevisiae* is used for the brewing of beer, wine and sake and production of bread. The gene is responsive to the stresses such as oxidative stress, osmotic pressure stress and glucose starvation stress. The present sequence represents a PCR primer for the yeast DOG2 stress responsive gene, which is used in an example from the present invention

XX SQ Sequence 26 BP; 3 A; 2 C; 2 G; 19 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 26;
 Best Local Similarity 75.0%; Pred. No. 2.3e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3113 AGTTTAAATTTTAACTATTGAC 3136
 DB 2 ATTTTATTTTATTTTATTTGAC 25

RESULT 2096
 ADA26181
 ID ADA26181 standard; DNA; 30 BP.
 XX ADA26181;
 AC ADA26181;
 XX 20-NOV-2003 (first entry)
 DE Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:26.
 XX genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;
 KW characteristic; single nucleotide polymorphism; SNP; genotyping;
 XX chromosome 1; gene; ds.
 XX Synthetic.
 OS *Oryza sativa*.
 XX WO2003070934-A1.
 XX 28-AUG-2003.
 XX 07-FEB-2003; 2003NO-JP001317.
 XX 25-FEB-2002; 2002JP-00048115.
 XX (PLAN-) PLANT GENOME CENT CO LTD.
 XX Minobe Y, Monna L, Kitazawa N, Yoshino R, Suzuki J;
 XX WPI; 2003-697617/66.

PT Judging the genotype of a region around a plant sd-1 gene with
 PT polymorphism-obtained markers isolated by positional cloning, useful in
 PT genotyping for examination of semi-dwarf character of rice.
 XX Disclosure; Page 15; 104pp; Japanese.
 XX The present invention describes a method for judging the genotype of a region around a plant semi-dwarf (sd-1) gene in which polymorphisms are present, by detecting the polymorphisms. Also described: (1) examining semi-dwarf characteristics of a plant using the judgment method with detection of polymorphisms; (2) oligonucleotides for amplifying sd-1 DNA regions, which are primers for judging the genotype of a region around a plant sd-1 gene; (3) reagents for judging the genotype of a region around a plant sd-1 gene containing these oligonucleotides; and (4) reagents for examining the semi-dwarf character of a plant containing the oligonucleotides. The method is for judging the genotype of a region around a plant sd-1 gene, which is applicable in genotyping by (d)CAPS ((derived) cleaved amplified polymorphic sequence) for examination of the semi-dwarf character of rice to identify desirable strains e.g. with high crop yield, pest resistance and resistance to flooded water. The method is easy and quick, in which a seedling is required for studying single nucleotide polymorphisms (SNPs) for genotyping, without needing cultivation of seedling to fully-grown plant for judging heterozygote and distinguishing morphology. The present sequence represents a rice sd-1 DNA fragment, which is given in the exemplification of the present invention. Rice sd-1 is located on chromosome 1.

XX SQ Sequence 30 BP; 0 A; 3 C; 0 G; 27 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.4; DB 1; Length 30;
 Best Local Similarity 75.0%; Pred. No. 2.6e+03;
 Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3262 TATTTATTGCTTGTCTTTT 3285
 DB 7 TCTTTTTCCTTTTTCCTTTT 30

RESULT 2097
 ABL56895
 ID ABL56895 standard; DNA; 30 BP.
 XX ABL56895;
 AC ABL56895;
 XX 26-JUL-2002 (first entry)
 DT Synthetic deoxyribonucleotide poly h.
 DE Concentration; quantification; mutation detection; polymorphic;
 KW polymerase chain reaction; PCR; ss.
 XX Synthetic.
 OS EP1046717-A2.
 XX 25-OCT-2000.
 XX 20-APR-2000; 2000EP-00108643.
 XX 20-APR-1999; 99JP-00111601.
 XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.
 PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
 PA (KANK-) KANKYO ENG CO LTD.
 XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
 PI Koyama O, Furusho K;
 XX WPI; 2000-657765/64.
 XX Determining the concentration of a target nucleic acid, useful e.g. for
 PT detecting genetic mutations, comprises using a fluorescently labeled
 PT probe in which emission is reduced by binding to the target nucleic acid.

XX Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces

CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by

CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for

CC quantifying microbial cells in co-cultures or symbiotic systems, for

CC detecting gene mutations or polymorphisms, and for analysing melting

CC curves of target nucleic acids to determine a Tm value. Methods of the

CC invention allow target nucleic acids to be quantified quickly, easily and

CC accurately. Particularly there is no need to remove unbound probe, and no

CC materials are introduced that inhibit amplification by Taq polymerase (so

CC conventional PCR conditions can be used). The specificity of PCR is kept

CC high (amplification of primer dimers is delayed), and the limit of

CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis

CC (automatically generated by a computer) has a higher correlation

CC coefficient than conventional graphs so more accurate quantitation is

CC possible. The current sequence represents a synthetic

CC deoxyribonucleotide that was used for investigating the base

CC selectivity of a target nucleic acid

XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 30;

Best Local Similarity 75.0%; Pred. No. 2.6e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATATATTTTATGAGTTTTT 3497

Db 1 ATATATATATTTTCTTTTTT 24

RESULT 2098

ABA97619

ID ABA97619 standard; DNA; 30 BP.

XX ABA97619;

AC ABA97619;

DT 11-APR-2002 (first entry)

XX Poly h nucleotide sequence.

DE ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

OS JP2001286300-A.

PN 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

XX 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEI2-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.

XX WPI; 2002-134193/18.

DR

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

PS This invention relates to a method for measuring nucleic acids using a

CC

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

CC target nucleic acid, the decrease in the fluorescence is measured. The

CC method can be used for measuring a target nucleic acid

XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 30;

Best Local Similarity 75.0%; Pred. No. 2.6e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATATTTTATGAGTTTTT 3497

Db 1 ATATATATATTTTCTTTTTT 24

RESULT 2099

ABL95892

ID ABL95892 standard; DNA; 30 BP.

XX ABL95892;

AC ABL95892;

DT 19-JUN-2002 (first entry)

XX Probe poly h for assaying nucleic acids.

DE

XX Probe; polymorphism detection; mutation detection; disease diagnosis;

KW microbial identification; ss.

XX Unidentified.

OS WO200208414-A1.

PN 31-JAN-2002.

XX 27-JUN-2001; 2001WO-IB001147.

XX 27-JUN-2000; 2000JP-00193133.

PR 03-AUG-2000; 2000JP-00236115.

PR 26-SEP-2000; 2000JP-00292483.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

PA (KANK-) KANKYO ENG CO LTD.

XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;

PI Yokomaku T;

XX WPI; 2002-195876/25.

DR

XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and

PT their polymorphism and mutation, particularly useful in science and

PT medicine for e.g. analytical applications, disease diagnosis and

PT microbial identification.

XX Example 12; Page 60; 152pp; Japanese.

XX The present invention relates to nucleic acid probes, which are useful

CC for assaying nucleic acids by hybridising with a target nucleic acid, in

CC which a single-stranded oligonucleotide is labelled with a fluorescent

CC substance and a quencher in a manner that the fluorescence intensity of

CC the hybridisation reaction system is increased after completion of the

CC hybridisation but no stem loop structure is formed. The probes are useful

CC for assaying nucleic acids and their polymorphism and mutation,

CC particularly useful for e.g. analytical applications, disease diagnosis

CC and microbial identification. The present sequence was used to illustrate

CC the invention

XX

SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 14.4; DB 1; Length 30;

Best Local Similarity 75.0%; Pred. No. 2.6e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY

Db

RESULT 2098

ABA97619

ID ABA97619 standard; DNA; 30 BP.

XX ABA97619;

AC ABA97619;

DT 11-APR-2002 (first entry)

XX Poly h nucleotide sequence.

DE ss; fluorochrome; nucleic acid probe; fluorescence.

XX Unidentified.

OS JP2001286300-A.

PN 16-OCT-2001.

XX 20-APR-2000; 2000JP-00120097.

XX 20-APR-1999; 99JP-00111601.

PR 24-AUG-1999; 99JP-00236666.

PR 30-AUG-1999; 99JP-00242693.

PR 01-FEB-2000; 2000JP-00028896.

XX (BIOI-) BIOINDUSTRY KYOKAI SH.

PA (KANK-) KANKYO ENG KK.

PA (KEI2-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.

XX WPI; 2002-134193/18.

DR

XX Measurement of nucleic acids, using a nucleic acid probe and analysis of

PT the obtained data.

XX Example 5; Page 17; 34pp; Japanese.

PS This invention relates to a method for measuring nucleic acids using a

CC


```
QY 3474 ATATATATAATTTATTGAGTTTT 3497
DB 1 ATATATATTTTTCCTTTT 24

RESULT 2100
AAI30470/c
ID AAI30470 standard; DNA; 31 BP.
XX
XX AAI30470;
AC
XX
XX 18-OCT-2001 (first entry)
DT
XX
DE Human single nucleotide polymorphism (SNP) FGFR3 2.
XX
XX Human; resequence; genotype; disease; forensic; paternity testing;
KW single nucleotide polymorphism; SNP; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Variation replace(16,G)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200166800-A2.
PN
XX
XX 13-SEP-2001.
PD
XX
XX 07-MAR-2001; 2001WO-US007268.
PF
XX
XX 07-MAR-2000; 2000US-0187510P.
PR
XX 22-MAY-2000; 2000US-0206129P.
PR
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA
XX
XX Cargill M, Ireland JS, Lander ES;
PI
XX WPI; 2001-522952/57.
DR
XX
XX Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or severity
PT of a particular phenotype or disorder (e.g. diabetes) associated with a
PT particular genotype.
XX
XX Claim 1; Page 87; 145pp; English.
PS
XX
XX The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing
XX
XX Sequence 31 BP; 3 A; 13 C; 12 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 31;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 529 CGGCCCATCTCGAGCGGGCTG 552
DB 26 CAGCCCCGCTCGAGGATGCGCG 3

RESULT 2101
AAQ87894
ID AAQ87894 standard; DNA; 32 BP.
XX
XX AAQ87894;
```

```
XX
DT 25-MAR-2003 (revised)
DT 29-NOV-1995 (first entry)
XX
XX Normalised library first strand cDNA synthesis primer.
XX
XX Normalised cDNA library; directionally cloned cDNA library; screening;
KW hybridisation; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 15..18
FT /tag= a
FT /note= "Characteristic sequence identifier"
XX
XX WO9508647-A1.
PN
XX
XX 30-MAR-1995.
PD
XX 23-SEP-1994; 94WO-US010821.
PF
XX 24-SEP-1993; 93US-00126594.
PR
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Soares MB, Efstratiadis A;
PI
XX WPI; 1995-139615/18.
DR
XX
XX New normalised directional cDNA libraries - used for isolating novel
PT cDNA's, including tissue-specific and development-specific DNA.
XX
XX Disclosure; Page 45; 186pp; English.
PS
XX
XX Human tissues were obtained for construction of a variety of cDNA
CC libraries, including infant brain, adult brain and adult hippocampus.
CC Each of the cDNA libraries had a characteristic sequence identifier,
CC provided by the oligonucleotide utilised to prime first strand cDNA
CC synthesis (see AQ87894-Q87907 for these primer sequences; all these
CC primers have the PacI restriction site for directional cloning of cDNAs).
CC Each of the libraries was propagated in the form of single-stranded (ss)
CC circles and normalised separately by a novel method. The method
CC comprises: generating fragments complementary to the 3' non-coding
CC sequence of the ss circles in the library to produce partial duplexes;
CC purifying the partial duplexes; melting and reassociating them to
CC appropriate Cot; and purifying the unassociated ss circles to generate a
CC normalised cDNA library. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 32 BP; 4 A; 0 C; 0 G; 28 T; 0 U; 0 Other;
SQ
Query Match 0.4%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3311 TTTTCTTAGGAGATTATTTT 3334
DB 1 TTTTCTTAGGAGATTATTTT 24

RESULT 2102
ABQ80395/c
ID ABQ80395 standard; DNA; 33 BP.
XX
XX ABQ80395;
AC
XX 06-NOV-2003 (first entry)
DT
XX
XX Probe APC 1-MUT.
DE
XX
XX Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW infection; screening; colour change; ss.
XX
```

```

OS Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1
XX FT /*tag= a
XX FT /*note= "Gold-S'-A"
XX PN
XX WO2003048769-A1.
XX
XX 12-JUN-2003.
XX
XX 27-NOV-2002; 2002WO-US038069.
XX
XX 30-NOV-2001; 2001US-0334644P.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Storhoff JJ, Fritz BM, Herrmann M;
XX
XX WPI; 2003-617993/58.
XX
XX Detecting target polynucleotide in a sample, by amplifying target,
XX hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
XX detection system, and determining amount of signal generated due to
XX binding.
XX
XX Example 1; Page 35; 74pp; English.
XX
XX The sequences given in ABQ80394-99 represent probes and targets which
XX were used in the method of the invention for detecting a target
XX polynucleotide in a sample. The method comprises amplifying the target,
XX hybridizing the target to oligonucleotides bound to nanoparticles in a
XX nanoparticle detection system, determining the amount of signal generated
XX as a result of binding, optionally repeating the above steps, and
XX detecting the presence of the target oligonucleotide by analysing for the
XX amount of signal produced after at least one amplification cycle. The
XX method is useful for detecting target polynucleotide in a sample, and for
XX determining the quantity of target polynucleotide in a sample. The method
XX is useful in research and analytical laboratories in DNA sequencing, in
XX the field to detect the presence of specific pathogens, in the doctor's
XX office for quick identification of an infection to assist in prescribing
XX a drug for treatment, and in homes and health centres for inexpensive
XX first-line screening. The method is based on observing colour change with
XX the naked eye, hence the method is cheap, fast, simple, robust, do not
XX require specialized or expensive equipment, and little or no
XX instrumentation is required
XX
XX Sequence 33 BP; 29 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 33;
XX Best Local Similarity 75.0%; Pred. No. 2.7e+03;
XX Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 3262 TATTTATTGCTTTCCTTTT 3285
XX | | | | | | | | | | | | | | | | | |
XX DB 32 TTTTTCCTGCTTTTTCCTTTT 9
XX
XX RESULT 2103
XX ABN89412/C
XX ID ABN89412 standard; DNA; 40 BP.
XX
XX AC ABN89412;
XX
XX DT 30-AUG-2002 (first entry)
XX
XX DE Polymorphism detection related oligonucleotide SEQ ID NO:4.
XX
XX KW Polymorphism; detection; mass spectroscopy; ss.
XX
XX OS Synthetic.
XX
XX PN WO200250307-A1.

```

```

XX 27-JUN-2002.
XX
XX 12-DEC-2001; 2001WO-JP010892.
XX
XX 12-DEC-2000; 2000JP-00378091.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Inoko H, Tamiya G, Nakajima K, Kimura N, Nagashima R, Morikawa M;
XX Okamoto K;
XX
XX WPI; 2002-508814/54.
XX
XX Detection of DNA polymorphism by mass spectroscopy for investigation and
XX diagnosis of gene-related diseases.
XX
XX Example 3; Page 28; 34pp; Japanese.
XX
XX The present invention describes a method for detecting polymorphisms in
XX DNA by: (a) preparing a DNA sample from patients containing the DNA
XX region in which the target polymorphism is located; (b) hybridising to an
XX appropriate oligonucleotide fragment, immobilised on a support; and (c)
XX detecting the hybridised target DNA by mass spectroscopy. The method can
XX be used for the investigation and diagnosis of gene-related diseases. The
XX method allows polymorphisms to be detected rapidly and effectively in a
XX large number of specimens. The present sequence represents an
XX oligonucleotide which is used in an example from the present invention
XX
XX Sequence 40 BP; 30 A; 0 C; 0 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 14.4; DB 1; Length 40;
XX Best Local Similarity 65.6%; Pred. No. 2.9e+03;
XX Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
XX
XX QY 3262 TATTTATTGCTTTCCTTTTTCAGGAGAA 3293
XX | | | | | | | | | | | | | | | | | |
XX DB 35 TTTTTCCTGCTTTTTCCTTTTTCAGGAGAA 4
XX
XX RESULT 2104
XX AD041321/C
XX ID AD041321 standard; cDNA; 40 BP.
XX
XX AC AD041321;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Human cDNA probe useful for disease diagnosis #472.
XX
XX ss; probe; human; bacteria; virus; prion; parasite; fungus; drug;
XX allergen; influenza; malaria; yellow fever; multiple sclerosis;
XX Alzheimer's disease; lung cancer; breast cancer; stomach cancer.
XX
XX OS Homo sapiens.
XX
XX PN WO2004046382-A2.
XX
XX PD 03-JUN-2004.
XX
XX PF 21-NOV-2003; 2003WO-GB005102.
XX
XX PR 21-NOV-2002; 2002GB-00027238.
XX
XX (DIAG-) DIAGENIC AS.
XX (JONE/) JONES E L.
XX
XX Sharma P, Sahni NS, Loenneborg A;
XX
XX WPI; 2004-420641/39.
XX
XX Set of oligonucleotide probes, useful for diagnosing breast cancer or
XX Alzheimer's disease, comprising specific number of oligonucleotides.
XX
XX PT

```


PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
PS Disclosure; SEQ ID NO 6971; 872bp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 6 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3463 TATATATATCTATATATAT 3481
Db 2 TTTATATATGATGATATAT 20
RESULT 2107
ABD27959
ID ABD27959 standard; DNA; 20 BP.
XX
AC ABD27959;
XX
DT 29-JUL-2004 (first entry)
DE AA497002-derived oligonucleotide SEQ ID 6971.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.

XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 6971; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 6 A; 1 C; 2 G; 11 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3463 TATATATATCTATATATAT 3481
Db 2 TTTATATATGATGATATAT 20
RESULT 2108
ABD27962
ID ABD27962 standard; DNA; 20 BP.
XX
AC ABD27962;
XX
DT 29-JUL-2004 (first entry)
DE AA497002-derived oligonucleotide SEQ ID 6974.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX

PD 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013143.
 XX
 XX 24-APR-2001; 2001US-0286036P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 XX WPI; 2003-093058/08.
 XX
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.
 XX
 XX Claim 15; SEQ ID NO 6974; 763pp; English.
 XX
 XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 XX
 XX Sequence 20 BP; 11 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3463 TATATATATCTATATATAT 3481
 DB 2 TATATATATGAAATATAT 20
 RESULT 2109
 ABZ98662
 ID ABZ98662 standard; DNA; 20 BP.
 XX
 AC ABZ98662;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human tryptase a oligonucleotide sequence.
 XX
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 XX lung inflammation; respiratory disease; ds.
 OS Homo sapiens.
 XX
 XX WO200285308-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX 24-APR-2001; 2001US-0286137P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 XX WPI; 2003-229219/22.
 DR
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Disclosure; SEQ ID NO 13904; 872pp; English.
 PS
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 20 BP; 2 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.9e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2100 GGACACCCCGCTCCAGC 2118
 DB 2 GGGCTCTCCAGCTCCAGC 20
 RESULT 2110
 ABD31693
 ID ABD31693 standard; DNA; 20 BP.
 XX
 AC ABD31693;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human Tryptase a-derived oligonucleotide SEQ ID 13904.
 XX
 XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW

AC ADO46030;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Human oligonucleotide #1396.
XX
XX KW Human; ss; interleukin-4 receptor; IL-4; interleukin-5 receptor; IL-5;
KW CCR1; CCR3; Eotaxin-1; RANTES; MCP4; CD23; ICAM; VCAM; tryptase a;
KW tryptase b; PDE4 A; PDE4 B; PDE4 C; PDE4 D; respiratory disease;
KW lung disease; hyper-responsiveness; adenosine; adenosine A receptor;
KW asthma; lung allergy; inflammation; inflammatory disease;
KW airway inflammation; allergy; impeded respiration; cystic fibrosis; CF;
KW chronic obstructive pulmonary disease; COPD; allergic rhinitis;
KW acute respiratory distress syndrome; pulmonary hypertension;
KW lung inflammation; bronchitis; airway obstruction; bronchoconstriction.
XX
XX OS Homo sapiens.
XX
XX FN US2004049022-A1.
XX
XX PD 11-MAR-2004.
XX
XX PF 25-JUL-2003; 2003US-00627930.
XX
XX PR 23-APR-2002; 2002WO-US013135.
XX PR 23-APR-2002; 2002WO-US013143.
XX
XX PA (NYCE/) NYCE J W.
XX PA (SAND/) SANDRASAGRA A.
XX PA (TANG/) TANG L.
XX PA (AGUI/) AGUILAR D.
XX PA (MILL/) MILLER S.
XX PA (SHAH/) SHAHABUDDIN S.
XX PA (LUHH/) LU H.
XX PA (CONG/) CONG H.
XX
XX PI Nyce JW, Sandrasagra A, Tang L, Aguilar D, Miller S;
XX PI Shahabuddin S, Lu H, Cong H;
XX DR WPI; 2004-293804/27.
XX
XX PT Novel single or multiple target oligonucleotide anti-sense to e.g.
XX PT initiation codon, intron of respiratory disease-relevant gene e.g. CCR1,
XX PT RANTES, MCP4, useful for prophylaxis or treating respiratory disease e.g.
XX PT asthma.
XX
XX PS Claim 2; SEQ ID NO 1397; 174pp; English.
XX
XX CC The invention relates to oligonucleotides anti-sense to an initiation
XX CC codon, coding region, 5' or 3' intron-exon junction, intron or region
XX CC with 2-10 nucleotides of the 5'-end or 3'-end of a nucleic acid target
XX CC chosen from a gene encoding interleukin (IL)-4 receptor, interleukin (IL)
XX CC -5 receptor, CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM,
XX CC tryptase a, tryptase b, PDE4 A, PDE4 B, PDE4 C or PDE4 D. The invention
XX CC also relates to a method of screening a candidate compound that binds to
XX CC one or more nucleic acid target(s) or expressed product(s), for the
XX CC prevention and/or treatment of a respiratory or lung disease. The
XX CC oligonucleotides are useful for reducing or inhibiting expression of a
XX CC gene or mRNA encoding interleukin-4 receptor, interleukin-5 receptor,
XX CC CCR1, CCR3, Eotaxin-1, RANTES, MCP4, CD23, ICAM, VCAM, tryptase a,
XX CC tryptase b, PDE4 A, PDE4 B, PDE4 C, or PDE4 D. The oligonucleotides are
XX CC useful for preventing or treating a respiratory or lung disease. The
XX CC respiratory or lung disease is associated with hyper-responsiveness to
XX CC and/or increased levels of, adenosine and/or levels of adenosine A
XX CC receptor(s), and/or asthma and/or lung allergies associated with
XX CC inflammation or an inflammatory disease. The respiratory or lung disease
XX CC is chosen from airway inflammation, allergy, asthma, impeded respiration,
XX CC cystic fibrosis (CF), chronic obstructive pulmonary disease (COPD),
XX CC allergic rhinitis, acute respiratory distress syndrome, pulmonary
XX CC hypertension, lung inflammation, bronchitis, airway obstruction or
XX CC bronchoconstriction. This sequence represents an oligonucleotide of the
XX CC invention.

SQ Sequence 20 BP; 2 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2100 GGACACCCCGCTCCAGC 2118
Db 2 GGGCTCCTCCAGCTCCAGC 20
Search completed: October 28, 2004, 12:04:30
Job time : 181 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 11:51:40 ; Search time 103 Seconds
(without alignments)
3.669 Million cell updates/sec

Title: US-10-630-401-10

Perfect score: 3799

Sequence: 1 aaggatggcagggctggt.....gacacctgttgtaacctg 3799

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 0.5

Searched: 2344 seqs, 49742 residues

Total number of hits satisfying chosen parameters: ~4688

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1504 summaries

Database : rge10.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.4	1.0	48	1	AR444606
2	35.6	0.9	50	1	E32208
3	35.6	0.9	50	1	E32228
4	35.6	0.9	50	1	E31183
5	35.6	0.9	50	1	I31274
6	34.8	0.9	48	1	AR444607
7	34.6	0.9	46	1	I31434
8	34.4	0.9	44	1	I31337
9	34.4	0.9	44	1	AR444608
10	34.2	0.9	42	1	I31141
11	34.2	0.9	47	1	I31171
12	34.2	0.9	47	1	I31180
13	34.2	0.9	47	1	I31309
14	34.2	0.9	47	1	A0047784
15	34	0.9	47	1	Q738314
16	33.8	0.9	38	1	BD251663
17	33.8	0.9	38	1	I31286
18	33.8	0.9	38	1	I31485
19	33.8	0.9	38	1	AX028364
20	33.8	0.9	39	1	I31225
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25	33.8	0.9	41	1	I31271
26	33.8	0.9	41	1	I31320
27	33.8	0.9	42	1	I31317
28	33.8	0.9	43	1	I31476
29	33.8	0.9	44	1	I31283
30	33.8	0.9	44	1	I31329
31	33.8	0.9	46	1	I31159
32	33.8	0.9	46	1	I31189
33	33.8	0.9	46	1	I31314

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C 36	33	0.9	41	1	AR222935
C 37	32.8	0.9	36	1	I31192
C 38	32.8	0.9	36	1	I31446
C 39	32.8	0.9	37	1	I31228
C 40	32.8	0.9	44	1	AR444609
C 41	32.8	0.9	45	1	I31291
C 42	32.4	0.9	34	1	I31268
C 43	32.4	0.9	35	1	I31277
C 44	32.2	0.8	38	1	E32209
C 45	32.2	0.8	38	1	I31156
C 46	32.2	0.8	39	1	I31174
C 47	32.2	0.8	40	1	I31240
C 48	32.2	0.8	40	1	I31263
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C 50	32.2	0.8	45	1	I31245
C 51	32	0.8	39	1	AR007163
C 52	31.4	0.8	33	1	I31147
C 53	31.4	0.8	33	1	I31306
C 54	31.4	0.8	34	1	I31198
C 55	31.4	0.8	34	1	I31260
C 56	31.4	0.8	34	1	I31280
C 57	31.4	0.8	34	1	I31410
C 58	31.4	0.8	43	1	I31458
C 59	30.8	0.8	42	1	I31431
C 60	30.6	0.8	31	1	AX248878
C 61	30.6	0.8	31	1	AX248879
C 62	30.6	0.8	31	1	AX248880
C 63	30.6	0.8	31	1	AX248881
C 64	30.6	0.8	42	1	A45638
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C 68	30.4	0.8	32	1	I31464
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C 75	29	0.8	39	1	I31419
C 76	28.8	0.8	32	1	I31494
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C 78	28.8	0.8	41	1	AX519258
C 79	28.4	0.7	30	1	I31461
C 80	28.4	0.7	30	1	BD107614
C 81	28	0.7	40	1	MMVIMV26
C 82	27.4	0.7	29	1	AR051257
C 83	27.4	0.7	29	1	I28386
C 84	27.4	0.7	29	1	I31168
C 85	27.4	0.7	29	1	I31326
C 86	26.4	0.7	28	1	A27175
C 87	26.4	0.7	28	1	I31539
C 88	26	0.7	34	1	A45639
C 89	26	0.7	34	1	AR033092
C 90	25.8	0.7	29	1	BD174950
C 91	25.8	0.7	30	1	E32218
C 92	25.4	0.7	27	1	AR051255
C 93	25.4	0.7	27	1	AR127802
C 94	25.4	0.7	27	1	I28384
C 95	25.4	0.7	27	1	I31231
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C 97	25.4	0.7	27	1	AX175241
C 98	25.4	0.7	27	1	AX175302
C 99	25.4	0.7	27	1	AX189457
C 100	25.2	0.7	30	1	I31503
C 101	25	0.7	25	1	AX482128
C 102	25	0.7	25	1	AX511367
C 103	25	0.7	25	1	AX721728
C 104	24	0.6	24	1	E11483
C 105	24	0.6	24	1	AX482129
C 106	24	0.6	24	1	AX511368

ACCESSION: I31452
ACCESSION: I31165
ACCESSION: AR222935
ACCESSION: I31192
ACCESSION: I31446
ACCESSION: I31228
ACCESSION: AR444609
ACCESSION: I31291
ACCESSION: I31268
ACCESSION: I31277
ACCESSION: E32209
ACCESSION: I31156
ACCESSION: I31174
ACCESSION: I31240
ACCESSION: I31263
ACCESSION: I31422
ACCESSION: I31245
ACCESSION: AR007163
ACCESSION: I31147
ACCESSION: I31306
ACCESSION: I31198
ACCESSION: I31260
ACCESSION: I31280
ACCESSION: I31410
ACCESSION: I31458
ACCESSION: I31431
ACCESSION: AX248878
ACCESSION: AX248879
ACCESSION: AX248880
ACCESSION: AX248881
ACCESSION: A45638
ACCESSION: AR033091
ACCESSION: E32203
ACCESSION: I31298
ACCESSION: I31464
ACCESSION: I31428
ACCESSION: I31303
ACCESSION: I31323
ACCESSION: I31359
ACCESSION: I31440
ACCESSION: I31443
ACCESSION: I31419
ACCESSION: AX513919
ACCESSION: AX519258
ACCESSION: I31461
ACCESSION: BD107614
ACCESSION: X89143
ACCESSION: AR031257
ACCESSION: I28386
ACCESSION: I31168
ACCESSION: I31326
ACCESSION: A27175
ACCESSION: I31539
ACCESSION: A45639
ACCESSION: AR033092
ACCESSION: BD174950
ACCESSION: E32218
ACCESSION: AR051255
ACCESSION: AR127802
ACCESSION: I28384
ACCESSION: I31231
ACCESSION: AX175237
ACCESSION: AX175241
ACCESSION: AX175302
ACCESSION: AX189457
ACCESSION: I31503
ACCESSION: AX482128
ACCESSION: AX511367
ACCESSION: AX721728
ACCESSION: E11483
ACCESSION: AX482129
ACCESSION: AX511368

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C 108	23.6	0.6	30	1	A29208	ACCESSION:A29208	C 181	18.8	0.5	22	1	AX486835	ACCESSION:AX486835
C 109	23.6	0.6	30	1	A29211	ACCESSION:A29211	C 182	18.8	0.5	23	1	AX926722	ACCESSION:AX926722
C 110	23.4	0.6	25	1	I31234	ACCESSION:I31234	C 183	18.8	0.5	24	1	AR058875	ACCESSION:AR058875
C 111	23.4	0.6	25	1	AX115976	ACCESSION:AX115976	C 184	18.8	0.5	24	1	AR058877	ACCESSION:AR058877
C 112	23.4	0.6	33	1	I31400	ACCESSION:I31400	C 185	18.8	0.5	24	1	AR079580	ACCESSION:AR079580
C 113	22.4	0.6	33	1	I31533	ACCESSION:I31533	C 186	18.8	0.5	24	1	AR079582	ACCESSION:AR079582
C 114	22.4	0.6	24	1	AX104876	ACCESSION:AX104876	C 187	18.8	0.5	24	1	AR123289	ACCESSION:AR123289
C 115	22.4	0.6	24	1	AX175257	ACCESSION:AX175257	C 188	18.8	0.5	24	1	AR123291	ACCESSION:AR123291
C 116	22.4	0.6	24	1	AX175258	ACCESSION:AX175258	C 189	18.8	0.5	24	1	AR146823	ACCESSION:AR146823
C 117	22.4	0.6	24	1	AX547929	ACCESSION:AX547929	C 190	18.8	0.5	24	1	BD188891	ACCESSION:BD188891
C 118	22.4	0.6	25	1	AX117836	ACCESSION:AX117836	C 191	18.8	0.5	24	1	BD188893	ACCESSION:BD188893
C 119	22.4	0.6	22	1	AR173691	ACCESSION:AR173691	C 192	18.8	0.5	24	1	I33252	ACCESSION:I33252
C 120	22	0.6	22	1	BD231722	ACCESSION:BD231722	C 193	18.8	0.5	24	1	I33254	ACCESSION:I33254
C 121	22	0.6	22	1	BD231723	ACCESSION:BD231723	C 194	18.8	0.5	24	1	I33517	ACCESSION:I33517
C 122	22	0.6	22	1	BD270911	ACCESSION:BD270911	C 195	18.8	0.5	24	1	I35519	ACCESSION:I35519
C 123	22	0.6	22	1	BD270912	ACCESSION:BD270912	C 196	18.8	0.5	24	1	I43127	ACCESSION:I43127
C 124	22	0.6	22	1	AR383046	ACCESSION:AR383046	C 197	18.8	0.5	24	1	I43129	ACCESSION:I43129
C 125	22	0.6	22	1	AR383047	ACCESSION:AR383047	C 198	18.8	0.5	24	1	I43129	ACCESSION:I43129
C 126	22	0.6	22	1	AX327687	ACCESSION:AX327687	C 199	18.8	0.5	24	1	I92005	ACCESSION:I92005
C 127	22	0.6	22	1	AX327688	ACCESSION:AX327688	C 200	18.6	0.5	24	1	I92007	ACCESSION:I92007
C 128	22	0.6	22	1	AX812159	ACCESSION:AX812159	C 201	18.6	0.5	25	1	AR177699	ACCESSION:AR177699
C 129	22	0.6	28	1	AR020621	ACCESSION:AR020621	C 202	18.6	0.5	25	1	AR028293	ACCESSION:AR028293
C 130	21.8	0.6	25	1	AR117832	ACCESSION:AR117832	C 203	18.4	0.5	25	1	AR434784	ACCESSION:AR434784
C 131	21.4	0.6	23	1	AR127801	ACCESSION:AR127801	C 204	18.4	0.5	20	1	A63570	ACCESSION:A63570
C 132	21.4	0.6	23	1	I31542	ACCESSION:I31542	C 205	18.4	0.5	20	1	AR084543	ACCESSION:AR084543
C 133	21	0.6	23	1	AR173690	ACCESSION:AR173690	C 206	18.4	0.5	20	1	AR123339	ACCESSION:AR123339
C 134	21	0.6	30	1	AR090052	ACCESSION:AR090052	C 207	18.4	0.5	20	1	AR129684	ACCESSION:AR129684
C 135	21	0.6	30	1	AR197087	ACCESSION:AR197087	C 208	18.4	0.5	20	1	E36173	ACCESSION:E36173
C 136	21	0.6	30	1	AR259241	ACCESSION:AR259241	C 209	18.4	0.5	20	1	AX179298	ACCESSION:AX179298
C 137	20.8	0.5	25	1	AX117828	ACCESSION:AX117828	C 210	18.4	0.5	20	1	AX179299	ACCESSION:AX179299
C 138	20.6	0.5	27	1	AR002279	ACCESSION:AR002279	C 211	18.4	0.5	20	1	BD016468	ACCESSION:BD016468
C 139	20.6	0.5	27	1	AR053130	ACCESSION:AR053130	C 212	18.4	0.5	20	1	BD084130	ACCESSION:BD084130
C 140	20.6	0.5	27	1	BD174951	ACCESSION:BD174951	C 213	18.4	0.5	20	1	BD084130	ACCESSION:BD084130
C 141	20.4	0.5	22	1	I31213	ACCESSION:I31213	C 214	18.4	0.5	20	1	BD097545	ACCESSION:BD097545
C 142	20	0.5	20	1	CQ759610	ACCESSION:CQ759610	C 215	18.4	0.5	20	1	BD105781	ACCESSION:BD105781
C 143	20	0.5	20	1	E23735	ACCESSION:E23735	C 216	18.4	0.5	21	1	AX398276	ACCESSION:AX398276
C 144	20	0.5	27	1	BD107438	ACCESSION:BD107438	C 217	18.4	0.5	21	1	AX398277	ACCESSION:AX398277
C 145	19.8	0.5	23	1	AX116678	ACCESSION:AX116678	C 218	18.4	0.5	24	1	AX926721	ACCESSION:AX926721
C 146	19.8	0.5	24	1	E32214	ACCESSION:E32214	C 219	18.2	0.5	25	1	AB086601	ACCESSION:AB086601
C 147	19.8	0.5	26	1	AR090987	ACCESSION:AR090987	C 220	18	0.5	18	1	AR071800	ACCESSION:AR071800
C 148	19.8	0.5	26	1	AR198032	ACCESSION:AR198032	C 221	18	0.5	18	1	AX482165	ACCESSION:AX482165
C 149	19.8	0.5	26	1	AR260176	ACCESSION:AR260176	C 222	18	0.5	18	1	AX511404	ACCESSION:AX511404
C 150	19.6	0.5	27	1	AX183949	ACCESSION:AX183949	C 223	18	0.5	18	1	AX721765	ACCESSION:AX721765
C 151	19.6	0.5	28	1	AR090230	ACCESSION:AR090230	C 224	18	0.5	20	1	E05497	ACCESSION:E05497
C 152	19.6	0.5	28	1	AR197265	ACCESSION:AR197265	C 225	18	0.5	22	1	BD192794	ACCESSION:BD192794
C 153	19.6	0.5	28	1	AR259419	ACCESSION:AR259419	C 226	17.8	0.5	21	1	I30547	ACCESSION:I30547
C 154	19.4	0.5	21	1	AR007164	ACCESSION:AR007164	C 227	17.8	0.5	21	1	AX020772	ACCESSION:AX020772
C 155	19.4	0.5	21	1	I31248	ACCESSION:I31248	C 228	17.8	0.5	21	1	AX116107	ACCESSION:AX116107
C 156	19.4	0.5	21	1	AX104715	ACCESSION:AX104715	C 229	17.8	0.5	21	1	AX556883	ACCESSION:AX556883
C 157	19.4	0.5	21	1	AX175255	ACCESSION:AX175255	C 230	17.8	0.5	21	1	AX556883	ACCESSION:AX556883
C 158	19.4	0.5	21	1	AX547768	ACCESSION:AX547768	C 231	17.8	0.5	21	1	BD089174	ACCESSION:BD089174
C 159	19.4	0.5	21	1	BD251661	ACCESSION:BD251661	C 232	17.8	0.5	21	1	AB068223	ACCESSION:AB068223
C 160	19.4	0.5	22	1	BD251661	ACCESSION:BD251661	C 233	17.8	0.5	24	1	AS7514	ACCESSION:AS7514
C 161	19.4	0.5	22	1	BD251661	ACCESSION:BD251661	C 234	17.8	0.5	24	1	AR052980	ACCESSION:AR052980
C 162	19.4	0.5	22	1	AX028362	ACCESSION:AX028362	C 235	17.6	0.5	24	1	AX117030	ACCESSION:AX117030
C 163	19.4	0.5	22	1	AX028362	ACCESSION:AX028362	C 236	17.6	0.5	24	1	BD249753	ACCESSION:BD249753
C 164	19.4	0.5	22	1	AX104718	ACCESSION:AX104718	C 237	17.6	0.5	24	1	AR302333	ACCESSION:AR302333
C 165	19.4	0.5	22	1	AX104718	ACCESSION:AX104718	C 238	17.6	0.5	24	1	AX740251	ACCESSION:AX740251
C 166	19.4	0.5	22	1	AX547771	ACCESSION:AX547771	C 239	17.6	0.5	25	1	AX743827	ACCESSION:AX743827
C 167	19.4	0.5	22	1	AX547771	ACCESSION:AX547771	C 240	17.6	0.5	25	1	AR028294	ACCESSION:AR028294
C 168	19.4	0.5	24	1	AX116747	ACCESSION:AX116747	C 241	17.6	0.5	25	1	AR434781	ACCESSION:AR434781
C 169	19.4	0.5	26	1	AS5962	ACCESSION:AS5962	C 242	17.6	0.5	25	1	AR434785	ACCESSION:AR434785
C 170	19.4	0.5	26	1	A82434	ACCESSION:A82434	C 243	17.6	0.5	25	1	AR434785	ACCESSION:AR434785
C 171	19.4	0.5	26	1	AR128125	ACCESSION:AR128125	C 244	17.4	0.5	19	1	BD174952	ACCESSION:BD174952
C 172	19.4	0.5	26	1	BD135484	ACCESSION:BD135484	C 245	17.4	0.5	19	1	I31530	ACCESSION:I31530
C 173	19.2	0.5	24	1	BD192781	ACCESSION:BD192781	C 246	17.4	0.5	19	1	AX040467	ACCESSION:AX040467
C 174	19.2	0.5	24	1	E32221	ACCESSION:E32221	C 247	17.4	0.5	19	1	AX040468	ACCESSION:AX040468
C 175	19	0.5	19	1	AX482164	ACCESSION:AX482164	C 248	17.4	0.5	19	1	AX132174	ACCESSION:AX132174
C 176	19	0.5	19	1	AX511403	ACCESSION:AX511403	C 249	17.4	0.5	20	1	AR129716	ACCESSION:AR129716
C 177	19	0.5	19	1	AX721764	ACCESSION:AX721764	C 250	17.4	0.5	20	1	I33568	ACCESSION:I33568
C 178	19	0.5	24	1	AR404118	ACCESSION:AR404118	C 251	17.4	0.5	20	1	AX462693	ACCESSION:AX462693
C 179	19	0.5	27	1	AX080281	ACCESSION:AX080281	C 252	17.4	0.5	20	1		

253	17.4	0.5	21	1	AR126570	ACCESSION:AR126570	326	17	0.4	18	1	AX115187	ACCESSION:AX115187
254	17.4	0.5	21	1	AR126571	ACCESSION:AR126571	327	17	0.4	18	1	AX175253	ACCESSION:AX175253
c 255	17.4	0.5	21	1	AX203572	ACCESSION:AX203572	328	17	0.4	18	1	AX175254	ACCESSION:AX175254
c 256	17.4	0.5	21	1	AX613777	ACCESSION:AX613777	329	17	0.4	18	1	BD087486	ACCESSION:BD087486
257	17.4	0.5	30	1	AR264920	ACCESSION:AR264920	c 330	17	0.4	20	1	CQ818365	ACCESSION:CQ818365
258	17.4	0.5	30	1	AR264926	ACCESSION:AR264926	c 331	17	0.4	20	1	CQ818387	ACCESSION:CQ818387
259	17.4	0.5	30	1	AR478201	ACCESSION:AR478201	c 332	16.8	0.4	20	1	AR010007	ACCESSION:AR010007
260	17.4	0.5	30	1	AR478207	ACCESSION:AR478207	c 333	16.8	0.4	20	1	AR034742	ACCESSION:AR034742
261	17.4	0.5	30	1	BD072865	ACCESSION:BD072865	334	16.8	0.4	20	1	AR058876	ACCESSION:AR058876
262	17.4	0.5	30	1	BD072871	ACCESSION:BD072871	c 335	16.8	0.4	20	1	AR058876	ACCESSION:AR058876
263	17.4	0.5	30	1	BD107492	ACCESSION:BD107492	336	16.8	0.4	20	1	AR079581	ACCESSION:AR079581
264	17.4	0.5	30	1	BD107498	ACCESSION:BD107498	c 337	16.8	0.4	20	1	AR079581	ACCESSION:AR079581
265	17.4	0.5	30	1	BD145024	ACCESSION:BD145024	338	16.8	0.4	20	1	AR123290	ACCESSION:AR123290
266	17.4	0.5	30	1	BD145030	ACCESSION:BD145030	c 339	16.8	0.4	20	1	AR123290	ACCESSION:AR123290
267	17.4	0.5	30	1	BD166025	ACCESSION:BD166025	c 340	16.8	0.4	20	1	AR130163	ACCESSION:AR130163
268	17.4	0.5	30	1	BD166030	ACCESSION:BD166030	c 341	16.8	0.4	20	1	AR177700	ACCESSION:AR177700
c 269	17.4	0.5	31	1	AX248881	ACCESSION:AX248881	342	16.8	0.4	20	1	BD188892	ACCESSION:BD188892
270	17.2	0.5	22	1	A38159	ACCESSION:A38159	c 343	16.8	0.4	20	1	BD188892	ACCESSION:BD188892
271	17.2	0.5	22	1	AR173686	ACCESSION:AR173686	c 344	16.8	0.4	20	1	E32219	ACCESSION:E32219
272	17.2	0.5	23	1	A27197	ACCESSION:A27197	c 345	16.8	0.4	20	1	I24757	ACCESSION:I24757
273	17.2	0.5	23	1	A32939	ACCESSION:A32939	346	16.8	0.4	20	1	I33253	ACCESSION:I33253
274	17.2	0.5	23	1	A33834	ACCESSION:A33834	c 347	16.8	0.4	20	1	I33253	ACCESSION:I33253
275	17.2	0.5	23	1	AR077343	ACCESSION:AR077343	348	16.8	0.4	20	1	I35518	ACCESSION:I35518
276	17.2	0.5	23	1	AR117963	ACCESSION:AR117963	c 349	16.8	0.4	20	1	I35518	ACCESSION:I35518
277	17.2	0.5	23	1	BD231857	ACCESSION:BD231857	350	16.8	0.4	20	1	I43128	ACCESSION:I43128
278	17.2	0.5	23	1	CQ802102	ACCESSION:CQ802102	c 351	16.8	0.4	20	1	I43128	ACCESSION:I43128
279	17.2	0.5	23	1	CQ846562	ACCESSION:CQ846562	352	16.8	0.4	20	1	I92006	ACCESSION:I92006
280	17.2	0.5	23	1	E09110	ACCESSION:E09110	c 353	16.8	0.4	20	1	I92006	ACCESSION:I92006
281	17.2	0.5	23	1	I27518	ACCESSION:I27518	c 354	16.8	0.4	20	1	AR199772	ACCESSION:AR199772
c 282	17.2	0.5	23	1	I44506	ACCESSION:I44506	c 355	16.8	0.4	20	1	AR242049	ACCESSION:AR242049
283	17.2	0.5	23	1	I95684	ACCESSION:I95684	c 356	16.8	0.4	20	1	AX956707	ACCESSION:AX956707
c 284	17.2	0.5	23	1	AR262782	ACCESSION:AR262782	357	16.8	0.4	20	1	DOGIT1A	ACCESSION:DOGIT1A
285	17.2	0.5	23	1	AR265406	ACCESSION:AR265406	c 358	16.8	0.4	21	1	AR074234	ACCESSION:AR074234
286	17.2	0.5	23	1	AR301927	ACCESSION:AR301927	c 359	16.8	0.4	21	1	AR098876	ACCESSION:AR098876
287	17.2	0.5	23	1	AR428817	ACCESSION:AR428817	c 360	16.8	0.4	21	1	I79716	ACCESSION:I79716
c 288	17.2	0.5	23	1	AR438219	ACCESSION:AR438219	c 361	16.8	0.4	21	1	AR301331	ACCESSION:AR301331
289	17.2	0.5	23	1	AR447097	ACCESSION:AR447097	c 362	16.8	0.4	21	1	AX020545	ACCESSION:AX020545
290	17.2	0.5	23	1	AX010545	ACCESSION:AX010545	c 363	16.8	0.4	21	1	AX032596	ACCESSION:AX032596
291	17.2	0.5	23	1	AX203707	ACCESSION:AX203707	c 364	16.8	0.4	22	1	AR171534	ACCESSION:AR171534
292	17.2	0.5	23	1	AX203708	ACCESSION:AX203708	c 365	16.8	0.4	22	1	BD005554	ACCESSION:BD005554
293	17.2	0.5	23	1	AX357138	ACCESSION:AX357138	c 366	16.8	0.4	22	1	BD107557	ACCESSION:BD107557
294	17.2	0.5	24	1	AR058875	ACCESSION:AR058875	367	16.8	0.4	23	1	BD271420	ACCESSION:BD271420
295	17.2	0.5	24	1	AR058877	ACCESSION:AR058877	c 368	16.8	0.4	23	1	BD271421	ACCESSION:BD271421
296	17.2	0.5	24	1	AR079580	ACCESSION:AR079580	369	16.8	0.4	23	1	BD074547	ACCESSION:BD074547
297	17.2	0.5	24	1	AR123289	ACCESSION:AR123289	370	16.8	0.4	23	1	AX455018	ACCESSION:AX455018
298	17.2	0.5	24	1	AR123289	ACCESSION:AR123289	371	16.8	0.4	23	1	AX785090	ACCESSION:AX785090
299	17.2	0.5	24	1	AR123291	ACCESSION:AR123291	372	16.8	0.4	23	1	AX799210	ACCESSION:AX799210
300	17.2	0.5	24	1	BD188891	ACCESSION:BD188891	c 373	16.8	0.4	24	1	A57513	ACCESSION:A57513
301	17.2	0.5	24	1	BD188893	ACCESSION:BD188893	c 374	16.8	0.4	24	1	A57516	ACCESSION:A57516
302	17.2	0.5	24	1	I33252	ACCESSION:I33252	c 375	16.8	0.4	24	1	AR052979	ACCESSION:AR052979
303	17.2	0.5	24	1	I33254	ACCESSION:I33254	376	16.8	0.4	24	1	AR052982	ACCESSION:AR052982
304	17.2	0.5	24	1	I35517	ACCESSION:I35517	c 377	16.8	0.4	24	1	CQ828722	ACCESSION:CQ828722
305	17.2	0.5	24	1	I35519	ACCESSION:I35519	c 378	16.8	0.4	24	1	E31758	ACCESSION:E31758
306	17.2	0.5	24	1	I43127	ACCESSION:I43127	c 379	16.6	0.4	23	1	A48768	ACCESSION:A48768
307	17.2	0.5	24	1	I43129	ACCESSION:I43129	c 380	16.6	0.4	23	1	AR157364	ACCESSION:AR157364
308	17.2	0.5	24	1	I92005	ACCESSION:I92005	c 381	16.6	0.4	23	1	BD195029	ACCESSION:BD195029
309	17.2	0.5	24	1	I92007	ACCESSION:I92007	c 382	16.6	0.4	23	1	CQ799557	ACCESSION:CQ799557
c 310	17	0.4	17	1	E11484	ACCESSION:E11484	c 383	16.6	0.4	23	1	CQ841335	ACCESSION:CQ841335
311	17	0.4	17	1	AR455908	ACCESSION:AR455908	384	16.6	0.4	23	1	CQ841340	ACCESSION:CQ841340
c 312	17	0.4	17	1	AR455910	ACCESSION:AR455910	c 385	16.6	0.4	23	1	AX020199	ACCESSION:AX020199
313	17	0.4	17	1	AX239678	ACCESSION:AX239678	c 386	16.6	0.4	23	1	AX452855	ACCESSION:AX452855
c 314	17	0.4	17	1	AX239680	ACCESSION:AX239680	c 387	16.6	0.4	23	1	AX685107	ACCESSION:AX685107
c 315	17	0.4	18	1	AR071773	ACCESSION:AR071773	c 388	16.6	0.4	23	1	AX794949	ACCESSION:AX794949
c 316	17	0.4	18	1	AR071777	ACCESSION:AR071777	c 389	16.6	0.4	23	1	AX926751	ACCESSION:AX926751
c 317	17	0.4	18	1	AR071778	ACCESSION:AR071778	c 390	16.4	0.4	18	1	AR071772	ACCESSION:AR071772
c 318	17	0.4	18	1	AR071779	ACCESSION:AR071779	c 391	16.4	0.4	18	1	AR071799	ACCESSION:AR071799
c 319	17	0.4	18	1	AR071801	ACCESSION:AR071801	392	16.4	0.4	18	1	E28534	ACCESSION:E28534
c 320	17	0.4	18	1	AR071802	ACCESSION:AR071802	c 393	16.4	0.4	18	1	E28534	ACCESSION:E28534
c 321	17	0.4	18	1	AR071803	ACCESSION:AR071803	394	16.4	0.4	18	1	AR241816	ACCESSION:AR241816
c 322	17	0.4	18	1	AR178165	ACCESSION:AR178165	395	16.4	0.4	18	1	AX355057	ACCESSION:AX355057
323	17	0.4	18	1	AR178166	ACCESSION:AR178166	c 396	16.4	0.4	18	1	AX355057	ACCESSION:AX355057
324	17	0.4	18	1	AR182079	ACCESSION:AR182079	c 397	16.4	0.4	20	1	AR338196	ACCESSION:AR338196
325	17	0.4	18	1	AR261503	ACCESSION:AR261503	398	16.4	0.4	21	1	AR393666	ACCESSION:AR393666

C 399	16.4	0.4	21	1	AX020767	472	16	0.4	30	1	BD166026	ACCESSION:BD166026
C 400	16.4	0.4	21	1	AX020767	473	16	0.4	30	1	BD166028	ACCESSION:BD166028
C 401	16.4	0.4	23	1	AX092707	474	15.8	0.4	19	1	AR074777	ACCESSION:AR074777
C 402	16.4	0.4	23	1	AX3578	475	15.8	0.4	19	1	BD192775	ACCESSION:BD192775
C 403	16.2	0.4	23	1	AX38978	476	15.8	0.4	19	1	AX132173	ACCESSION:AX132173
C 404	16.2	0.4	21	1	A25398	477	15.8	0.4	20	1	A80994	ACCESSION:A80994
C 405	16.2	0.4	21	1	A25416	478	15.8	0.4	20	1	A88143	ACCESSION:A88143
C 406	16.2	0.4	21	1	A27176	479	15.8	0.4	20	1	A90110	ACCESSION:A90110
C 407	16.2	0.4	21	1	AR031310	480	15.8	0.4	20	1	A95373	ACCESSION:A95373
C 408	16.2	0.4	21	1	AR084555	481	15.8	0.4	20	1	AR070856	ACCESSION:AR070856
C 409	16.2	0.4	21	1	AR084555	482	15.8	0.4	20	1	AR074792	ACCESSION:AR074792
C 410	16.2	0.4	21	1	AR084576	483	15.8	0.4	20	1	AR117573	ACCESSION:AR117573
C 411	16.2	0.4	21	1	AR121232	484	15.8	0.4	20	1	AR125552	ACCESSION:AR125552
C 412	16.2	0.4	21	1	AR121232	485	15.8	0.4	20	1	AR190536	ACCESSION:AR190536
C 413	16.2	0.4	21	1	I32944	486	15.8	0.4	20	1	BD250309	ACCESSION:BD250309
C 414	16.2	0.4	21	1	I87090	487	15.8	0.4	20	1	E32215	ACCESSION:E32215
C 415	16.2	0.4	21	1	BD132045	488	15.8	0.4	20	1	AR228858	ACCESSION:AR228858
C 416	16.2	0.4	21	1	BD140705	489	15.8	0.4	20	1	AR271190	ACCESSION:AR271190
C 417	16.2	0.4	22	1	AR074772	490	15.8	0.4	20	1	AX029182	ACCESSION:AX029182
C 418	16.2	0.4	22	1	AR074786	491	15.8	0.4	20	1	AX224874	ACCESSION:AX224874
C 419	16.2	0.4	22	1	AR074787	492	15.8	0.4	20	1	AX224884	ACCESSION:AX224884
C 420	16.2	0.4	22	1	AR074787	493	15.8	0.4	20	1	AX250713	ACCESSION:AX250713
C 421	16.2	0.4	22	1	AR074787	494	15.8	0.4	20	1	AX469446	ACCESSION:AX469446
C 422	16.2	0.4	22	1	AR074787	495	15.8	0.4	20	1	AX476807	ACCESSION:AX476807
C 423	16.2	0.4	23	1	AR316862	496	15.8	0.4	20	1	BD016057	ACCESSION:BD016057
C 424	16.2	0.4	23	1	AR329402	497	15.8	0.4	20	1	BD016176	ACCESSION:BD016176
C 425	16.2	0.4	23	1	AR329402	498	15.8	0.4	20	1	BD017328	ACCESSION:BD017328
C 426	16.2	0.4	23	1	AR329402	499	15.8	0.4	20	1	BD065656	ACCESSION:BD065656
C 427	16.2	0.4	23	1	AR329402	500	15.8	0.4	20	1	BD174235	ACCESSION:BD174235
C 428	16.2	0.4	23	1	AR329402	501	15.8	0.4	21	1	E14785	ACCESSION:E14785
C 429	16.2	0.4	23	1	AR329402	502	15.8	0.4	21	1	BD056548	ACCESSION:BD056548
C 430	16.2	0.4	23	1	AR329402	503	15.8	0.4	30	1	AR264925	ACCESSION:AR264925
C 431	16.2	0.4	23	1	AR329402	504	15.8	0.4	30	1	AR478206	ACCESSION:AR478206
C 432	16.2	0.4	23	1	AR329402	505	15.8	0.4	30	1	BD072870	ACCESSION:BD072870
C 433	16.2	0.4	23	1	AR329402	506	15.8	0.4	30	1	BD107497	ACCESSION:BD107497
C 434	16.2	0.4	23	1	AR329402	507	15.8	0.4	30	1	BD145029	ACCESSION:BD145029
C 435	16.2	0.4	23	1	AR329402	508	15.8	0.4	30	1	BD166029	ACCESSION:BD166029
C 436	16.2	0.4	23	1	AR329402	509	15.8	0.4	41	1	AR309630	ACCESSION:AR309630
C 437	16.2	0.4	23	1	AR329402	510	15.8	0.4	42	1	BD238391	ACCESSION:BD238391
C 438	16.2	0.4	23	1	AR329402	511	15.8	0.4	42	1	AR279817	ACCESSION:AR279817
C 439	16.2	0.4	23	1	AR329402	512	15.6	0.4	21	1	AR138717	ACCESSION:AR138717
C 440	16.2	0.4	23	1	AR329402	513	15.6	0.4	21	1	AX094910	ACCESSION:AX094910
C 441	16.2	0.4	23	1	AR329402	514	15.6	0.4	22	1	A39908	ACCESSION:A39908
C 442	16.2	0.4	23	1	AR329402	515	15.6	0.4	22	1	AR036420	ACCESSION:AR036420
C 443	16.2	0.4	23	1	AR329402	516	15.6	0.4	22	1	AR048932	ACCESSION:AR048932
C 444	16.2	0.4	23	1	AR329402	517	15.6	0.4	22	1	CQ812601	ACCESSION:CQ812601
C 445	16.2	0.4	23	1	AR329402	518	15.6	0.4	22	1	I29861	ACCESSION:I29861
C 446	16.2	0.4	23	1	AR329402	519	15.6	0.4	22	1	I34465	ACCESSION:I34465
C 447	16.2	0.4	23	1	AR329402	520	15.6	0.4	22	1	AX252963	ACCESSION:AX252963
C 448	16.2	0.4	23	1	AR329402	521	15.6	0.4	22	1	AX367061	ACCESSION:AX367061
C 449	16.2	0.4	23	1	AR329402	522	15.6	0.4	22	1	AX740255	ACCESSION:AX740255
C 450	16.2	0.4	23	1	AR329402	523	15.6	0.4	22	1	AX743831	ACCESSION:AX743831
C 451	16.2	0.4	23	1	AR329402	524	15.6	0.4	22	1	AX937575	ACCESSION:AX937575
C 452	16.2	0.4	23	1	AR329402	525	15.4	0.4	17	1	A95626	ACCESSION:A95626
C 453	16.2	0.4	23	1	AR329402	526	15.4	0.4	17	1	AR023742	ACCESSION:AR023742
C 454	16.2	0.4	23	1	AR329402	527	15.4	0.4	17	1	AR036967	ACCESSION:AR036967
C 455	16.2	0.4	23	1	AR329402	528	15.4	0.4	17	1	BD199067	ACCESSION:BD199067
C 456	16.2	0.4	23	1	AR329402	529	15.4	0.4	17	1	BD226525	ACCESSION:BD226525
C 457	16.2	0.4	23	1	AR329402	530	15.4	0.4	17	1	CQ623256	ACCESSION:CQ623256
C 458	16.2	0.4	23	1	AR329402	531	15.4	0.4	17	1	AR188722	ACCESSION:AR188722
C 459	16.2	0.4	23	1	AR329402	532	15.4	0.4	17	1	AR188754	ACCESSION:AR188754
C 460	16.2	0.4	23	1	AR329402	533	15.4	0.4	17	1	AR286400	ACCESSION:AR286400
C 461	16.2	0.4	23	1	AR329402	534	15.4	0.4	17	1	AR324575	ACCESSION:AR324575
C 462	16.2	0.4	23	1	AR329402	535	15.4	0.4	17	1	AR324607	ACCESSION:AR324607
C 463	16.2	0.4	23	1	AR329402	536	15.4	0.4	17	1	AR329327	ACCESSION:AR329327
C 464	16.2	0.4	23	1	AR329402	537	15.4	0.4	17	1	AR329328	ACCESSION:AR329328
C 465	16.2	0.4	23	1	AR329402	538	15.4	0.4	17	1	AR329329	ACCESSION:AR329329
C 466	16.2	0.4	23	1	AR329402	539	15.4	0.4	17	1	AR329330	ACCESSION:AR329330
C 467	16.2	0.4	23	1	AR329402	540	15.4	0.4	17	1	AR329331	ACCESSION:AR329331
C 468	16.2	0.4	23	1	AR329402	541	15.4	0.4	17	1	AR329332	ACCESSION:AR329332
C 469	16.2	0.4	23	1	AR329402	542	15.4	0.4	17	1	AR329333	ACCESSION:AR329333
C 470	16.2	0.4	23	1	AR329402	543	15.4	0.4	17	1	AR329334	ACCESSION:AR329334
C 471	16.2	0.4	23	1	AR329402	544	15.4	0.4	17	1	AR329335	ACCESSION:AR329335

545	15.4	0.4	17	1	AX734179	ACCESSION:AX734179	C 618	15.2	0.4	20	1	AX293956	ACCESSION:AX293956
546	15.4	0.4	17	1	AX738591	ACCESSION:AX738591	C 619	15.2	0.4	20	1	AX452336	ACCESSION:AX452336
547	15.4	0.4	17	1	BD091430	ACCESSION:BD091430	620	15.2	0.4	20	1	AX477161	ACCESSION:AX477161
548	15.4	0.4	18	1	AX241816	ACCESSION:AX241816	621	15.2	0.4	20	1	AX526537	ACCESSION:AX526537
549	15.4	0.4	19	1	A95063	ACCESSION:A95063	622	15.2	0.4	20	1	AX712200	ACCESSION:AX712200
550	15.4	0.4	19	1	AX072218	ACCESSION:AX072218	623	15.2	0.4	20	1	AX787161	ACCESSION:AX787161
551	15.4	0.4	19	1	CQ802798	ACCESSION:CQ802798	624	15.2	0.4	20	1	AX799916	ACCESSION:AX799916
552	15.4	0.4	19	1	I26329	ACCESSION:I26329	625	15.2	0.4	20	1	BD072884	ACCESSION:BD072884
553	15.4	0.4	19	1	AX222435	ACCESSION:AX222435	626	15.2	0.4	20	1	BD072895	ACCESSION:BD072895
554	15.4	0.4	19	1	BD102783	ACCESSION:BD102783	627	15.2	0.4	20	1	BD106032	ACCESSION:BD106032
555	15.4	0.4	20	1	AX733540	ACCESSION:AX733540	628	15.2	0.4	20	1	BD107511	ACCESSION:BD107511
556	15.4	0.4	20	1	AX074776	ACCESSION:AX074776	629	15.2	0.4	20	1	BD107522	ACCESSION:BD107522
557	15.4	0.4	20	1	AR103195	ACCESSION:AR103195	630	15.2	0.4	20	1	BD138221	ACCESSION:BD138221
558	15.4	0.4	20	1	AR199773	ACCESSION:AR199773	631	15.2	0.4	20	1	BD138283	ACCESSION:BD138283
559	15.4	0.4	20	1	AR214196	ACCESSION:AR214196	632	15.2	0.4	20	1	BD145043	ACCESSION:BD145043
560	15.4	0.4	20	1	AR214200	ACCESSION:AR214200	633	15.2	0.4	20	1	BD145054	ACCESSION:BD145054
561	15.4	0.4	20	1	AX370498	ACCESSION:AX370498	634	15.2	0.4	20	1	BD166043	ACCESSION:BD166043
562	15.4	0.4	20	1	AX527818	ACCESSION:AX527818	635	15.2	0.4	20	1	BD166054	ACCESSION:BD166054
563	15.4	0.4	20	1	AX601143	ACCESSION:AX601143	636	15.2	0.4	20	1	DOGH0X7B	ACCESSION:L77371
564	15.4	0.4	20	1	BD144226	ACCESSION:BD144226	637	15.2	0.4	21	1	BD140705	ACCESSION:BD140705
565	15.4	0.4	21	1	AR177588	ACCESSION:AR177588	638	15.2	0.4	21	1	A28676	ACCESSION:A28676
566	15.4	0.4	21	1	CQ788487	ACCESSION:CQ788487	639	15.2	0.4	21	1	AR073030	ACCESSION:AR073030
567	15.4	0.4	21	1	AX146144	ACCESSION:AX146144	640	15.2	0.4	21	1	AR084556	ACCESSION:AR084556
568	15.4	0.4	21	1	AX395564	ACCESSION:AX395564	641	15.2	0.4	21	1	AR084560	ACCESSION:AR084560
569	15.4	0.4	21	1	AX395585	ACCESSION:AX395585	642	15.2	0.4	21	1	AR084593	ACCESSION:AR084593
570	15.4	0.4	21	1	AX955606	ACCESSION:AX955606	643	15.2	0.4	21	1	AR084597	ACCESSION:AR084597
571	15.4	0.4	25	1	AX042549	ACCESSION:AX042549	644	15.2	0.4	21	1	BD250646	ACCESSION:BD250646
572	15.4	0.4	25	1	AX043230	ACCESSION:AX043230	645	15.2	0.4	21	1	BD266134	ACCESSION:BD266134
573	15.4	0.4	30	1	AX351715	ACCESSION:AX351715	646	15.2	0.4	21	1	CQ769152	ACCESSION:CQ769152
574	15.4	0.4	31	1	A08914	ACCESSION:A08914	647	15.2	0.4	21	1	CQ797933	ACCESSION:CQ797933
575	15.4	0.4	35	1	AR029831	ACCESSION:AR029831	648	15.2	0.4	21	1	E08187	ACCESSION:E08187
576	15.4	0.4	41	1	I31440	ACCESSION:I31440	649	15.2	0.4	21	1	I27608	ACCESSION:I27608
577	15.4	0.4	41	1	I31443	ACCESSION:I31443	650	15.2	0.4	21	1	AR279803	ACCESSION:AR279803
578	15.2	0.4	40	1	AR181773	ACCESSION:AR181773	651	15.2	0.4	21	1	AR351501	ACCESSION:AR351501
579	15.2	0.4	20	1	A65910	ACCESSION:A65910	652	15.2	0.4	21	1	AR483457	ACCESSION:AR483457
580	15.2	0.4	20	1	AR050627	ACCESSION:AR050627	653	15.2	0.4	21	1	AX203590	ACCESSION:AX203590
581	15.2	0.4	20	1	AR067440	ACCESSION:AR067440	654	15.2	0.4	21	1	AX226447	ACCESSION:AX226447
582	15.2	0.4	20	1	AR100070	ACCESSION:AR100070	655	15.2	0.4	21	1	AX250034	ACCESSION:AX250034
583	15.2	0.4	20	1	AR117533	ACCESSION:AR117533	656	15.2	0.4	21	1	AX740291	ACCESSION:AX740291
584	15.2	0.4	20	1	AR129685	ACCESSION:AR129685	657	15.2	0.4	22	1	BD140700	ACCESSION:BD140700
585	15.2	0.4	20	1	AR163998	ACCESSION:AR163998	658	15.2	0.4	29	1	AR438517	ACCESSION:AR438517
586	15.2	0.4	20	1	AR170760	ACCESSION:AR170760	659	15.2	0.4	29	1	AX430216	ACCESSION:AX430216
587	15.2	0.4	20	1	AR176139	ACCESSION:AR176139	660	15.2	0.4	29	1	BD165919	ACCESSION:BD165919
588	15.2	0.4	20	1	BD250269	ACCESSION:BD250269	661	15.2	0.4	30	1	I30206	ACCESSION:I30206
589	15.2	0.4	20	1	CQ754256	ACCESSION:CQ754256	662	15.2	0.4	30	1	A79651	ACCESSION:A79651
590	15.2	0.4	20	1	CQ759158	ACCESSION:CQ759158	663	15.2	0.4	37	1	HS0BR105	ACCESSION:U62489
591	15.2	0.4	20	1	CQ762434	ACCESSION:CQ762434	664	15	0.4	15	1	AR074710	ACCESSION:AR074710
592	15.2	0.4	20	1	CQ762603	ACCESSION:CQ762603	665	15	0.4	15	1	AR074711	ACCESSION:AR074711
593	15.2	0.4	20	1	CQ763381	ACCESSION:CQ763381	666	15	0.4	15	1	AR074712	ACCESSION:AR074712
594	15.2	0.4	20	1	E12301	ACCESSION:E12301	667	15	0.4	15	1	AR074713	ACCESSION:AR074713
595	15.2	0.4	20	1	E25559	ACCESSION:E25559	668	15	0.4	15	1	AR127803	ACCESSION:AR127803
596	15.2	0.4	20	1	I16675	ACCESSION:I16675	669	15	0.4	15	1	AX175252	ACCESSION:AX175252
597	15.2	0.4	20	1	I18759	ACCESSION:I18759	670	15	0.4	15	1	AX721631	ACCESSION:AX721631
598	15.2	0.4	20	1	I19017	ACCESSION:I19017	671	15	0.4	16	1	AR328668	ACCESSION:AR328668
599	15.2	0.4	20	1	AR9428	ACCESSION:AR9428	672	15	0.4	17	1	AR074719	ACCESSION:AR074719
600	15.2	0.4	20	1	AR199806	ACCESSION:AR199806	673	15	0.4	17	1	AX687933	ACCESSION:AX687933
601	15.2	0.4	20	1	AR208740	ACCESSION:AR208740	674	15	0.4	17	1	AX687934	ACCESSION:AX687934
602	15.2	0.4	20	1	AR211982	ACCESSION:AR211982	675	15	0.4	17	1	AX687935	ACCESSION:AX687935
603	15.2	0.4	20	1	AR214733	ACCESSION:AR214733	676	15	0.4	18	1	AR076354	ACCESSION:AR076354
604	15.2	0.4	20	1	AR225997	ACCESSION:AR225997	677	15	0.4	18	1	BD234297	ACCESSION:BD234297
605	15.2	0.4	20	1	AR228818	ACCESSION:AR228818	678	15	0.4	19	1	AR127806	ACCESSION:AR127806
606	15.2	0.4	20	1	AR264939	ACCESSION:AR264939	679	15	0.4	20	1	AR163975	ACCESSION:AR163975
607	15.2	0.4	20	1	AR304132	ACCESSION:AR304132	680	15	0.4	20	1	AR208748	ACCESSION:AR208748
608	15.2	0.4	20	1	AR305121	ACCESSION:AR305121	681	15	0.4	20	1	AX482068	ACCESSION:AX482068
609	15.2	0.4	20	1	AR309225	ACCESSION:AR309225	682	15	0.4	20	1	AX511307	ACCESSION:AX511307
610	15.2	0.4	20	1	AR399605	ACCESSION:AR399605	683	15	0.4	20	1	AX721667	ACCESSION:AX721667
611	15.2	0.4	20	1	AR399627	ACCESSION:AR399627	684	15	0.4	23	1	S61964	ACCESSION:S61964
612	15.2	0.4	20	1	AR478220	ACCESSION:AR478220	685	14.8	0.4	18	1	AR7890	ACCESSION:AR7890
613	15.2	0.4	20	1	AR489949	ACCESSION:AR489949	686	14.8	0.4	18	1	A89857	ACCESSION:A89857
614	15.2	0.4	20	1	AR489951	ACCESSION:AR489951	687	14.8	0.4	18	1	AR187533	ACCESSION:AR187533
615	15.2	0.4	20	1	AX035957	ACCESSION:AX035957	688	14.8	0.4	18	1	AR190756	ACCESSION:AR190756
616	15.2	0.4	20	1	AX149223	ACCESSION:AX149223	689	14.8	0.4	18	1	AR219474	ACCESSION:AR219474
617	15.2	0.4	20	1	AX224921	ACCESSION:AX224921	690	14.8	0.4	18	1	AR324047	ACCESSION:AR324047

691	14.8	0.4	18	1	AR325602	764	14.8	0.4	20	1	AX295588
692	14.8	0.4	18	1	AR325602	765	14.8	0.4	20	1	AX295588
693	14.8	0.4	18	1	AR325602	766	14.8	0.4	20	1	AX295588
694	14.8	0.4	18	1	AR325602	767	14.8	0.4	20	1	AX295588
695	14.8	0.4	18	1	AR325602	768	14.8	0.4	20	1	AX295588
696	14.8	0.4	18	1	AR325602	769	14.8	0.4	20	1	AX295588
697	14.8	0.4	18	1	AR325602	770	14.8	0.4	20	1	AX295588
698	14.8	0.4	18	1	AR325602	771	14.8	0.4	20	1	AX295588
699	14.8	0.4	18	1	AR325602	772	14.8	0.4	20	1	AX295588
700	14.8	0.4	18	1	AR325602	773	14.8	0.4	20	1	AX295588
701	14.8	0.4	18	1	AR325602	774	14.8	0.4	20	1	AX295588
702	14.8	0.4	18	1	AR325602	775	14.8	0.4	20	1	AX295588
703	14.8	0.4	18	1	AR325602	776	14.8	0.4	20	1	AX295588
704	14.8	0.4	18	1	AR325602	777	14.8	0.4	20	1	AX295588
705	14.8	0.4	18	1	AR325602	778	14.8	0.4	20	1	AX295588
706	14.8	0.4	18	1	AR325602	779	14.8	0.4	20	1	AX295588
707	14.8	0.4	18	1	AR325602	780	14.8	0.4	20	1	AX295588
708	14.8	0.4	18	1	AR325602	781	14.8	0.4	20	1	AX295588
709	14.8	0.4	18	1	AR325602	782	14.8	0.4	20	1	AX295588
710	14.8	0.4	18	1	AR325602	783	14.8	0.4	20	1	AX295588
711	14.8	0.4	18	1	AR325602	784	14.8	0.4	20	1	AX295588
712	14.8	0.4	18	1	AR325602	785	14.8	0.4	20	1	AX295588
713	14.8	0.4	18	1	AR325602	786	14.8	0.4	20	1	AX295588
714	14.8	0.4	18	1	AR325602	787	14.8	0.4	20	1	AX295588
715	14.8	0.4	18	1	AR325602	788	14.8	0.4	20	1	AX295588
716	14.8	0.4	18	1	AR325602	789	14.8	0.4	20	1	AX295588
717	14.8	0.4	18	1	AR325602	790	14.8	0.4	20	1	AX295588
718	14.8	0.4	18	1	AR325602	791	14.8	0.4	20	1	AX295588
719	14.8	0.4	18	1	AR325602	792	14.8	0.4	20	1	AX295588
720	14.8	0.4	18	1	AR325602	793	14.8	0.4	20	1	AX295588
721	14.8	0.4	18	1	AR325602	794	14.8	0.4	20	1	AX295588
722	14.8	0.4	18	1	AR325602	795	14.8	0.4	20	1	AX295588
723	14.8	0.4	18	1	AR325602	796	14.8	0.4	20	1	AX295588
724	14.8	0.4	18	1	AR325602	797	14.8	0.4	20	1	AX295588
725	14.8	0.4	18	1	AR325602	798	14.8	0.4	20	1	AX295588
726	14.8	0.4	18	1	AR325602	799	14.8	0.4	20	1	AX295588
727	14.8	0.4	18	1	AR325602	800	14.8	0.4	20	1	AX295588
728	14.8	0.4	18	1	AR325602	801	14.8	0.4	20	1	AX295588
729	14.8	0.4	18	1	AR325602	802	14.8	0.4	20	1	AX295588
730	14.8	0.4	18	1	AR325602	803	14.8	0.4	20	1	AX295588
731	14.8	0.4	18	1	AR325602	804	14.8	0.4	20	1	AX295588
732	14.8	0.4	18	1	AR325602	805	14.8	0.4	20	1	AX295588
733	14.8	0.4	18	1	AR325602	806	14.8	0.4	20	1	AX295588
734	14.8	0.4	18	1	AR325602	807	14.8	0.4	20	1	AX295588
735	14.8	0.4	18	1	AR325602	808	14.8	0.4	20	1	AX295588
736	14.8	0.4	18	1	AR325602	809	14.8	0.4	20	1	AX295588
737	14.8	0.4	18	1	AR325602	810	14.8	0.4	20	1	AX295588
738	14.8	0.4	18	1	AR325602	811	14.8	0.4	20	1	AX295588
739	14.8	0.4	18	1	AR325602	812	14.8	0.4	20	1	AX295588
740	14.8	0.4	18	1	AR325602	813	14.8	0.4	20	1	AX295588
741	14.8	0.4	18	1	AR325602	814	14.8	0.4	20	1	AX295588
742	14.8	0.4	18	1	AR325602	815	14.8	0.4	20	1	AX295588
743	14.8	0.4	18	1	AR325602	816	14.8	0.4	20	1	AX295588
744	14.8	0.4	18	1	AR325602	817	14.8	0.4	20	1	AX295588
745	14.8	0.4	18	1	AR325602	818	14.8	0.4	20	1	AX295588
746	14.8	0.4	18	1	AR325602	819	14.8	0.4	20	1	AX295588
747	14.8	0.4	18	1	AR325602	820	14.8	0.4	20	1	AX295588
748	14.8	0.4	18	1	AR325602	821	14.8	0.4	20	1	AX295588
749	14.8	0.4	18	1	AR325602	822	14.8	0.4	20	1	AX295588
750	14.8	0.4	18	1	AR325602	823	14.8	0.4	20	1	AX295588
751	14.8	0.4	18	1	AR325602	824	14.8	0.4	20	1	AX295588
752	14.8	0.4	18	1	AR325602	825	14.8	0.4	20	1	AX295588
753	14.8	0.4	18	1	AR325602	826	14.8	0.4	20	1	AX295588
754	14.8	0.4	18	1	AR325602	827	14.8	0.4	20	1	AX295588
755	14.8	0.4	18	1	AR325602	828	14.8	0.4	20	1	AX295588
756	14.8	0.4	18	1	AR325602	829	14.8	0.4	20	1	AX295588
757	14.8	0.4	18	1	AR325602	830	14.8	0.4	20	1	AX295588
758	14.8	0.4	18	1	AR325602	831	14.8	0.4	20	1	AX295588
759	14.8	0.4	18	1	AR325602	832	14.8	0.4	20	1	AX295588
760	14.8	0.4	18	1	AR325602	833	14.8	0.4	20	1	AX295588
761	14.8	0.4	18	1	AR325602	834	14.8	0.4	20	1	AX295588
762	14.8	0.4	18	1	AR325602	835	14.8	0.4	20	1	AX295588
763	14.8	0.4	18	1	AR325602	836	14.8	0.4	20	1	AX295588

837	14.4	0.4	16	1	I33563	ACCSSION:I33563	910	14.4	0.4	18	1	BD086292	ACCSSION:BD086292
838	14.4	0.4	16	1	I33563	ACCSSION:I33563	911	14.4	0.4	18	1	BD172416	ACCSSION:BD172416
839	14.4	0.4	16	1	I38642	ACCSSION:I38642	912	14.4	0.4	18	1	BD172735	ACCSSION:BD172735
840	14.4	0.4	16	1	I38642	ACCSSION:I38642	913	14.4	0.4	18	1	BD173054	ACCSSION:BD173054
841	14.4	0.4	16	1	I51790	ACCSSION:I51790	914	14.4	0.4	18	1	BD173373	ACCSSION:BD173373
842	14.4	0.4	16	1	I84399	ACCSSION:I84399	915	14.4	0.4	19	1	AR131366	ACCSSION:AR131366
843	14.4	0.4	16	1	AR204607	ACCSSION:AR204607	916	14.4	0.4	19	1	CQ785575	ACCSSION:CQ785575
844	14.4	0.4	16	1	AR307317	ACCSSION:AR307317	917	14.4	0.4	19	1	E09395	ACCSSION:E09395
845	14.4	0.4	16	1	AR328417	ACCSSION:AR328417	918	14.4	0.4	19	1	AR482127	ACCSSION:AR482127
846	14.4	0.4	16	1	AR328446	ACCSSION:AR328446	919	14.4	0.4	19	1	AX117795	ACCSSION:AX117795
847	14.4	0.4	16	1	AR328669	ACCSSION:AR328669	920	14.4	0.4	19	1	AX131096	ACCSSION:AX131096
848	14.4	0.4	16	1	AX067878	ACCSSION:AX067878	921	14.4	0.4	19	1	BD001771	ACCSSION:BD001771
849	14.4	0.4	16	1	AX135452	ACCSSION:AX135452	922	14.4	0.4	20	1	AR020466	ACCSSION:AR020466
850	14.4	0.4	16	1	BD002055	ACCSSION:BD002055	923	14.4	0.4	20	1	AR026501	ACCSSION:AR026501
851	14.4	0.4	16	1	BD016434	ACCSSION:BD016434	924	14.4	0.4	20	1	AR063688	ACCSSION:AR063688
852	14.4	0.4	17	1	AR046263	ACCSSION:AR046263	925	14.4	0.4	20	1	AR116436	ACCSSION:AR116436
853	14.4	0.4	17	1	AR057459	ACCSSION:AR057459	926	14.4	0.4	20	1	AR130803	ACCSSION:AR130803
854	14.4	0.4	17	1	AR057807	ACCSSION:AR057807	927	14.4	0.4	20	1	BD233551	ACCSSION:BD233551
855	14.4	0.4	17	1	AR115217	ACCSSION:AR115217	928	14.4	0.4	20	1	I25851	ACCSSION:I25851
856	14.4	0.4	17	1	AR115565	ACCSSION:AR115565	929	14.4	0.4	20	1	I43488	ACCSSION:I43488
857	14.4	0.4	17	1	CQ617262	ACCSSION:CQ617262	930	14.4	0.4	20	1	AR208766	ACCSSION:AR208766
858	14.4	0.4	17	1	CQ617263	ACCSSION:CQ617263	931	14.4	0.4	20	1	AR435720	ACCSSION:AR435720
859	14.4	0.4	17	1	CQ617265	ACCSSION:CQ617265	932	14.4	0.4	20	1	AR475721	ACCSSION:AR475721
860	14.4	0.4	17	1	CQ617266	ACCSSION:CQ617266	933	14.4	0.4	20	1	AX006846	ACCSSION:AX006846
861	14.4	0.4	17	1	CQ623255	ACCSSION:CQ623255	934	14.4	0.4	20	1	AX078019	ACCSSION:AX078019
862	14.4	0.4	17	1	CQ623257	ACCSSION:CQ623257	935	14.4	0.4	20	1	AX304783	ACCSSION:AX304783
863	14.4	0.4	17	1	I53315	ACCSSION:I53315	936	14.4	0.4	20	1	AX404655	ACCSSION:AX404655
864	14.4	0.4	17	1	AR190295	ACCSSION:AR190295	937	14.4	0.4	20	1	AX494234	ACCSSION:AX494234
865	14.4	0.4	17	1	AR325248	ACCSSION:AR325248	938	14.4	0.4	20	1	AX553634	ACCSSION:AX553634
866	14.4	0.4	17	1	AR327351	ACCSSION:AR327351	939	14.4	0.4	20	1	AX740160	ACCSSION:AX740160
867	14.4	0.4	17	1	AR229330	ACCSSION:AR229330	940	14.4	0.4	20	1	AX785898	ACCSSION:AX785898
868	14.4	0.4	17	1	AR458325	ACCSSION:AR458325	941	14.4	0.4	20	1	AX926289	ACCSSION:AX926289
869	14.4	0.4	17	1	AR458326	ACCSSION:AR458326	942	14.4	0.4	20	1	AX926579	ACCSSION:AX926579
870	14.4	0.4	17	1	AR458328	ACCSSION:AR458328	943	14.4	0.4	20	1	BD074593	ACCSSION:BD074593
871	14.4	0.4	17	1	AR458329	ACCSSION:AR458329	944	14.4	0.4	25	1	BD244864	ACCSSION:BD244864
872	14.4	0.4	17	1	AR464318	ACCSSION:AR464318	945	14.4	0.4	25	1	AX043454	ACCSSION:AX043454
873	14.4	0.4	17	1	AR464320	ACCSSION:AR464320	946	14.4	0.4	26	1	AG3569	ACCSSION:AG3569
874	14.4	0.4	17	1	AX216365	ACCSSION:AX216365	947	14.4	0.4	26	1	E33560	ACCSSION:E33560
875	14.4	0.4	17	1	AX217982	ACCSSION:AX217982	948	14.4	0.4	30	1	AR264927	ACCSSION:AR264927
876	14.4	0.4	17	1	AX272813	ACCSSION:AX272813	949	14.4	0.4	30	1	AR478208	ACCSSION:AR478208
877	14.4	0.4	17	1	AX273076	ACCSSION:AX273076	950	14.4	0.4	30	1	BD072872	ACCSSION:BD072872
878	14.4	0.4	17	1	AX273311	ACCSSION:AX273311	951	14.4	0.4	30	1	BD107499	ACCSSION:BD107499
879	14.4	0.4	17	1	AX530932	ACCSSION:AX530932	952	14.4	0.4	30	1	BD145031	ACCSSION:BD145031
880	14.4	0.4	17	1	AX530934	ACCSSION:AX530934	953	14.4	0.4	30	1	BD166031	ACCSSION:BD166031
881	14.4	0.4	17	1	AX530935	ACCSSION:AX530935	954	14.4	0.4	32	1	AR051291	ACCSSION:AR051291
882	14.4	0.4	17	1	AX530936	ACCSSION:AX530936	955	14.4	0.4	32	1	I16939	ACCSSION:I16939
883	14.4	0.4	17	1	AX634548	ACCSSION:AX634548	956	14.4	0.4	32	1	I45733	ACCSSION:I45733
884	14.4	0.4	17	1	AX634866	ACCSSION:AX634866	957	14.4	0.4	40	1	BD170449	ACCSSION:BD170449
885	14.4	0.4	17	1	AX687337	ACCSSION:AX687337	958	14.4	0.4	40	1	CQ820328	ACCSSION:CQ820328
886	14.4	0.4	17	1	AX687398	ACCSSION:AX687398	959	14.4	0.4	44	1	AR038858	ACCSSION:AR038858
887	14.4	0.4	17	1	AX734671	ACCSSION:AX734671	960	14.4	0.4	19	1	A37552	ACCSSION:A37552
888	14.4	0.4	17	1	AX759120	ACCSSION:AX759120	961	14.2	0.4	19	1	A42357	ACCSSION:A42357
889	14.4	0.4	17	1	AX762817	ACCSSION:AX762817	962	14.2	0.4	19	1	A44390	ACCSSION:A44390
890	14.4	0.4	18	1	A34808	ACCSSION:A34808	963	14.2	0.4	19	1	A47177	ACCSSION:A47177
891	14.4	0.4	18	1	A47305	ACCSSION:A47305	964	14.2	0.4	19	1	A56651	ACCSSION:A56651
892	14.4	0.4	18	1	AR87891	ACCSSION:AR87891	965	14.2	0.4	19	1	AR0372	ACCSSION:AR0372
893	14.4	0.4	18	1	AR89858	ACCSSION:AR89858	966	14.2	0.4	19	1	AR111775	ACCSSION:AR111775
894	14.4	0.4	18	1	AR035673	ACCSSION:AR035673	967	14.2	0.4	19	1	AR179815	ACCSSION:AR179815
895	14.4	0.4	18	1	AR104208	ACCSSION:AR104208	968	14.2	0.4	19	1	BD266251	ACCSSION:BD266251
896	14.4	0.4	18	1	AR134314	ACCSSION:AR134314	969	14.2	0.4	19	1	CQ800200	ACCSSION:CQ800200
897	14.4	0.4	18	1	AR165360	ACCSSION:AR165360	970	14.2	0.4	19	1	I46926	ACCSSION:I46926
898	14.4	0.4	18	1	BD175407	ACCSSION:BD175407	971	14.2	0.4	19	1	I84730	ACCSSION:I84730
899	14.4	0.4	18	1	AR410785	ACCSSION:AR410785	972	14.2	0.4	19	1	AR193516	ACCSSION:AR193516
900	14.4	0.4	18	1	AR439149	ACCSSION:AR439149	973	14.2	0.4	19	1	AR254165	ACCSSION:AR254165
901	14.4	0.4	18	1	AR473169	ACCSSION:AR473169	974	14.2	0.4	19	1	AR292967	ACCSSION:AR292967
902	14.4	0.4	18	1	AX352818	ACCSSION:AX352818	975	14.2	0.4	19	1	AR294648	ACCSSION:AR294648
903	14.4	0.4	18	1	AX362663	ACCSSION:AX362663	976	14.2	0.4	19	1	AX081351	ACCSSION:AX081351
904	14.4	0.4	18	1	AX683709	ACCSSION:AX683709	977	14.2	0.4	19	1	AX128989	ACCSSION:AX128989
905	14.4	0.4	18	1	AX697638	ACCSSION:AX697638	978	14.2	0.4	19	1	AX128990	ACCSSION:AX128990
906	14.4	0.4	18	1	AX773279	ACCSSION:AX773279	979	14.2	0.4	19	1	AX129129	ACCSSION:AX129129
907	14.4	0.4	18	1	AX773295	ACCSSION:AX773295	980	14.2	0.4	19	1	AX129166	ACCSSION:AX129166
908	14.4	0.4	18	1	BD065404	ACCSSION:BD065404	981	14.2	0.4	19	1	AX129367	ACCSSION:AX129367
909	14.4	0.4	18	1	BD075556	ACCSSION:BD075556	982	14.2	0.4	19	1	AX129652	ACCSSION:AX129652

983	14.2	0.4	19	1	AX130617	ACCESSION:AX130617	CI056	14.2	0.4	20	1	I28186	ACCESSION:I28186
984	14.2	0.4	19	1	AX131319	ACCESSION:AX131319	1057	14.2	0.4	20	1	I33357	ACCESSION:I33357
985	14.2	0.4	19	1	AX132490	ACCESSION:AX132490	CI058	14.2	0.4	20	1	I33959	ACCESSION:I33959
986	14.2	0.4	19	1	AX204959	ACCESSION:AX204959	1059	14.2	0.4	20	1	I75371	ACCESSION:I75371
987	14.2	0.4	19	1	AX283191	ACCESSION:AX283191	CI060	14.2	0.4	20	1	I84306	ACCESSION:I84306
988	14.2	0.4	19	1	AX283247	ACCESSION:AX283247	CI061	14.2	0.4	20	1	I88636	ACCESSION:I88636
989	14.2	0.4	19	1	AX384647	ACCESSION:AX384647	CI062	14.2	0.4	20	1	AR182775	ACCESSION:AR182775
990	14.2	0.4	19	1	AX474023	ACCESSION:AX474023	CI063	14.2	0.4	20	1	AR198529	ACCESSION:AR198529
991	14.2	0.4	19	1	AX513754	ACCESSION:AX513754	1064	14.2	0.4	20	1	AR207423	ACCESSION:AR207423
992	14.2	0.4	19	1	AX644866	ACCESSION:AX644866	CI065	14.2	0.4	20	1	AR208741	ACCESSION:AR208741
993	14.2	0.4	19	1	AX928387	ACCESSION:AX928387	1065	14.2	0.4	20	1	AR211282	ACCESSION:AR211282
994	14.2	0.4	19	1	AX956746	ACCESSION:AX956746	CI067	14.2	0.4	20	1	AR217715	ACCESSION:AR217715
995	14.2	0.4	19	1	BD002098	ACCESSION:BD002098	CI068	14.2	0.4	20	1	AR217726	ACCESSION:AR217726
996	14.2	0.4	19	1	BD002141	ACCESSION:BD002141	CI069	14.2	0.4	20	1	AR217729	ACCESSION:AR217729
997	14.2	0.4	19	1	BD008057	ACCESSION:BD008057	CI070	14.2	0.4	20	1	AR221053	ACCESSION:AR221053
998	14.2	0.4	19	1	AB067988	ACCESSION:AB067988	CI071	14.2	0.4	20	1	AR223313	ACCESSION:AR223313
999	14.2	0.4	20	1	A32748	ACCESSION:A32748	CI072	14.2	0.4	20	1	AR223403	ACCESSION:AR223403
1000	14.2	0.4	20	1	A47852	ACCESSION:A47852	CI073	14.2	0.4	20	1	AR224513	ACCESSION:AR224513
1001	14.2	0.4	20	1	A63042	ACCESSION:A63042	1074	14.2	0.4	20	1	AR225072	ACCESSION:AR225072
1002	14.2	0.4	20	1	A97518	ACCESSION:A97518	CI075	14.2	0.4	20	1	AR231256	ACCESSION:AR231256
1003	14.2	0.4	20	1	AR012029	ACCESSION:AR012029	CI076	14.2	0.4	20	1	AR242698	ACCESSION:AR242698
1004	14.2	0.4	20	1	AR062662	ACCESSION:AR062662	CI077	14.2	0.4	20	1	AR243570	ACCESSION:AR243570
1005	14.2	0.4	20	1	AR062829	ACCESSION:AR062829	CI078	14.2	0.4	20	1	AR255972	ACCESSION:AR255972
1006	14.2	0.4	20	1	AR076718	ACCESSION:AR076718	CI079	14.2	0.4	20	1	AR268291	ACCESSION:AR268291
1007	14.2	0.4	20	1	AR079558	ACCESSION:AR079558	CI080	14.2	0.4	20	1	AR272010	ACCESSION:AR272010
1008	14.2	0.4	20	1	AR104765	ACCESSION:AR104765	1081	14.2	0.4	20	1	AR279110	ACCESSION:AR279110
1009	14.2	0.4	20	1	AR105587	ACCESSION:AR105587	1082	14.2	0.4	20	1	AR299882	ACCESSION:AR299882
1010	14.2	0.4	20	1	AR108646	ACCESSION:AR108646	CI083	14.2	0.4	20	1	AR300855	ACCESSION:AR300855
1011	14.2	0.4	20	1	AR116480	ACCESSION:AR116480	CI084	14.2	0.4	20	1	AR311304	ACCESSION:AR311304
1012	14.2	0.4	20	1	AR122482	ACCESSION:AR122482	1085	14.2	0.4	20	1	AR312921	ACCESSION:AR312921
1013	14.2	0.4	20	1	AR122500	ACCESSION:AR122500	CI086	14.2	0.4	20	1	AR314131	ACCESSION:AR314131
1014	14.2	0.4	20	1	AR122507	ACCESSION:AR122507	CI087	14.2	0.4	20	1	AR314261	ACCESSION:AR314261
1015	14.2	0.4	20	1	AR123249	ACCESSION:AR123249	CI088	14.2	0.4	20	1	AR314448	ACCESSION:AR314448
1016	14.2	0.4	20	1	AR127702	ACCESSION:AR127702	1089	14.2	0.4	20	1	AR315253	ACCESSION:AR315253
1017	14.2	0.4	20	1	AR129756	ACCESSION:AR129756	1090	14.2	0.4	20	1	AR316159	ACCESSION:AR316159
1018	14.2	0.4	20	1	AR142705	ACCESSION:AR142705	CI091	14.2	0.4	20	1	AR342815	ACCESSION:AR342815
1019	14.2	0.4	20	1	AR162412	ACCESSION:AR162412	CI092	14.2	0.4	20	1	AR361086	ACCESSION:AR361086
1020	14.2	0.4	20	1	AR163862	ACCESSION:AR163862	CI093	14.2	0.4	20	1	AR366100	ACCESSION:AR366100
1021	14.2	0.4	20	1	AR163934	ACCESSION:AR163934	1094	14.2	0.4	20	1	AR370587	ACCESSION:AR370587
1022	14.2	0.4	20	1	AR164041	ACCESSION:AR164041	CI095	14.2	0.4	20	1	AR382073	ACCESSION:AR382073
1023	14.2	0.4	20	1	AR174372	ACCESSION:AR174372	CI096	14.2	0.4	20	1	AR382084	ACCESSION:AR382084
1024	14.2	0.4	20	1	AR177628	ACCESSION:AR177628	CI097	14.2	0.4	20	1	AR382087	ACCESSION:AR382087
1025	14.2	0.4	20	1	BD181148	ACCESSION:BD181148	CI098	14.2	0.4	20	1	AR382950	ACCESSION:AR382950
1026	14.2	0.4	20	1	BD181159	ACCESSION:BD181159	CI099	14.2	0.4	20	1	AR408461	ACCESSION:AR408461
1027	14.2	0.4	20	1	BD181162	ACCESSION:BD181162	CI100	14.2	0.4	20	1	AR437052	ACCESSION:AR437052
1028	14.2	0.4	20	1	BD196159	ACCESSION:BD196159	1101	14.2	0.4	20	1	AR437053	ACCESSION:AR437053
1029	14.2	0.4	20	1	BD225060	ACCESSION:BD225060	CI102	14.2	0.4	20	1	AR437098	ACCESSION:AR437098
1030	14.2	0.4	20	1	BD230252	ACCESSION:BD230252	CI103	14.2	0.4	20	1	AR451291	ACCESSION:AR451291
1031	14.2	0.4	20	1	BD272738	ACCESSION:BD272738	1104	14.2	0.4	20	1	AR488805	ACCESSION:AR488805
1032	14.2	0.4	20	1	Q762181	ACCESSION:Q762181	CI105	14.2	0.4	20	1	AR492019	ACCESSION:AR492019
1033	14.2	0.4	20	1	Q762365	ACCESSION:Q762365	1106	14.2	0.4	20	1	AR492377	ACCESSION:AR492377
1034	14.2	0.4	20	1	Q762759	ACCESSION:Q762759	CI107	14.2	0.4	20	1	AR492685	ACCESSION:AR492685
1035	14.2	0.4	20	1	Q762880	ACCESSION:Q762880	1108	14.2	0.4	20	1	AX080337	ACCESSION:AX080337
1036	14.2	0.4	20	1	Q763511	ACCESSION:Q763511	CI109	14.2	0.4	20	1	AX080338	ACCESSION:AX080338
1037	14.2	0.4	20	1	Q764464	ACCESSION:Q764464	CI110	14.2	0.4	20	1	AX148837	ACCESSION:AX148837
1038	14.2	0.4	20	1	Q764591	ACCESSION:Q764591	1111	14.2	0.4	20	1	AX149220	ACCESSION:AX149220
1039	14.2	0.4	20	1	Q779747	ACCESSION:Q779747	1112	14.2	0.4	20	1	AX167126	ACCESSION:AX167126
1040	14.2	0.4	20	1	Q779749	ACCESSION:Q779749	1113	14.2	0.4	20	1	AX224922	ACCESSION:AX224922
1041	14.2	0.4	20	1	Q786731	ACCESSION:Q786731	1114	14.2	0.4	20	1	AX224927	ACCESSION:AX224927
1042	14.2	0.4	20	1	Q819706	ACCESSION:Q819706	1115	14.2	0.4	20	1	AX295702	ACCESSION:AX295702
1043	14.2	0.4	20	1	Q821690	ACCESSION:Q821690	1116	14.2	0.4	20	1	AX296663	ACCESSION:AX296663
1044	14.2	0.4	20	1	E02948	ACCESSION:E02948	1117	14.2	0.4	20	1	AX298596	ACCESSION:AX298596
1045	14.2	0.4	20	1	E04077	ACCESSION:E04077	CI118	14.2	0.4	20	1	AX298894	ACCESSION:AX298894
1046	14.2	0.4	20	1	E11000	ACCESSION:E11000	1119	14.2	0.4	20	1	AX317742	ACCESSION:AX317742
1047	14.2	0.4	20	1	E13769	ACCESSION:E13769	CI120	14.2	0.4	20	1	AX342778	ACCESSION:AX342778
1048	14.2	0.4	20	1	E29869	ACCESSION:E29869	1121	14.2	0.4	20	1	AX356852	ACCESSION:AX356852
1049	14.2	0.4	20	1	E30661	ACCESSION:E30661	CI122	14.2	0.4	20	1	AX462663	ACCESSION:AX462663
1050	14.2	0.4	20	1	E31396	ACCESSION:E31396	1123	14.2	0.4	20	1	AX462663	ACCESSION:AX462663
1051	14.2	0.4	20	1	E37366	ACCESSION:E37366	1124	14.2	0.4	20	1	AX487048	ACCESSION:AX487048
1052	14.2	0.4	20	1	E39123	ACCESSION:E39123	1125	14.2	0.4	20	1	AX488257	ACCESSION:AX488257
1053	14.2	0.4	20	1	E59332	ACCESSION:E59332	1126	14.2	0.4	20	1	AX589229	ACCESSION:AX589229
1054	14.2	0.4	20	1	I12350	ACCESSION:I12350	CI127	14.2	0.4	20	1	AX658511	ACCESSION:AX658511
1055	14.2	0.4	20	1	I20664	ACCESSION:I20664	1128	14.2	0.4	20	1	AX665329	ACCESSION:AX665329

c1129	14.2	0.4	20	1	AX719302	ACCESSION:AX719302	c1202	14	0.4	20	1	AX149325	ACCESSION:AX149325
c1130	14.2	0.4	20	1	AX743793	ACCESSION:AX743793	c1203	14	0.4	20	1	AX613800	ACCESSION:AX613800
c1131	14.2	0.4	20	1	AX776233	ACCESSION:AX776233	c1204	14	0.4	20	1	BD013149	ACCESSION:BD013149
c1132	14.2	0.4	20	1	AX804534	ACCESSION:AX804534	c1205	14	0.4	20	1	BD167763	ACCESSION:BD167763
c1133	14.2	0.4	20	1	AX923443	ACCESSION:AX923443	c1206	14	0.4	22	1	AX103869	ACCESSION:AX103869
c1134	14.2	0.4	20	1	AX938959	ACCESSION:AX938959	c1207	14	0.4	22	1	AX546922	ACCESSION:AX546922
c1135	14.2	0.4	20	1	AX958421	ACCESSION:AX958421	c1208	14	0.4	22	1	AX184223	ACCESSION:AX184223
c1136	14.2	0.4	20	1	AX962209	ACCESSION:AX962209	c1209	14	0.4	39	1	I31174	ACCESSION:I31174
c1137	14.2	0.4	20	1	BD016082	ACCESSION:BD016082	c1210	14	0.4	44	1	I31337	ACCESSION:I31337
c1138	14.2	0.4	20	1	BD016201	ACCESSION:BD016201	c1211	13.8	0.4	17	1	AR046263	ACCESSION:AR046263
c1139	14.2	0.4	20	1	BD017353	ACCESSION:BD017353	c1212	13.8	0.4	17	1	I53315	ACCESSION:I53315
c1140	14.2	0.4	20	1	BD074637	ACCESSION:BD074637	c1213	13.8	0.4	17	1	AO2372	ACCESSION:AO2372
c1141	14.2	0.4	20	1	BD081247	ACCESSION:BD081247	c1214	13.8	0.4	17	1	AO6173	ACCESSION:AO6173
c1142	14.2	0.4	20	1	BD123453	ACCESSION:BD123453	c1215	13.8	0.4	17	1	AR039211	ACCESSION:AR039211
c1143	14.2	0.4	20	1	BD140699	ACCESSION:BD140699	c1216	13.8	0.4	17	1	AR046566	ACCESSION:AR046566
c1144	14.2	0.4	20	1	BD167962	ACCESSION:BD167962	c1217	13.8	0.4	17	1	AR047368	ACCESSION:AR047368
c1145	14.2	0.4	23	1	BD271421	ACCESSION:BD271421	c1218	13.8	0.4	17	1	BD234970	ACCESSION:BD234970
c1146	14.2	0.4	23	1	AR409907	ACCESSION:AR409907	c1219	13.8	0.4	17	1	BD241250	ACCESSION:BD241250
c1147	14.2	0.4	30	1	AR264929	ACCESSION:AR264929	c1220	13.8	0.4	17	1	BD241618	ACCESSION:BD241618
c1148	14.2	0.4	30	1	AR478210	ACCESSION:AR478210	c1221	13.8	0.4	17	1	BD253988	ACCESSION:BD253988
c1149	14.2	0.4	30	1	BD145033	ACCESSION:BD145033	c1222	13.8	0.4	17	1	BD253989	ACCESSION:BD253989
c1150	14.2	0.4	30	1	BD072869	ACCESSION:BD072869	c1223	13.8	0.4	17	1	BD253989	ACCESSION:BD253989
c1151	14.2	0.4	30	1	BD072874	ACCESSION:BD072874	c1224	13.8	0.4	17	1	BD254375	ACCESSION:BD254375
c1152	14.2	0.4	30	1	BD107496	ACCESSION:BD107496	c1225	13.8	0.4	17	1	BD254495	ACCESSION:BD254495
c1153	14.2	0.4	30	1	BD107501	ACCESSION:BD107501	c1226	13.8	0.4	17	1	BD254752	ACCESSION:BD254752
c1154	14.2	0.4	30	1	BD145028	ACCESSION:BD145028	c1227	13.8	0.4	17	1	CO617474	ACCESSION:CO617474
c1155	14.2	0.4	30	1	BD145033	ACCESSION:BD145033	c1228	13.8	0.4	17	1	CO617930	ACCESSION:CO617930
c1156	14.2	0.4	30	1	BD166033	ACCESSION:BD166033	c1229	13.8	0.4	17	1	CO618036	ACCESSION:CO618036
c1157	14.2	0.4	30	1	BD166129	ACCESSION:BD166129	c1230	13.8	0.4	17	1	CO618038	ACCESSION:CO618038
c1158	14.2	0.4	31	1	AR248879	ACCESSION:AR248879	c1231	13.8	0.4	17	1	CO623102	ACCESSION:CO623102
c1159	14.2	0.4	38	1	AR222444	ACCESSION:AR222444	c1232	13.8	0.4	17	1	CO623258	ACCESSION:CO623258
c1160	14	0.4	42	1	I31428	ACCESSION:I31428	c1233	13.8	0.4	17	1	CO623261	ACCESSION:CO623261
c1161	14	0.4	14	1	BD185612	ACCESSION:BD185612	c1234	13.8	0.4	17	1	CO623347	ACCESSION:CO623347
c1162	14	0.4	14	1	BD185613	ACCESSION:BD185613	c1235	13.8	0.4	17	1	CO623985	ACCESSION:CO623985
c1163	14	0.4	14	1	E32202	ACCESSION:E32202	c1236	13.8	0.4	17	1	CO623986	ACCESSION:CO623986
c1164	14	0.4	14	1	I31524	ACCESSION:I31524	c1237	13.8	0.4	17	1	CO624607	ACCESSION:CO624607
c1165	14	0.4	15	1	AX175251	ACCESSION:AX175251	c1238	13.8	0.4	17	1	CO624974	ACCESSION:CO624974
c1166	14	0.4	16	1	AR241795	ACCESSION:AR241795	c1239	13.8	0.4	17	1	CO625121	ACCESSION:CO625121
c1167	14	0.4	16	1	BD234638	ACCESSION:BD234638	c1240	13.8	0.4	17	1	I53618	ACCESSION:I53618
c1168	14	0.4	16	1	AR302865	ACCESSION:AR302865	c1241	13.8	0.4	17	1	I54420	ACCESSION:I54420
c1169	14	0.4	17	1	AR057463	ACCESSION:AR057463	c1242	13.8	0.4	17	1	AR187317	ACCESSION:AR187317
c1170	14	0.4	17	1	AR115221	ACCESSION:AR115221	c1243	13.8	0.4	17	1	AR187357	ACCESSION:AR187357
c1171	14	0.4	17	1	BD241576	ACCESSION:BD241576	c1244	13.8	0.4	17	1	AR188717	ACCESSION:AR188717
c1172	14	0.4	17	1	BD272846	ACCESSION:BD272846	c1245	13.8	0.4	17	1	AR188718	ACCESSION:AR188718
c1173	14	0.4	17	1	AR483077	ACCESSION:AR483077	c1246	13.8	0.4	17	1	AR188755	ACCESSION:AR188755
c1174	14	0.4	17	1	AX634556	ACCESSION:AX634556	c1247	13.8	0.4	17	1	AR190226	ACCESSION:AR190226
c1175	14	0.4	17	1	AX687746	ACCESSION:AX687746	c1248	13.8	0.4	17	1	AR190240	ACCESSION:AR190240
c1176	14	0.4	17	1	AX687747	ACCESSION:AX687747	c1249	13.8	0.4	17	1	AR190291	ACCESSION:AR190291
c1177	14	0.4	17	1	AX687748	ACCESSION:AX687748	c1250	13.8	0.4	17	1	AR190292	ACCESSION:AR190292
c1178	14	0.4	17	1	AX687749	ACCESSION:AX687749	c1251	13.8	0.4	17	1	AR190292	ACCESSION:AR190292
c1179	14	0.4	17	1	AX687932	ACCESSION:AX687932	c1252	13.8	0.4	17	1	AR190307	ACCESSION:AR190307
c1180	14	0.4	17	1	AX687936	ACCESSION:AX687936	c1253	13.8	0.4	17	1	AR192109	ACCESSION:AR192109
c1181	14	0.4	17	1	AX688344	ACCESSION:AX688344	c1254	13.8	0.4	17	1	AR261711	ACCESSION:AR261711
c1182	14	0.4	17	1	AX688345	ACCESSION:AX688345	c1255	13.8	0.4	17	1	AR286089	ACCESSION:AR286089
c1183	14	0.4	17	1	AX688346	ACCESSION:AX688346	c1256	13.8	0.4	17	1	AR286406	ACCESSION:AR286406
c1184	14	0.4	17	1	AX688347	ACCESSION:AX688347	c1257	13.8	0.4	17	1	AR286445	ACCESSION:AR286445
c1185	14	0.4	17	1	AX728804	ACCESSION:AX728804	c1258	13.8	0.4	17	1	AR286463	ACCESSION:AR286463
c1186	14	0.4	17	1	AX759001	ACCESSION:AX759001	c1259	13.8	0.4	17	1	AR317230	ACCESSION:AR317230
c1187	14	0.4	18	1	A31423	ACCESSION:A31423	c1260	13.8	0.4	17	1	AR323927	ACCESSION:AR323927
c1188	14	0.4	18	1	A57884	ACCESSION:A57884	c1261	13.8	0.4	17	1	AR323967	ACCESSION:AR323967
c1189	14	0.4	18	1	CO821210	ACCESSION:CO821210	c1262	13.8	0.4	17	1	AR324570	ACCESSION:AR324570
c1190	14	0.4	18	1	AX441362	ACCESSION:AX441362	c1263	13.8	0.4	17	1	AR324571	ACCESSION:AR324571
c1191	14	0.4	18	1	AX453148	ACCESSION:AX453148	c1264	13.8	0.4	17	1	AR324608	ACCESSION:AR324608
c1192	14	0.4	18	1	AX599908	ACCESSION:AX599908	c1265	13.8	0.4	17	1	AR325195	ACCESSION:AR325195
c1193	14	0.4	18	1	AX599910	ACCESSION:AX599910	c1266	13.8	0.4	17	1	AR325206	ACCESSION:AR325206
c1194	14	0.4	20	1	A30762	ACCESSION:A30762	c1267	13.8	0.4	17	1	AR325259	ACCESSION:AR325259
c1195	14	0.4	20	1	A36727	ACCESSION:A36727	c1268	13.8	0.4	17	1	AR325989	ACCESSION:AR325989
c1196	14	0.4	20	1	AR126637	ACCESSION:AR126637	c1269	13.8	0.4	17	1	AR327329	ACCESSION:AR327329
c1197	14	0.4	20	1	BD270088	ACCESSION:BD270088	c1270	13.8	0.4	17	1	AR327483	ACCESSION:AR327483
c1198	14	0.4	20	1	CO818366	ACCESSION:CO818366	c1271	13.8	0.4	17	1	AR328712	ACCESSION:AR328712
c1199	14	0.4	20	1	CO818386	ACCESSION:CO818386	c1272	13.8	0.4	17	1	AR329331	ACCESSION:AR329331
c1200	14	0.4	20	1	E30319	ACCESSION:E30319	c1273	13.8	0.4	17	1	AR329361	ACCESSION:AR329361
c1201	14	0.4	20	1	AR266079	ACCESSION:AR266079	c1274	13.8	0.4	17	1	AR398079	ACCESSION:AR398079

1275	13.8	0.4	17	1	AR398396	1348	13.8	0.4	17	1	AX783664
1276	13.8	0.4	17	1	AR398397	1349	13.8	0.4	17	1	AX783665
1277	13.8	0.4	17	1	AR398435	1350	13.8	0.4	17	1	BD002054
1278	13.8	0.4	17	1	AR398453	1351	13.8	0.4	17	1	BD067798
1279	13.8	0.4	17	1	AR402298	1352	13.8	0.4	17	1	BD104450
1280	13.8	0.4	17	1	AR433728	c1353	13.8	0.4	17	1	DOGP36202
1281	13.8	0.4	17	1	AR433961	c1354	13.8	0.4	18	1	A88197
1282	13.8	0.4	17	1	AR433962	c1355	13.8	0.4	18	1	A90154
1283	13.8	0.4	17	1	AR433963	c1356	13.8	0.4	18	1	A90829
1284	13.8	0.4	17	1	AR433964	c1357	13.8	0.4	18	1	A91171
1285	13.8	0.4	17	1	AR458537	c1358	13.8	0.4	18	1	AR036682
1286	13.8	0.4	17	1	AR458933	c1359	13.8	0.4	18	1	AR062605
1287	13.8	0.4	17	1	AR459099	c1360	13.8	0.4	18	1	AR078582
1288	13.8	0.4	17	1	AR459101	1361	13.8	0.4	18	1	AR080699
1289	13.8	0.4	17	1	AR464165	1362	13.8	0.4	18	1	AR082993
1290	13.8	0.4	17	1	AR464321	c1363	13.8	0.4	18	1	AR104708
1291	13.8	0.4	17	1	AR464324	c1364	13.8	0.4	18	1	AR105530
1292	13.8	0.4	17	1	AR464410	c1365	13.8	0.4	18	1	AR119310
1293	13.8	0.4	17	1	AR465048	c1366	13.8	0.4	18	1	AR121140
1294	13.8	0.4	17	1	AR465049	c1367	13.8	0.4	18	1	AR123192
1295	13.8	0.4	17	1	AR465670	c1368	13.8	0.4	18	1	AR138072
1296	13.8	0.4	17	1	AR466037	1369	13.8	0.4	18	1	AR145511
1297	13.8	0.4	17	1	AR466184	1370	13.8	0.4	18	1	AR162682
1298	13.8	0.4	17	1	AR482439	c1371	13.8	0.4	18	1	AR178738
1299	13.8	0.4	17	1	AR483119	1372	13.8	0.4	18	1	BD226623
1300	13.8	0.4	17	1	AX009041	1373	13.8	0.4	18	1	BD227742
1301	13.8	0.4	17	1	AX216115	1374	13.8	0.4	18	1	BD250528
1302	13.8	0.4	17	1	AX216149	1375	13.8	0.4	18	1	BD250528
1303	13.8	0.4	17	1	AX217295	c1376	13.8	0.4	18	1	BD250528
1304	13.8	0.4	17	1	AX217292	c1377	13.8	0.4	18	1	BD250528
1305	13.8	0.4	17	1	AX217292	1378	13.8	0.4	18	1	BD250528
1306	13.8	0.4	17	1	AX217310	c1379	13.8	0.4	18	1	BD250528
1307	13.8	0.4	17	1	AX225317	c1380	13.8	0.4	18	1	BD250528
1308	13.8	0.4	17	1	AX225318	c1381	13.8	0.4	18	1	BD250528
1309	13.8	0.4	17	1	AX225319	c1382	13.8	0.4	18	1	BD250528
1310	13.8	0.4	17	1	AX225320	1383	13.8	0.4	18	1	BD250528
1311	13.8	0.4	17	1	AX225321	c1384	13.8	0.4	18	1	BD250528
1312	13.8	0.4	17	1	AX225322	c1385	13.8	0.4	18	1	BD250528
1313	13.8	0.4	17	1	AX225323	1386	13.8	0.4	18	1	BD250528
1314	13.8	0.4	17	1	AX225324	1387	13.8	0.4	18	1	BD250528
1315	13.8	0.4	17	1	AX225325	c1388	13.8	0.4	18	1	BD250528
1316	13.8	0.4	17	1	AX225326	c1389	13.8	0.4	18	1	BD250528
1317	13.8	0.4	17	1	AX225327	c1390	13.8	0.4	18	1	BD250528
1318	13.8	0.4	17	1	AX225328	c1391	13.8	0.4	18	1	BD250528
1319	13.8	0.4	17	1	AX225329	c1392	13.8	0.4	18	1	BD250528
1320	13.8	0.4	17	1	AX225330	1393	13.8	0.4	18	1	BD250528
1321	13.8	0.4	17	1	AX225331	c1394	13.8	0.4	18	1	BD250528
1322	13.8	0.4	17	1	AX225332	c1395	13.8	0.4	18	1	BD250528
1323	13.8	0.4	17	1	AX225333	1396	13.8	0.4	18	1	BD250528
1324	13.8	0.4	17	1	AX225334	c1397	13.8	0.4	18	1	BD250528
1325	13.8	0.4	17	1	AX225335	1398	13.8	0.4	18	1	BD250528
1326	13.8	0.4	17	1	AX225336	1399	13.8	0.4	18	1	BD250528
1327	13.8	0.4	17	1	AX225337	1400	13.8	0.4	18	1	BD250528
1328	13.8	0.4	17	1	AX225338	1401	13.8	0.4	18	1	BD250528
1329	13.8	0.4	17	1	AX225339	c1402	13.8	0.4	18	1	BD250528
1330	13.8	0.4	17	1	AX225340	c1403	13.8	0.4	18	1	BD250528
1331	13.8	0.4	17	1	AX225341	1404	13.8	0.4	18	1	BD250528
1332	13.8	0.4	17	1	AX225342	c1405	13.8	0.4	18	1	BD250528
1333	13.8	0.4	17	1	AX225343	c1406	13.8	0.4	18	1	BD250528
1334	13.8	0.4	17	1	AX225344	1407	13.8	0.4	18	1	BD250528
1335	13.8	0.4	17	1	AX225345	c1408	13.8	0.4	18	1	BD250528
1336	13.8	0.4	17	1	AX225346	c1409	13.8	0.4	18	1	BD250528
1337	13.8	0.4	17	1	AX225347	1410	13.8	0.4	18	1	BD250528
1338	13.8	0.4	17	1	AX225348	c1411	13.8	0.4	18	1	BD250528
1339	13.8	0.4	17	1	AX225349	c1412	13.8	0.4	18	1	BD250528
1340	13.8	0.4	17	1	AX225350	c1413	13.8	0.4	18	1	BD250528
1341	13.8	0.4	17	1	AX225351	1414	13.8	0.4	18	1	BD250528
1342	13.8	0.4	17	1	AX225352	c1415	13.8	0.4	18	1	BD250528
1343	13.8	0.4	17	1	AX225353	c1416	13.8	0.4	18	1	BD250528
1344	13.8	0.4	17	1	AX225354	c1417	13.8	0.4	18	1	BD250528
1345	13.8	0.4	17	1	AX225355	c1418	13.8	0.4	18	1	BD250528
1346	13.8	0.4	17	1	AX225356	c1419	13.8	0.4	18	1	BD250528
1347	13.8	0.4	17	1	AX225357	c1420	13.8	0.4	18	1	BD250528
1348	13.8	0.4	17	1	AX225358						
1349	13.8	0.4	17	1	AX225359						
1350	13.8	0.4	17	1	AX225360						
1351	13.8	0.4	17	1	AX225361						
1352	13.8	0.4	17	1	AX225362						
1353	13.8	0.4	17	1	AX225363						
1354	13.8	0.4	17	1	AX225364						
1355	13.8	0.4	17	1	AX225365						
1356	13.8	0.4	17	1	AX225366						
1357	13.8	0.4	17	1	AX225367						
1358	13.8	0.4	17	1	AX225368						
1359	13.8	0.4	17	1	AX225369						
1360	13.8	0.4	17	1	AX225370						
1361	13.8	0.4	17	1	AX225371						
1362	13.8	0.4	17	1	AX225372						
1363	13.8	0.4	17	1	AX225373						
1364	13.8	0.4	17	1	AX225374						
1365	13.8	0.4	17	1	AX225375						
1366	13.8	0.4	17	1	AX225376						
1367	13.8	0.4	17	1	AX225377						
1368	13.8	0.4	17	1	AX225378						
1369	13.8	0.4	17	1	AX225379						
1370	13.8	0.4	17	1	AX225380						
1371	13.8	0.4	17	1	AX225381						
1372	13.8	0.4	17	1	AX225382						
1373	13.8	0.4	17	1	AX225383						
1374	13.8	0.4	17	1	AX225384						
1375	13.8	0.4	17	1	AX225385						
1376	13.8	0.4	17	1	AX225386						
1377	13.8	0.4	17	1	AX225387						
1378	13.8	0.4	17	1	AX225388						
1379	13.8	0.4	17	1	AX225389						
1380	13.8	0.4	17	1	AX225390						
1381	13.8	0.4	17	1	AX225391						
1382	13.8	0.4	17	1	AX225392						
1383	13.8	0.4	17	1	AX225393						
1384	13.8	0.4	17	1	AX225394						
1385	13.8	0.4	17	1	AX225395						
1386	13.8	0.4	17	1	AX225396						
1387	13.8	0.4	17	1	AX225397						
1388	13.8	0.4	17	1	AX225398						
1389	13.8	0.4	17	1	AX225399						
1390	13.8	0.4	17	1	AX225400						
1391	13.8	0.4	17	1	AX225401						
1392	13.8	0.4	17	1	AX225402						
1393	13.8	0.4	17	1	AX225403						
1394	13.8	0.4	17	1	AX225404						
1395	13.8	0.4	17	1	AX225405						
1396	13.8	0.4	17	1	AX225406						
1397	13.8	0.4	17	1	AX225407						
1398	13.8	0.4	17	1	AX225408						
1399	13.8	0.4	17	1	AX225409						
1400	13.8	0.4	17	1	AX225410						
1401	13.8	0.4	17	1	AX225411						
1402	13.8	0.4	17	1	AX225412						
1403</											

c1421	13.8	0.4	18	1	AX826442	ACCESSION:AX826442
c1422	13.8	0.4	18	1	AX826683	ACCESSION:AX826683
c1423	13.8	0.4	18	1	BD023630	ACCESSION:BD023630
c1424	13.8	0.4	18	1	BD064969	ACCESSION:BD064969
c1425	13.8	0.4	18	1	BD065700	ACCESSION:BD065700
c1426	13.8	0.4	18	1	BD070462	ACCESSION:BD070462
c1427	13.8	0.4	18	1	BD089937	ACCESSION:BD089937
c1428	13.8	0.4	19	1	SSAJ787	ACCESSION:AJ000787
c1429	13.8	0.4	19	1	A36743	ACCESSION:A36743
c1430	13.8	0.4	19	1	A36744	ACCESSION:A36744
c1431	13.8	0.4	19	1	AR030969	ACCESSION:AR030969
c1432	13.8	0.4	19	1	AR030972	ACCESSION:AR030972
c1433	13.8	0.4	19	1	AR030974	ACCESSION:AR030974
c1434	13.8	0.4	19	1	AR030975	ACCESSION:AR030975
c1435	13.8	0.4	19	1	AR030976	ACCESSION:AR030976
c1436	13.8	0.4	19	1	AR030977	ACCESSION:AR030977
c1437	13.8	0.4	19	1	AR030978	ACCESSION:AR030978
c1438	13.8	0.4	19	1	AR030981	ACCESSION:AR030981
c1439	13.8	0.4	19	1	AR030982	ACCESSION:AR030982
c1440	13.8	0.4	19	1	AR030983	ACCESSION:AR030983
c1441	13.8	0.4	19	1	AR030984	ACCESSION:AR030984
c1442	13.8	0.4	19	1	AR066286	ACCESSION:AR066286
c1443	13.8	0.4	19	1	AR066287	ACCESSION:AR066287
c1444	13.8	0.4	19	1	AR066714	ACCESSION:AR066714
c1445	13.8	0.4	19	1	AR083027	ACCESSION:AR083027
c1446	13.8	0.4	19	1	AR108814	ACCESSION:AR108814
c1447	13.8	0.4	19	1	AR108817	ACCESSION:AR108817
c1448	13.8	0.4	19	1	AR108819	ACCESSION:AR108819
c1449	13.8	0.4	19	1	AR108820	ACCESSION:AR108820
c1450	13.8	0.4	19	1	AR108821	ACCESSION:AR108821
c1451	13.8	0.4	19	1	AR108822	ACCESSION:AR108822
c1452	13.8	0.4	19	1	AR108823	ACCESSION:AR108823
c1453	13.8	0.4	19	1	AR108826	ACCESSION:AR108826
c1454	13.8	0.4	19	1	AR108827	ACCESSION:AR108827
c1455	13.8	0.4	19	1	AR108828	ACCESSION:AR108828
c1456	13.8	0.4	19	1	AR108829	ACCESSION:AR108829
c1457	13.8	0.4	19	1	BD196756	ACCESSION:BD196756
c1458	13.8	0.4	19	1	BD226482	ACCESSION:BD226482
c1459	13.8	0.4	19	1	BD232821	ACCESSION:BD232821
c1460	13.8	0.4	19	1	BD232822	ACCESSION:BD232822
c1461	13.8	0.4	19	1	I33095	ACCESSION:I33095
c1462	13.8	0.4	19	1	I33096	ACCESSION:I33096
c1463	13.8	0.4	19	1	I62823	ACCESSION:I62823
c1464	13.8	0.4	19	1	AR205763	ACCESSION:AR205763
c1465	13.8	0.4	19	1	AR205766	ACCESSION:AR205766
c1466	13.8	0.4	19	1	AR205768	ACCESSION:AR205768
c1467	13.8	0.4	19	1	AR205769	ACCESSION:AR205769
c1468	13.8	0.4	19	1	AR205770	ACCESSION:AR205770
c1469	13.8	0.4	19	1	AR205771	ACCESSION:AR205771
c1470	13.8	0.4	19	1	AR205772	ACCESSION:AR205772
c1471	13.8	0.4	19	1	AR205775	ACCESSION:AR205775
c1472	13.8	0.4	19	1	AR205776	ACCESSION:AR205776
c1473	13.8	0.4	19	1	AR205777	ACCESSION:AR205777
c1474	13.8	0.4	19	1	AR205778	ACCESSION:AR205778
c1475	13.8	0.4	19	1	AR224942	ACCESSION:AR224942
c1476	13.8	0.4	19	1	AR224943	ACCESSION:AR224943
c1477	13.8	0.4	19	1	AR241182	ACCESSION:AR241182
c1478	13.8	0.4	19	1	AR241929	ACCESSION:AR241929

[illegible]

Best Local Similarity 94.6%; Pred. No. 8.6;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGCGGTGTGTGTGTGTGTG 2351
|||
Db 38 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 2

RESULT 21
LOCUS I31207/c 40 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 119 from patent US 5582979.
ACCESSION I31207
VERSION I31207.1 GI:1821998
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 119 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 33.8; DB 1; Length 40;
Best Local Similarity 94.6%; Pred. No. 8.8;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGCGGTGTGTGTGTGTG 2351
|||
Db 40 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 4

RESULT 22
LOCUS I31488/c 40 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 400 from patent US 5582979.
ACCESSION I31488
VERSION I31488.1 GI:1822279
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 400 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 33.8; DB 1; Length 40;
Best Local Similarity 94.6%; Pred. No. 8.8;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGCGGTGTGTGTGTGTG 2351
|||
Db 40 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 4

RESULT 23
LOCUS I31491/c 40 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 403 from patent US 5582979.
ACCESSION I31491
VERSION I31491.1 GI:1822282
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 403 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..40
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 33.8; DB 1; Length 40;
Best Local Similarity 94.6%; Pred. No. 8.8;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGCGGTGTGTGTGTGTG 2351
|||
Db 39 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 3

RESULT 24
LOCUS I31162/c 41 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 74 from patent US 5582979.
ACCESSION I31162
VERSION I31162.1 GI:1821953
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 74 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..41
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 33.8; DB 1; Length 41;
Best Local Similarity 94.6%; Pred. No. 9.1;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGCGGTGTGTGTGTGTG 2351
|||
Db 40 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 4

RESULT 25
LOCUS I31271/c 41 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 183 from patent US 5582979.
ACCESSION I31271
VERSION I31271.1 GI:1822062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 183 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..41
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 33.8; DB 1; Length 41;
Best Local Similarity 94.6%; Pred. No. 9.1;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same	Patent: US 5582979-A 189 10-DEC-1996;	Location/Qualifiers	source
FEATURES	Query Match	0.9%; Score 32.4; DB 1; Length 35;	Best Local Similarity 97.1%; Pred. No. 12;	Mismatches 33; Conservative 0; Indels 0; Gaps 0;
LOCUS	131291	45 bp	DNA	linear
DEFINITION	Sequence 203 from patent US 5582979.			
ACCESSION	131291			
VERSION	131291.1	GI:1822082		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 45)			
AUTHORS	Weber, J.L.			
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same			
JOURNAL	Patent: US 5582979-A 203 10-DEC-1996;			
FEATURES	Query Match	0.9%; Score 32.8; DB 1; Length 45;	Best Local Similarity 94.4%; Pred. No. 13;	Mismatches 34; Conservative 0; Indels 0; Gaps 0;
LOCUS	131268	34 bp	DNA	linear
DEFINITION	Sequence 180 from patent US 5582979.			
ACCESSION	131268			
VERSION	131268.1	GI:1822059		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 34)			
AUTHORS	Weber, J.L.			
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same			
JOURNAL	Patent: US 5582979-A 180 10-DEC-1996;			
FEATURES	Query Match	0.9%; Score 32.4; DB 1; Length 34;	Best Local Similarity 97.1%; Pred. No. 11;	Mismatches 33; Conservative 0; Indels 0; Gaps 0;
LOCUS	131277	35 bp	DNA	linear
DEFINITION	Sequence 189 from patent US 5582979.			
ACCESSION	131277			
VERSION	131277.1	GI:1822068		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 35)			
AUTHORS	Weber, J.L.			
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same			
JOURNAL	Patent: US 5582979-A 189 10-DEC-1996;			
FEATURES	Query Match	0.8%; Score 32.2; DB 1; Length 38;	Best Local Similarity 91.9%; Pred. No. 13;	Mismatches 34; Conservative 0; Indels 0; Gaps 0;
LOCUS	131156	38 bp	DNA	linear
DEFINITION	Sequence 68 from patent US 5582979.			
ACCESSION	131156			
VERSION	131156.1	GI:1821947		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 38)			
AUTHORS	Weber, J.L.			
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same			
JOURNAL	Patent: US 5582979-A 189 10-DEC-1996;			
FEATURES	Query Match	0.9%; Score 32.4; DB 1; Length 35;	Best Local Similarity 97.1%; Pred. No. 12;	Mismatches 33; Conservative 0; Indels 0; Gaps 0;
LOCUS	131291	45 bp	DNA	linear
DEFINITION	Sequence 203 from patent US 5582979.			
ACCESSION	131291			
VERSION	131291.1	GI:1822082		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 45)			
AUTHORS	Weber, J.L.			
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same			
JOURNAL	Patent: US 5582979-A 203 10-DEC-1996;			
FEATURES	Query Match	0.9%; Score 32.8; DB 1; Length 45;	Best Local Similarity 94.4%; Pred. No. 13;	Mismatches 34; Conservative 0; Indels 0; Gaps 0;
LOCUS	131268	34 bp	DNA	linear
DEFINITION	Sequence 180 from patent US 5582979.			
ACCESSION	131268			
VERSION	131268.1	GI:1822059		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 34)			
AUTHORS	Weber, J.L.			
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same			
JOURNAL	Patent: US 5582979-A 180 10-DEC-1996;			
FEATURES	Query Match	0.9%; Score 32.4; DB 1; Length 34;	Best Local Similarity 97.1%; Pred. No. 11;	Mismatches 33; Conservative 0; Indels 0; Gaps 0;
LOCUS	131277	35 bp	DNA	linear
DEFINITION	Sequence 189 from patent US 5582979.			
ACCESSION	131277			
VERSION	131277.1	GI:1822068		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 35)			
AUTHORS	Weber, J.L.			
TITLE	Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same			
JOURNAL	Patent: US 5582979-A 189 10-DEC-1996;			
FEATURES	Query Match	0.8%; Score 32.2; DB 1; Length 38;	Best Local Similarity 91.9%; Pred. No. 13;	Mismatches 34; Conservative 0; Indels 0; Gaps 0;
LOCUS	131156	38 bp	DNA	linear
DEFINITION	Sequence 68 from patent US 5582979.			

RESULT 58
I31458/C

Qy 642 GCACGTGGAGGTGAATGGCAGCAAGGTGGC 672

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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 42)
AUTHORS       Barton,C.Howard., White,J.Katie. and Blackwell,J.Mary.
TITLE         Natural resistance associated macrophage protein and uses thereof
JOURNAL       Patent: US 5869247-A 32 09-FEB-1999;
FEATURES      Location/Qualifiers
source        1..42
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.8%; Score 30.6; DB 1; Length 42;
Best Local Similarity 89.2%; Pred. No. 23;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2315 GTCGTGTGTGTGTGTGCGGTGTGTGTGTGTGTGTGTG 2351
      |||||
DB 6 GTGTGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 42

RESULT 66
E32203/c
LOCUS       E32203 Method for isolating satellite sequence. linear PAT 18-JUN-2001
DEFINITION E32203
ACCESSION  E32203
VERSION     E32203.1 GI:13021740
KEYWORDS   JP 2000060559-A/5;
SOURCE     Haliotis discus discus
ORGANISM   Haliotis discus discus
            Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
            Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.

REFERENCE   1 (bases 1 to 32)
AUTHORS     Hideaki,T. and Masashi,S.
TITLE       Method for isolating satellite sequence
JOURNAL     Patent: JP 2000060559-A 5 29-FEB-2000;
COMMENT     NATL INST OF AGROBIOLOGICAL RESOURCES
            OS Haliotis discus discus
            PN JP 2000060559-A/5
            PD 29-FEB-2000
            PF 18-AUG-1998 JP 1998232153
            PR
            PI HIDEAKI TAKAHASHI,MASASHI SEKINO
            CC C12N15/09,C12Q1/68,C12N15/00
            PH Key Location/Qualifiers
            FT source 1..32
            /organism='Haliotis discus discus'.
FEATURES     source
              1..32
              /organism="Haliotis discus discus"
              /mol_type="genomic DNA"
              /sub_species="discus"
              /db_xref="taxon:91233"

Query Match      0.8%; Score 30.4; DB 1; Length 32;
Best Local Similarity 96.9%; Pred. No. 19;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGCGGTGTGTGTGTGTGTGTG 2349
      |||||
DB 32 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 67
E32298/c
LOCUS       E32298 Sequence 210 from patent US 5582979. linear PAT 06-FEB-1997
DEFINITION  E32298
ACCESSION  E32298
VERSION     E32298.1 GI:1822089
KEYWORDS   .
SOURCE     Unknown.

Query Match      0.8%; Score 30.4; DB 1; Length 42;
Best Local Similarity 96.9%; Pred. No. 25;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTCGTGTGTGTGTGCGGTGTGTGTGTGTGTGTGTG 2350
      |||||
DB 32 GTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 68
E32299/c
LOCUS       E32299 Sequence 376 from patent US 5582979. linear PAT 06-FEB-1997
DEFINITION  E32299
ACCESSION  E32299
VERSION     E32299.1 GI:1822255
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 32)
AUTHORS     Weber,J.L.
TITLE       Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
JOURNAL     Patent: US 5582979-A 376 10-DEC-1996;
COMMENT     Location/Qualifiers
            source 1..32
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.8%; Score 30.4; DB 1; Length 32;
Best Local Similarity 96.9%; Pred. No. 19;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTCGTGTGTGTGTGCGGTGTGTGTGTGTGTGTGTG 2350
      |||||
DB 32 GTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 69
E32299/c
LOCUS       E32299 Sequence 340 from patent US 5582979. linear PAT 06-FEB-1997
DEFINITION  E32299
ACCESSION  E32299
VERSION     E32299.1 GI:1822219
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 42)
AUTHORS     Weber,J.L.
TITLE       Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
            method of using the same
JOURNAL     Patent: US 5582979-A 340 10-DEC-1996;
COMMENT     Location/Qualifiers
            source 1..42
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.8%; Score 30.4; DB 1; Length 42;
Best Local Similarity 96.9%; Pred. No. 25;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTCGTGTGTGTGTGCGGTGTGTGTGTGTGTGTGTG 2350
      |||||
DB 32 GTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1
```


AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected macromolecular structures
JOURNAL Patent: US 5571677-A 25 05-NOV-1996;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 41;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTCGTCGTGTGTGTGTG 2347
|||||
Db 29 GTGTGTGTGTGTCGTGTGTGTGTGTG 1

RESULT 84
I31168/c
LOCUS I31168 29 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 80 from patent US 5582979.
ACCESSION I31168
VERSION I31168.1 GI:1821959
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 80 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 41;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTCGTCGTGTGTGTGTG 2346
|||||
Db 29 TGTGTGTGTGTGTCGTGTGTGTGTGTG 1

RESULT 85
I31326/c
LOCUS I31326 29 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 238 from patent US 5582979.
ACCESSION I31326
VERSION I31326.1 GI:1822117
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 238 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 41;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTCGTCGTGTGTGTGTG 2347
|||||
Db 29 GTGTGTGTGTGTCGTGTGTGTGTGTG 1

RESULT 86
A27175/c
LOCUS A27175 28 bp DNA linear PAT 23-JUN-1995
DEFINITION Synthetic oligonucleotide primer.
ACCESSION A27175
VERSION A27175.1 GI:1248379
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS
TITLE CLONING OF A NEW MEMBER OF THE FIBROBLAST GROWTH FACTOR (FGF) RECEPTOR FAMILY
JOURNAL Patent: WO 9213948-A 5 20-AUG-1992;
FEATURES Location/Qualifiers
source 1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 53;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1632 TGCCCGCAATGCTGCTGACCGAGGAC 1659
|||||
Db 28 TGCCCGCAATGCTGCTGACTGAGGAC 1

RESULT 87
I31539/c
LOCUS I31539 28 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 451 from patent US 5582979.
ACCESSION I31539
VERSION I31539.1 GI:1822230
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 451 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 53;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTCGTCGTGTGTGTGTG 2346
|||||
Db 28 GTGTGTGTGTGTCGTGTGTGTGTGTG 1

RESULT 88
A45639
LOCUS A45639 34 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 33 from Patent WO9520044.
ACCESSION A45639
VERSION A45639.1 GI:2300037
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 34)

TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 5 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
source

1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 68;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGTGTGTGTG 2344

Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 98
AX175302

LOCUS AX175302 27 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 66 from Patent WO0144465.

ACCESSION AX175302
VERSION AX175302.1 GI:14598670

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 66 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
Location/Qualifiers

source

1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 68;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGCGTGTGTGTGTG 2345

Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 99
AX189457

LOCUS AX189457 27 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from Patent WO0147561.

ACCESSION AX189457
VERSION AX189457.1 GI:15142969

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Hyaluronic acid in the treatment of cancer
JOURNAL Patent: WO 0147561-A 2 05-JUL-2001;
Bioniche Life Sciences Inc. (CA)

FEATURES
Location/Qualifiers

source

1. .27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide"

Query Match 0.7%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 68;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGCGTGTGTGTGTG 2345

Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 100
I31503/c

LOCUS I31503 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 415 from patent US 5582979.

ACCESSION I31503
VERSION I31503.1 GI:1822294

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same

JOURNAL Patent: US 5582979-A 415 10-DEC-1996;
FEATURES Location/Qualifiers

source

1.30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 25.2; DB 1; Length 30;

Best Local Similarity 90.0%; Pred. No. 79;

Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGTGTGTGTG 2347

Db 30 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 101
AX482128

LOCUS AX482128 25 bp DNA linear PAT 17-AUG-2002
DEFINITION Sequence 105 from Patent EP1225233.

ACCESSION AX482128
VERSION AX482128.1 GI:22316850

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1225233-A 105 24-JUL-2002;
Amsterdam Support Diagnostics B.V. (NL)

FEATURES
Location/Qualifiers

source

1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="5'TAG019GENE"

Query Match 0.7%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 71;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTGACCGAGGACACGTGTGTGAAGA 1672

Db 1 GTGACCGAGGACACGTGTGTGAAGA 25

RESULT 102
AX511367

LOCUS AX511367 25 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 105 from Patent WO02059558.

ACCESSION AX511367
VERSION AX511367.1 GI:23392244

KEYWORDS

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SOURCE          synthetic construct
ORGANISM         synthetic construct
REFERENCE        1
AUTHORS          van der Kuyl,A.C. and Cornelissen,M.
TITLE            Means and methods for treatment evaluation
JOURNAL          Patent: WO 02059558-A 105 01-AUG-2002;
                  Amsterdam Support Diagnostics B.V. (NL)
FEATURES
  source
    1..25
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="5'TAG019GENE"
  Query Match      0.7%; Score 25; DB 1; Length 25;
  Best Local Similarity 100.0%; Pred. No. 71;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTGACCGAGGACAACTGTGATGAAGA 1672
Db 1 GTGACCGAGGACAACTGTGATGAAGA 25

RESULT 103
LOCUS          AX7211728          25 bp DNA linear PAT 07-MAY-2003
DEFINITION     Sequence 107 from Patent EP1298221.
ACCESSION      AX7211728
VERSION        AX7211728.1 GI:30422319
KEYWORDS       synthetic construct
               synthetic construct
               artificial sequences.
ORGANISM       van der Kuyl,A.C. and Cornelissen,M.
AUTHORS        Means and methods for treatment evaluation
TITLE          Patent: EP 1298221-A 107 02-APR-2003;
JOURNAL        PrimaGen Holding B.V. (NL)
FEATURES
  source
    1..25
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="primer 5'TAG019GENE"
  Query Match      0.7%; Score 25; DB 1; Length 25;
  Best Local Similarity 100.0%; Pred. No. 71;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1648 GTGACCGAGGACAACTGTGATGAAGA 1672
Db 1 GTGACCGAGGACAACTGTGATGAAGA 25

RESULT 104
LOCUS          E11483            24 bp DNA linear PAT 29-SEP-1997
DEFINITION     Primer for gaining probe which is for screening human Tie gene.
ACCESSION      E11483
VERSION        E11483.1 GI:22025119
KEYWORDS       JP 1996143598-A/1.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Yasunaga,K., Suda,T., Iwama,A., Kurozumi,K., Shimizu,Y., Nakada,S.
               and Masuyasu,Y.
TITLE          ANTI-TIE MONOCLONAL ANTIBODY AND HYBRIDOMA
JOURNAL        Patent: JP 1996143598-A 1 04-JUN-1996;
               YAMANOUCHI PHARMACEUT CO LTD
COMMENT        OS None
               OC Artificial sequences.

PN JP 1996143598-A/1
PD 04-JUN-1996
PF 17-NOV-1994 JP 1994308249
PI YASUNAGA KUNIO, SUDA TOSHIO, IWAMA ATSUSHI, KUROZUMI KOICHI,
   SHIMIZU YASUAKI, NAKADA SUSUMU, MASUYASU YASUHIKO PC
C07K16/28 C12N5/10 C12P21/08 G01N33/53 G01N33/53, PC
G01N33/577//C12N15/02;
PC (C12P21/08,C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
FH Key
FT source
FT 1..24
   /organism='Artificial sequences'.
FEATURES
  source
    1..24
      /organism="unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"
  Query Match      0.6%; Score 24; DB 1; Length 24;
  Best Local Similarity 100.0%; Pred. No. 90;
  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1622 GGGACCTGGCTGCCCGCAATGTGC 1645
Db 1 GGGACCTGGCTGCCCGCAATGTGC 24

RESULT 105
LOCUS          AX482129/c        24 bp DNA linear PAT 16-AUG-2002
DEFINITION     Sequence 106 from Patent EPI225233.
ACCESSION      AX482129
VERSION        AX482129.1 GI:22316851
KEYWORDS       synthetic construct
               synthetic construct
               artificial sequences.
ORGANISM       van der Kuyl,A.C. and Cornelissen,M.
AUTHORS        Means and methods for treatment evaluation
TITLE          Patent: EP 1225233-A 106 24-JUL-2002;
JOURNAL        Amsterdam Support Diagnostics B.V. (NL)
FEATURES
  source
    1..24
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="3'TAG019GENE"
  Query Match      0.6%; Score 24; DB 1; Length 24;
  Best Local Similarity 100.0%; Pred. No. 90;
  Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 ACACAGCAGCTGTACATGATCATG 1956
Db 24 ACACAGCAGCTGTACATGATCATG 1

RESULT 106
LOCUS          AX511368/c        24 bp DNA linear PAT 27-SEP-2002
DEFINITION     Sequence 106 from Patent WO02059558.
ACCESSION      AX511368
VERSION        AX511368.1 GI:23192245
KEYWORDS       synthetic construct
               synthetic construct
               artificial sequences.
ORGANISM       1
REFERENCE      1
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AUTHORS van der Kuyl, A.C. and Cornelissen, M.
 TITLE Means and methods for treatment evaluation
 JOURNAL Patent: WO 02059558-A 106 01-AUG-2002;
 Amsterdam Support Diagnostics B.V. (NL)
 FEATURES Location/Qualifiers
 1..24
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="3'TAG019GENE"

Query Match 0.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 ACACAGCCTGTACATGATCATG 1956
 Db 24 ACACAGCCTGTACATGATCATG 1

RESULT 107
 A29208/c
 LOCUS AX721729 24 bp DNA linear PAT 07-MAY-2003
 DEFINITION Sequence 108 from Patent EP1298221.
 ACCESSION AX721729
 VERSION AX721729.1 GI:30422320
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS van der Kuyl, A.C. and Cornelissen, M.
 TITLE Means and methods for treatment evaluation
 JOURNAL Patent: EP 1298221-A 108 02-APR-2003;
 PrismaGen Holding B.V. (NL)
 FEATURES Location/Qualifiers
 1..24
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="primer 3'TAG019GENE"

Query Match 0.6%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1933 ACACAGCCTGTACATGATCATG 1956
 Db 24 ACACAGCCTGTACATGATCATG 1

RESULT 108
 A29208/c
 LOCUS A29208 30 bp DNA linear PAT 30-JUN-1995
 DEFINITION DNA probe from patent WO9111459.
 ACCESSION A29208
 VERSION A29208.1 GI:1248929
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS EXTRACELLULAR FORM OF THE HUMAN FIBROBLAST GROWTH FACTOR RECEPTOR
 TITLE Patent: WO 9111459-A 2 08-AUG-1991;
 JOURNAL Location/Qualifiers
 1..30
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

Query Match 0.6%; Score 23.6; DB 1; Length 30;
 Best Local Similarity 86.7%; Pred. No. 1.3e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1963 TGCTGGCATGCGCGCCCTCCACAGAGCCC 1992
 Db 30 TGCTGGCATGCGCGCCCTCCACAGAGCCC 1

RESULT 109
 A29211/c
 LOCUS A29211 30 bp DNA linear PAT 30-JUN-1995
 DEFINITION Oligonucleotide OAB984 from patent WO9111459.
 ACCESSION A29211
 VERSION A29211.1 GI:1248932
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 30)
 AUTHORS EXTRACELLULAR FORM OF THE HUMAN FIBROBLAST GROWTH FACTOR RECEPTOR
 TITLE Patent: WO 9111459-A 6 08-AUG-1991;
 JOURNAL Location/Qualifiers
 1..30
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

Query Match 0.6%; Score 23.6; DB 1; Length 30;
 Best Local Similarity 86.7%; Pred. No. 1.3e+02;
 Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1963 TGCTGGCATGCGCGCCCTCCACAGAGCCC 1992
 Db 30 TGCTGGCATGCGCGCCCTCCACAGAGCCC 1

RESULT 110
 I31234/c
 LOCUS I31234 25 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 146 from patent US 5582979.
 ACCESSION I31234
 VERSION I31234.1 GI:1822025
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Weber, J.L.
 TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
 JOURNAL method of using the same
 FEATURES Patent: US 5582979-A 146 10-DEC-1996;
 Location/Qualifiers
 1..25
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.6%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 1.1e+02;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2342
 Db 25 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 111
 AX115976
 LOCUS AX115976 25 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 1099 from Patent WO0129262.
 ACCESSION AX115976
 VERSION AX115976.1 GI:14032918
 KEYWORDS synthetic construct
 SOURCE synthetic construct


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ACCESSION AX175258
VERSION AX175258.1 GI:14598626
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 014445-A 22 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
    Location/Qualifiers
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    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
Query Match 0.6%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2319 GTGTGTGTGTGTGCGTGTGTGT 2342
Db 1 GTGTGTGTGTGTGTGTGTGTGT 24

RESULT 117
AX547929
LOCUS AX547929 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 1068 from Patent WO02053141.
ACCESSION AX547929
VERSION AX547929.1 GI:25813073
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 1068 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
    Location/Qualifiers
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    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Synthetic Sequence"
Query Match 0.6%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGCGTGTGTGT 2341
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 118
AX117836/c
LOCUS AX117836 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2959 from Patent WO0129262.
ACCESSION AX117836
VERSION AX117836.1 GI:14034787
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2959 28-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
    Location/Qualifiers
    ..25
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Primer"
Query Match 0.6%; Score 22.4; DB 1; Length 25;
Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2319 GTGTGTGTGTGTGCGTGTGTGT 2342
Db 24 GTGTGTGTGTGTGTGTGTGTGT 1

RESULT 119
ARI73691/c
LOCUS ARI73691 22 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6306591.
ACCESSION ARI73691
VERSION ARI73691.1 GI:17914011
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Cockett,N.E. and Beever,J.E.
TITLE Screening for the molecular defect causing spider lamb syndrome in sheep
JOURNAL Patent: US 6306591-A 8 23-OCT-2001;
Location/Qualifiers
    ..22
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match 0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1985 AGAGGCCACCTTCAAGCAGCT 2006
Db 22 AGAGGCCACCTTCAAGCAGCT 1

RESULT 120
BD231722
LOCUS BD231722 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Low oxygen culturing of cells.
ACCESSION BD231722
VERSION BD231722.1 GI:33041492
KEYWORDS JP 2002530067-A/21.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Ceste,M., Doyle,J., Wold,B.J., Morrison,S.J. and Anderson,D.
TITLE Low oxygen culturing of cells
JOURNAL Patent: JP 2002530067-A 21 17-SEP-2002;
CALIFORNIA INSTITUTE OF TECHNOLOGY
COMMENT
    OS Artificial Sequence
    PN JP 2002530067-A/21
    PD 17-SEP-2002
    PF 18-NOV-1999 JP 2000582533
    PR 18-NOV-1998 US 09/195569,22-OCT-1999 US 09/425462 PI
    MARIE CESTE, JOHN DOYLE, BARBARA J WOLD, SEAN J MORRISON, DAVID PI
    ANDERSON
    PC C12N15/09,C12N5/06,C12N5/10,C12Q1/02,C12N15/00,C12N5/
    CC Description of Artificial Sequence:Forward PCR primer for CC
    FGFR3
    PH Key Location/Qualifiers
    FT source 1..22
    /organism='Artificial Sequence'

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AR383046
LOCUS       AR383046                22 bp    DNA                linear    PAT 18-DEC-2003
DEFINITION   Sequence 21 from patent US 6610540.
ACCESSION   AR383046
VERSION     AR383046.1 GI:40091859
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Csete,M., Doyle,J., Wold,B.J., McKay,R. and Studer,L.
TITLE       Low oxygen culturing of central nervous system progenitor cells
JOURNAL     Patent: US 6610540-A 21 26-AUG-2003;
FEATURES
source
1..22
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAAGAC 183
|||||
Db 1 ATCTCGGAGATGACGAAGAC 22

RESULT 125
LOCUS       AR383047/c              22 bp    DNA                linear    PAT 18-DEC-2003
DEFINITION   Sequence 22 from patent US 6610540.
ACCESSION   AR383047
VERSION     AR383047.1 GI:40091860
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Csete,M., Doyle,J., Wold,B.J., McKay,R. and Studer,L.
TITLE       Low oxygen culturing of central nervous system progenitor cells
JOURNAL     Patent: US 6610540-A 22 26-AUG-2003;
FEATURES
source
1..22
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAAGAC 183
|||||
Db 1 ATCTCGGAGATGACGAAGAC 22

RESULT 126
LOCUS       AR327687              22 bp    DNA                linear    PAT 07-JAN-2002
DEFINITION   Sequence 23 from Patent WO0183715.
ACCESSION   AX327687
VERSION     AX327687.1 GI:18098018
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
artificial sequences.
REFERENCE   1
AUTHORS     Inoue,K., Kim,D., Gu,Y. and Ishii,M.
TITLE       Method for inducing differentiation of embryonic stem cells into
            functioning cells
JOURNAL     Patent: WO 03062405-A 47 31-JUL-2003;
            Inoue, Kazutomo (JP) ; Yugengaisha Okuma Contactlens Kenkyujo (JP)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide Primer"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGAACAAAGTTTGGCAGCATCC 487
|||||
Db 22 GAGAACAAAGTTTGGCAGCATCC 1

RESULT 127
LOCUS       AX327688/c              22 bp    DNA                linear    PAT 07-JAN-2002
DEFINITION   Sequence 24 from Patent WO0183715.
ACCESSION   AX327688
VERSION     AX327688.1 GI:18098019
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
artificial sequences.
REFERENCE   1
AUTHORS     Lee,S.H., Lumelsky,N., Studer,L. and McKay,R.D.
TITLE       Derivation of midbrain dopaminergic neurons from embryonic stem
            cells
JOURNAL     Patent: WO 0183715-A 24 08-NOV-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ;
            Lee, Sang-Hun (KR) ; Lumelsky, Nadya (US) ; Studer, Lorenz (US) ;
            McKay, Ron D. G. (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGAACAAAGTTTGGCAGCATCC 487
|||||
Db 22 GAGAACAAAGTTTGGCAGCATCC 1

RESULT 128
LOCUS       AX812159              22 bp    DNA                linear    PAT 02-DEC-2003
DEFINITION   Sequence 47 from Patent WO03062405.
ACCESSION   AX812159
VERSION     AX812159.1 GI:38635795
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
artificial sequences.
REFERENCE   1
AUTHORS     Inoue,K., Kim,D., Gu,Y. and Ishii,M.
TITLE       Method for inducing differentiation of embryonic stem cells into
            functioning cells
JOURNAL     Patent: WO 03062405-A 47 31-JUL-2003;
            Inoue, Kazutomo (JP) ; Yugengaisha Okuma Contactlens Kenkyujo (JP)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide Primer"

Query Match      0.6%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GAGAACAAAGTTTGGCAGCATCC 487
|||||
Db 22 GAGAACAAAGTTTGGCAGCATCC 1

```

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 162 ATCTCGGAGATGACGAAGAC 183
Db 1 ATCTCGGAGATGACGAAGAC 22

RESULT 129
LOCUS AR020621/c
DEFINITION Sequence 5 from patent US 5789182.
ACCESSION AR020621
VERSION AR020621.1 GI:3975236
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yayon,A., Ornitz,D.M., Klagesbrun,M., Leder,P. and Planagan,J.G.
TITLE System for assaying binding to a heparin-binding growth factor
JOURNAL Patent: US 5789182-A 5 04-AUG-1998;
FEATURES Location/Qualifiers
source 1..28
/mol_type="unassigned DNA"

Query Match 0.6%; Score 22; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1348 GAGATGGAGATGATGAAGATGA 1369
Db 28 GAGATGGAGATGATGAAGATGA 7

RESULT 130
LOCUS AX117832/c
DEFINITION Sequence 2955 from Patent WO0129262.
ACCESSION AX117832
VERSION AX117832.1 GI:14034783
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2955 26-APR-2001;
JOURNAL Orchid BioSciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..25
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match 0.6%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGTGTGTGTG 2341
Db 25 CCGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 131
LOCUS AR127801/c
DEFINITION Sequence 22 from patent US 6180777.
ACCESSION AR127801
VERSION AR127801.1 GI:14114396

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cockett,N.E. and Beever,J.E.
TITLE Screening for the molecular defect causing spider lamb syndrome in
JOURNAL Sheep
FEATURES Patent: US 6306591-A 7 23-OCT-2001;
Location/Qualifiers
source 1..21
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 22 30-JAN-2001;
FEATURES Location/Qualifiers
source 1..23
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTG 2341
Db 23 GTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 132
LOCUS I31542/c
DEFINITION Sequence 454 from patent US 5582979.
ACCESSION I31542
VERSION I31542.1 GI:1822333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
JOURNAL Patent: US 5582979-A 454 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..23
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTG 2340
Db 23 TGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 133
LOCUS AR173690
DEFINITION Sequence 7 from patent US 6306591.
ACCESSION AR173690
VERSION AR173690.1 GI:17914010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cockett,N.E. and Beever,J.E.
TITLE Screening for the molecular defect causing spider lamb syndrome in
JOURNAL Sheep
FEATURES Patent: US 6306591-A 7 23-OCT-2001;
Location/Qualifiers
source 1..21
/mol_type="unassigned DNA"

Query Match 0.6%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1425 CCTGTACGTGCTGGTGGAGTA 1445
    |||||
Db 1 CCTGTACGTGCTGGTGGAGTA 21

RESULT 134
AR090052/c
LOCUS AR090052 30 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 172 from patent US 5994076.
ACCESSION AR090052
VERSION AR090052.1 GI:10016807
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chenchik,A., Jolkhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 172 30-NOV-1999;
FEATURES
    Location/Qualifiers
        source
            1..30
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.6%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1572 CCAGTGGCCCGGGCATGGAGTACTTGG 1600
    |||||
Db 29 CCAAGTGGCTAAGGGCATGGAGTCTTGG 1

RESULT 135
AR197087/c
LOCUS AR197087 30 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 172 from patent US 6352829.
ACCESSION AR197087
VERSION AR197087.1 GI:20246936
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chenchik,A., Jolkhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 172 05-MAR-2002;
FEATURES
    Location/Qualifiers
        source
            1..30
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.6%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1572 CCAGTGGCCCGGGCATGGAGTACTTGG 1600
    |||||
Db 29 CCAAGTGGCTAAGGGCATGGAGTCTTGG 1

RESULT 136
AR259241/c
LOCUS AR259241 30 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 172 from patent US 6489455.
ACCESSION AR259241
VERSION AR259241.1 GI:27309752
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Chenchik,A., Jolkhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 172 03-DEC-2002;
FEATURES
    Location/Qualifiers
        source
            1..30
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 0.6%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1572 CCAGTGGCCCGGGCATGGAGTACTTGG 1600
    |||||
Db 29 CCAAGTGGCTAAGGGCATGGAGTCTTGG 1

RESULT 137
AX117828/c
LOCUS AX117828 25 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 2951 from Patent WO0129262.
ACCESSION AX117828
VERSION AX117828.1 GI:14034779
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2951 26-APR-2001;
FEATURES
    Location/Qualifiers
        source
            1..25
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match 0.5%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 2.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGTGTGTGTGT 2340
    |||||
Db 24 CCGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 138
AR002279/c
LOCUS AR002279 27 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 18 from patent US 5741645.
ACCESSION AR002279
VERSION AR002279.1 GI:3963833
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Orr,H.T., Ranum,L.P.W., Chung,M.-Y. and Zoghbi,H.Y.
TITLE Gene sequence for spinocerebellar ataxia type 1 and method for
diagnosis
JOURNAL Patent: US 5741645-A 18 21-APR-1998;
FEATURES
    Location/Qualifiers
        source
            1..27
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.5%; Score 20.6; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 2.6e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```



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ORGANISM      unidentified
REFERENCE      1 (bases 1 to 20)
AUTHORS        Jun,S., Eriko,T., Chika,H., Akihiro,I., Masahiro,T. and Hiroshi,H.
TITLE          Immortalized human papilla pili cell and method for evaluating hair
JOURNAL        Growth stimulants with the use of the same
                Patent: JP 199089565-A 24 06-APR-1999;
                SHISEIDO CO LTD
COMMENT        OS Unidentified
                PN JP 199089565-A/24
                PD 06-APR-1999
                PF 19-SEP-1997 JP 1997271927
                PR
                PI JUN SUZUKI, ERIKO TAKEOKA, CHIKA HAMADA, AKIHIRO ISHINO, PI
                MASAHIRO TAJIMA,
                PI HIROSHI HANDA
                PC C12N5/10,A61K7/06, C12N15/09, C12P21/02, C12Q1/02, C12N5/10, PC
                C12R1/91),
                PC (C12P21/02, C12R1:91), C12N5/00, C12N15/00, (C12N5/00, C12R1:91) CC
                Strandedness: Single;
                CC Topology: Linear;
                FH Key Location/Qualifiers
                FT source 1..20
                FT Location/Qualifiers
                FT /organism='Unidentified'.
                FT 1..20
                FT /organism='unidentified'
                FT /mol_type='genomic DNA'
                FT /db_xref='taxon:32644'

Query Match      0.5%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1297 AGATGCTGAAGACGATGC 1316
DB      20 AGATGCTGAAGACGATGC 1

RESULT 144
BD107438/c
LOCUS      BD107438      27 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION Novel microsatellite DNA of pears.
ACCESSION      BD107438
VERSION      BD107438.1 GI:23202256
KEYWORDS      JP 2002034562-A/47.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 27)
AUTHORS        Yamamoto,T., Sawamura,Y., Matsuda,N. and Hayashi,K.
TITLE          Novel microsatellite DNA of pears
JOURNAL        Patent: JP 2002034562-A 47 05-FEB-2002;
COMMENT        OS Artificial Sequence
                PN JP 2002034562-A/47
                PD 05-FEB-2002
                PF 21-JUL-2000 JP 2000220340
                PR TOSHIYA YAMAMOTO, YUTAKA SAWAMURA, NAGAO MATSUDA, KENKI HAYASHI
                PC C12N15/09, C12N15/00
                CC Description of Artificial Sequence: Primer
                CC 1
                FH Key Location/Qualifiers
                FT modified base (1)..(2).
                FT Location/Qualifiers
                FT 1..27
                FT /organism='synthetic construct'
                FT /mol_type='genomic DNA'
                FT /db_xref='taxon:32630'

Query Match      0.5%; Score 20; DB 1; Length 27;
Best Local Similarity 79.2%; Pred. No. 3.1e+02;
Matches 19; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY      2332 TCGTGTGTGTGTGTGTGTGCACA 2355
DB      27 TGTGTGTGTGTGTGTGTGTGVMMV 4

RESULT 145
AX116678
LOCUS      AX116678      23 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 1801 from Patent WO0129262.
ACCESSION      AX116678
VERSION      AX116678.1 GI:14033620
KEYWORDS      synthetic construct
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1
AUTHORS        Picoult-Newburg,L. and Pohl,M.
TITLE          Genotyping reagents, Kits and methods of use thereof
JOURNAL        Patent: WO 0129262-A 1801 26-APR-2001;
                Orchid Biosciences, Inc. (US)
FEATURES        Location/Qualifiers
                1..23
                source
                /organism='synthetic construct'
                /mol_type='unassigned DNA'
                /db_xref='taxon:32630'
                /note='Primer'

Query Match      0.5%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2311 TTTGTCTGTGTGTGTGTGTGTG 2333
DB      1 TTTTGTGTGTGTGTGTGTGTGTG 23

RESULT 146
E32214/c
LOCUS      E32214      24 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION      E32214
VERSION      E32214.1 GI:13021823
KEYWORDS      JP 2000060559-A/16.
SOURCE      Haliotis discus discus
ORGANISM      Haliotis discus discus
                Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Hideaki,T. and Masashi,S.
TITLE          Method for isolating satellite sequence
JOURNAL        Patent: JP 2000060559-A 16 29-FEB-2000;
                NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT        OS Haliotis discus discus
                PN JP 2000060559-A/16
                PD 29-FEB-2000
                PF 18-AUG-1998 JP 1998232153
                PR
                PR HIDEAKI TAKAHASHI, MASASHI SEKINO
                PC C12N15/09, C12Q1/68, C12N15/00
                CC
                CC Key Location/Qualifiers
                FT source 1..24
                FT /organism='Haliotis discus discus'.
                FT Location/Qualifiers
                FT 1..24
                FT /organism='Haliotis discus discus'
                FT /mol_type='genomic DNA'
                FT /sub_species='discus'
                FT /db_xref='taxon:91233'

Query Match      0.5%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 3e+02;

```



```
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 GTGTGGGTGTGTGTGTGTGTG 2351
| | | | | | | | | | | | | | |
Db 23 GCGGCGGTGTGTGTGTGTGTG 1

RESULT 147
AR090987
LOCUS AR090987 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1107 from patent US 5994076.
ACCESSION AR090987
VERSION AR090987.1 GI:10017742
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1107 30-NOV-1999;
FEATURES
source
Location/Qualifiers
1..26
/mol_type="unknown"
/organism="unassigned DNA"

Query Match 0.5%; Score 19.8; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2546 TGGCTCGGCTCTGCCTTTGCAC 2568
| | | | | | | | | | | | | | |
Db 1 TGGGTGGGCTCTACCTTTGCAC 23

RESULT 148
AR198022
LOCUS AR198022 26 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1107 from patent US 6352829.
ACCESSION AR198022
VERSION AR198022.1 GI:20247871
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1107 05-MAR-2002;
FEATURES
source
Location/Qualifiers
1..26
/mol_type="unknown"
/organism="unassigned DNA"

Query Match 0.5%; Score 19.8; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2546 TGGCTCGGCTCTGCCTTTGCAC 2568
| | | | | | | | | | | | | | |
Db 1 TGGGTGGGCTCTACCTTTGCAC 23

RESULT 149
AR260176
LOCUS AR260176 26 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1107 from patent US 6489455.
ACCESSION AR260176
VERSION AR260176.1 GI:27310687
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 1107 03-DEC-2002;
FEATURES
source
Location/Qualifiers
1..26
/mol_type="unknown"
/organism="unassigned DNA"

Query Match 0.5%; Score 19.8; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2546 TGGCTCGGCTCTGCCTTTGCAC 2568
| | | | | | | | | | | | | | |
Db 1 TGGGTGGGCTCTACCTTTGCAC 23

RESULT 150
AR183949
LOCUS AR183949 27 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1702 from Patent WO0142511.
ACCESSION AR183949
VERSION AR183949.1 GI:15135282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1702 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
source
Location/Qualifiers
1..27
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.5%; Score 19.6; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTGTGTGTGTGTGT 2342
| | | | | | | | | | | | | | |
Db 27 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 151
AR090230/c
LOCUS AR090230 28 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 350 from patent US 5994076.
ACCESSION AR090230
VERSION AR090230.1 GI:10016985
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 350 30-NOV-1999;
FEATURES
source
Location/Qualifiers
1..28
/mol_type="unknown"
/organism="unassigned DNA"

Query Match 0.5%; Score 19.6; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1765 GAGGCCTGTTTGACCGAGTCTACAC 1790
||||| ||||| ||||| |||||
Db 27 GAGGCATTATTGACCGGATCTACAC 2

RESULT 152
AR197265/c
LOCUS AR197265 28 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 350 from patent US 6352829.
ACCESSION AR197265
VERSION AR197265.1 GI:20247114
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 350 05-MAR-2002;
FEATURES
source
Location/Qualifiers
1..28
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 19.6; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1765 GAGGCCTGTTTGACCGAGTCTACAC 1790
||||| ||||| ||||| |||||
Db 27 GAGGCATTATTGACCGGATCTACAC 2

RESULT 153
AR259419/c
LOCUS AR259419 28 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 350 from patent US 6489455.
ACCESSION AR259419
VERSION AR259419.1 GI:27309930
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6489455-A 350 03-DEC-2002;
FEATURES
source
Location/Qualifiers
1..28
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 19.6; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 3.6e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1765 GAGGCCTGTTTGACCGAGTCTACAC 1790
||||| ||||| ||||| |||||
Db 27 GAGGCATTATTGACCGGATCTACAC 2

RESULT 154
AR007164
LOCUS AR007164 21 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 16 from patent US 5750371.
ACCESSION AR007164
VERSION AR007164.1 GI:3966648
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Senoo,M., Watanabe,T. and Igarashi,K.

TITLE Water-soluble mutein of FGF receptor, DNA and production thereof
JOURNAL Patent: US 5750371-A 16 12-MAY-1998;
FEATURES
source
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 TCTGAGATGGAGATGATGAAG 1365
||||| ||||| ||||| |||||
Db 1 TCAGAGATGGAGATGATGAAG 21

RESULT 155
I31248/c
LOCUS I31248 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 160 from patent US 5582979.
ACCESSION I31248
VERSION I31248.1 GI:1822039
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 160 10-DEC-1996;
FEATURES
source
Location/Qualifiers
1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGT 2338
||||| ||||| ||||| |||||
Db 21 TGTGTGTGTGTGTGTTGTGT 1

RESULT 156
AX104715
LOCUS AX104715 21 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 907 from Patent WO0122972.
ACCESSION AX104715
VERSION AX104715.1 GI:13920912
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 907 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGT 2338
||||| ||||| ||||| |||||
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Db      1  TGTGTGTGTGTGTGTGTGT 21

RESULT 157
AX175255
LOCUS      21 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 19 from Patent WO0144465.
ACCESSION AX175255
VERSION    AX175255.1 GI:14598623
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE 1
AUTHORS     Phillips,N.C. and Filion,M.C.
TITLE       Therapeutically useful synthetic oligonucleotides
JOURNAL     Patent: WO 0144465-A 19 21-JUN-2001;
            Bioniche Life Sciences Inc. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTGTGT 2338
Db      1  TGTGTGTGTGTGTGTGTGT 21

RESULT 160
BD251661
LOCUS      22 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Selection of animal based on character imprinted by parent.
ACCESSION BD251661
VERSION    BD251661.1 GI:33061431
KEYWORDS   JP 2002535963-A/181.
SOURCE     Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 22)
AUTHORS     Anderson,L., Georges,M., Spincemaille,G. and Nezer,C.D.A.
TITLE       Selection of animal based on character imprinted by parent
JOURNAL     Patent: JP 2002535963-A 181 29-OCT-2002;
            UNIVERSITY OF LIEGE,MELICA HB, SEGHERS GENTEC NV
COMMENT      OS Sus scrofa (pig)
            PN JP 2002535963-A/181
            PD 29-OCT-2002
            PF 16-DEC-1999 JP 2000588390
            PR 16-DEC-1998 EP 98204291.3
            PI LEIF ANDERSSON,MICHEL GEORGES,GEERT SPINCEMAILLE, PI CARINE
            DANIELLE ANDREE NEZER
            PC C12N15/09,A01K67/027,C12N5/06,C12Q1/68,C12N15/00,C12N5/00 CC
            /note="Microsatellite"
            FH Key      Location/Qualifiers
            FT source    1. .22
                        /organism="Sus scrofa (pig)".

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source
1. .22
/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"

Query Match      0.5%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2824 ATATATACATATATATATATA 2844
Db      1  ATATATATATATATATATATA 21

RESULT 161
BD251661/C
LOCUS      22 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Selection of animal based on character imprinted by parent.
ACCESSION BD251661
VERSION    BD251661.1 GI:33061431
KEYWORDS   JP 2002535963-A/181.
SOURCE     Sus scrofa (pig)
ORGANISM    Sus scrofa

Db      1  TGTGTGTGTGTGTGTGTGT 21

RESULT 158
AX175256
LOCUS      21 bp      DNA      linear      PAT 03-JUL-2001
DEFINITION Sequence 20 from Patent WO0144465.
ACCESSION AX175256
VERSION    AX175256.1 GI:14598624
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

REFERENCE 1
AUTHORS     Phillips,N.C. and Filion,M.C.
TITLE       Therapeutically useful synthetic oligonucleotides
JOURNAL     Patent: WO 0144465-A 20 21-JUN-2001;
            Bioniche Life Sciences Inc. (CA)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2319 GTGTGTGTGTGTGTGTGTGT 2339
Db      1  GTGTGTGTGTGTGTGTGTGT 21

RESULT 159
AX547768
LOCUS      21 bp      DNA      linear      PAT 01-MAR-2003
DEFINITION Sequence 907 from Patent WO20053141.
ACCESSION AX547768
VERSION    AX547768.1 GI:25812912
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.

```

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. (bases 1 to 22)

Andersson, L., Georges, M., Spincemaille, G. and Nezer, C.D.A. Selection of animal based on character imprinted by parent Patent: JP 2002535963-A 181 29-OCT-2002; UNIVERSITY OF LIEGE, MELICA HB, SEGHERS GENTEC NV

OS Sus scrofa (pig)
 PN JP 2002535963-A/181
 PD 29-OCT-2002
 PF 16-DEC-1999 JP 2000588390
 PR 16-DEC-1998 EP 98204291.3
 PI LEIF ANDERSSON, MICHEL GEORGES, GEERT SPINCEMAILLE, PI CARINE DANIELLE ANDREE NEZER
 PC C12N15/09 A01K67/027, C12N5/06, C12N15/00, C12N5/00 CC
 /note='Microsatellite'

FT Key Location/Qualifiers
 FT source 1..22
 /organism='Sus scrofa (pig)'
 /organism='Sus scrofa'
 /mol_type='genomic DNA'
 /db_xref='taxon:9823'

Query Match 0.5%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 3.1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
 Db 22 ATATATATATATATATATA 2

RESULT 162
 AX028362 22 bp DNA linear PAT 16-SEP-2000
 LOCUS Sequence 181 from Patent WO0036143.
 DEFINITION AX028362
 ACCESSION AX028362
 VERSION AX028362.1 GI:10189575
 KEYWORDS
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCES
 1 Georges, M., Spincemaille, G. and Andersson, L. Selecting animals for parentally imprinted traits Patent: WO 0036143-A 181 22-JUN-2000; SEGHERSGENTEC N V (BE) ; GEORGES MICHEL (BE) ; UNIV LIEGE (BE) ; SPINCEMAILLE GEERT (BE) ; MELICA HB (SE) ; ANDERSSON LEIF (SE)

FEATURES
 source 1..22
 /organism='Sus scrofa'
 /mol_type='unassigned DNA'
 /db_xref='taxon:9823'
 /note='Microsatellite'

Query Match 0.5%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 3.1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
 Db 1 ATATATATATATATATATA 21

RESULT 163
 AX028362/c 22 bp DNA linear PAT 16-SEP-2000
 LOCUS Sequence 181 from Patent WO0036143.
 DEFINITION AX028362
 ACCESSION AX028362
 VERSION AX028362.1 GI:10189575

KEYWORDS
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCES
 1 Georges, M., Spincemaille, G. and Andersson, L. Selecting animals for parentally imprinted traits Patent: WO 0036143-A 181 22-JUN-2000; SEGHERSGENTEC N V (BE) ; GEORGES MICHEL (BE) ; UNIV LIEGE (BE) ; SPINCEMAILLE GEERT (BE) ; MELICA HB (SE) ; ANDERSSON LEIF (SE)

FEATURES
 source 1..22
 /organism='Sus scrofa'
 /mol_type='unassigned DNA'
 /db_xref='taxon:9823'
 /note='Microsatellite'

Query Match 0.5%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 3.1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
 Db 22 ATATATATATATATATATA 2

RESULT 164
 AX104718 22 bp DNA linear PAT 30-APR-2001
 LOCUS Sequence 910 from Patent WO0122972.
 DEFINITION AX104718
 ACCESSION AX104718
 VERSION AX104718.1 GI:13920915
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCES
 1 Krieg, A.M., Schetter, C. and Vollmer, J.C. Immunostimulatory nucleic acids Patent: WO 0122972-A 910 05-APR-2001; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)

FEATURES
 source 1..22
 /organism='synthetic construct'
 /mol_type='unassigned DNA'
 /db_xref='taxon:32630'

Query Match 0.5%; Score 19.4; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 3.1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
 Db 1 ATATATATATATATATATA 21

RESULT 165
 AX104718/c 22 bp DNA linear PAT 30-APR-2001
 LOCUS Sequence 910 from Patent WO0122972.
 DEFINITION AX104718
 ACCESSION AX104718
 VERSION AX104718.1 GI:13920915
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCES
 1 Krieg, A.M., Schetter, C. and Vollmer, J.C. Immunostimulatory nucleic acids Patent: WO 0122972-A 910 05-APR-2001; UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical

QY	2824	ATATATACATATATATATATA	2844
Db	22	ATATATATATATATATATATA	2
RESULT 168			
AX116747/C			
LOCUS	AX116747	24 bp	DNA
DEFINITION	Sequence 1870 from Patent WO0129262.		
ACCESSION	AX116747		
VERSION	AX116747.1	GI:14033689	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1		
AUTHORS	Picoult-Newburg,L. and Pohl,M.		
TITLE	Genotyping reagents, kits and methods of use thereof		
JOURNAL	Patent: WO 0129262-A 1870 26-APR-2001;		
FEATURES	Orchid Biosciences, Inc. (US)		
source	Location/Qualifiers		
	1..24		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="Primer"		
Query Match	0.5%;	Score 19.4;	DB 1;
Best Local Similarity	95.2%;	Pred. No. 3.3e+02;	
Matches	20;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
QY	2318	TGTGTGTGTGTGTGTGTGT 2338	
Db	21	TGTGTGTGTGTGTGTGTGT 1	
RESULT 169			
LOCUS	A59562	26 bp	DNA
DEFINITION	Sequence 15 from Patent WO9705278.		
ACCESSION	A59562		
VERSION	A59562.1	GI:3714874	
KEYWORDS			
SOURCE	unidentified		
ORGANISM	unidentified		
REFERENCE	1		
AUTHORS	Andersson,L., Moller,M.J., Wales,R., Siggins,K.W. and Plastow,G.S.		
TITLE	METHODS FOR DETERMINING THE COAT COLOUR GENOTYPE OF A PIG		
JOURNAL	Patent: WO 9705278-A 15 13-FEB-1997;		
FEATURES	DALGETY PLC (GB)		
source	Location/Qualifiers		
	1..26		
	/organism="unidentified"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32644"		
Query Match	0.5%;	Score 19.4;	DB 1;
Best Local Similarity	80.0%;	Pred. No. 3.6e+02;	
Matches	20;	Conservative 2;	Mismatches 3; Indels 0; Gaps 0;
QY	1796	ACAGTGACGCTCTGGTCCTTTGGGT 1820	
Db	2	AAAGTGAYCTGGTCCTATSGAT 26	
RESULT 170			
LOCUS	A82434	26 bp	DNA
DEFINITION	Sequence 22 from Patent WO9854360.		
ACCESSION	A82434		
VERSION	A82434.1	GI:6732182	
KEYWORDS			

QY	2824	ATATATACATATATATATATA	2844
Db	22	ATATATATATATATATATATA	2
RESULT 168			
AX116747/C			
LOCUS	AX116747	24 bp	DNA
DEFINITION	Sequence 1870 from Patent WO0129262.		
ACCESSION	AX116747		
VERSION	AX116747.1	GI:14033689	
KEYWORDS	synthetic construct		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1		
AUTHORS	Picoult-Newburg,L. and Pohl,M.		
TITLE	Genotyping reagents, kits and methods of use thereof		
JOURNAL	Patent: WO 0129262-A 1870 26-APR-2001;		
FEATURES	Orchid Biosciences, Inc. (US)		
source	Location/Qualifiers		
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	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="Primer"		
Query Match	0.5%;	Score 19.4;	DB 1;
Best Local Similarity	95.2%;	Pred. No. 3.3e+02;	
Matches	20;	Conservative 0;	Mismatches 1;
		Indels 0;	Gaps 0;
Length	24;		
QY	2318	TGTGTGTGTGTGTGTGTGT 2338	
Db	21	TGTGTGTGTGTGTGTGTGT 1	
RESULT 169			
AX59562			
LOCUS	AX59562	26 bp	DNA
DEFINITION	Sequence 15 from Patent WO9705278.		
ACCESSION	AX59562		
VERSION	AX59562.1	GI:3714874	
KEYWORDS	unidentified		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1		
AUTHORS	Andersson,L., Moller,M.J., Wales,R., Siggins,K.W. and Plastow,G.S.		
TITLE	METHODS FOR DETERMINING THE COAT COLOUR GENOTYPE OF A PIG		
JOURNAL	Patent: WO 9705278-A 15 13-FEB-1997;		
FEATURES	DALGETY PLC (GB)		
source	Location/Qualifiers		
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	/organism="unidentified"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32644"		
Query Match	0.5%;	Score 19.4;	DB 1;
Best Local Similarity	80.0%;	Pred. No. 3.6e+02;	
Matches	20;	Conservative 2;	Mismatches 3;
		Indels 0;	Gaps 0;
Length	26;		
QY	1796	ACAGTGACGCTCTGGTCCTTTGGGT 1820	
Db	2	AAAGTGATGCTGGTCCTATSGAT 26	
RESULT 170			
AX82434			
LOCUS	AX82434	26 bp	DNA
DEFINITION	Sequence 22 from Patent WO9854360.		
ACCESSION	AX82434		
VERSION	AX82434.1	GI:6732182	
KEYWORDS			

FEATURES	source	Location/Qualifiers	Score	DB	Length	Indels	Gaps
Query Match			0.5%	19.4	26		
Best Local Similarity			80.0%				
Matches	20	Conservative	2	Mismatches	3	Indels	0
Qy	1796	AGAGTGACGCTCGTCTTTGGGGT 1820					
Db	2	AAAGTGAYGCTCGTCTCTATSGGAT 26					
RESULT 173							
BD192781/c							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							
FEATURES	source	Location/Qualifiers	Score <td>DB<td>Length</td><td>Indels</td><td>Gaps</td></td>	DB <td>Length</td> <td>Indels</td> <td>Gaps</td>	Length	Indels	Gaps
Query Match			0.5%	19.2	24		
Best Local Similarity			87.5%				
Matches	21	Conservative	0	Mismatches	3	Indels	0
Qy	984	GAAGGCTGGGCTCCCGCCCGT 1007					
Db	24	GAAGGCTGGGCTCGCCACCGT 1					
RESULT 174							
E32221/c							
LOCUS							
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							

		/mol_type="genomic DNA"	
Query Match		0.5%; Score 19; DB 1; Length 24;	
Best Local Similarity		69.6%; Pred. No. 3.7e+02;	
Matches		16; Conservative	6; Mismatches 1; Indels 0; Gaps 0;
Qy		1618 CACAGGACCTGGCTCCGCCGAA 1640	
Db		24 CAYCGGAYCTGGCGYCGGSAA 2	
RESULT 179			
AX080281/c		27 bp	DNA linear PAT 22-FEB-2001
LOCUS		AX080281	
DEFINITION		Sequence 8 from Patent WO0107632.	
ACCESSION		AX080281	
VERSION		AX080281.1	GI:13159750
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1	
AUTHORS		Perez, P. and Garcia, D.	
TITLE		Method for obtaining isogenic transgenic lines	
JOURNAL		Patent: WO 0107632-A 8 01-FEB-2001;	
Rhubio (FR)			
FEATURES		Location/Qualifiers	
source		1. .27	
		/organism="synthetic construct"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:32630"	
		/note="synthetic construct"	
Query Match		0.5%; Score 19; DB 1; Length 27;	
Best Local Similarity		81.5%; Pred. No. 4.1e+02;	
Matches		22; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
Qy		3639 GGGCAGCTGTCCTTGTGCTGCAG 3665	
Db		27 GAGCAGCTGAAGCTTGATGCTGCAG 1	
RESULT 180			
BD192780		22 bp	DNA linear PAT 17-JUL-2003
LOCUS		BD192780	
DEFINITION		Generation, characterization and isolation of neuroepithelial stem cells and lineage restricted intermediate precursor.	
ACCESSION		BD192780	
VERSION		BD192780.1	GI:33002519
KEYWORDS		JP 2002513291-A/7.	
SOURCE		Staphylococcus aureus	
ORGANISM		Staphylococcus aureus	
REFERENCE		1	
AUTHORS		Bacteria; Firmicutes; Bacillales; Staphylococcus.	
TITLE		Rao, M.S., Proschel, M.M. and Muftaba, T.	
JOURNAL		Generation, characterization and isolation of neuroepithelial stem cells and lineage restricted intermediate precursor	
COMMENT		Patent: JP 2002513291-A 7 08-MAY-2002;	
		UNIVERSITY OF UTAH RESEARCH FOUNDATION	
		PN JP 2002513291-A/7	
		PD 08-MAY-2002	
		PF 07-MAY-1998	JP 1998548581
		PR 07-MAY-1997	US 08/852744, 06-MAY-1998 US 09/073881 PI
		MAHENDRA S RAO, MARGOT WAYER PROSCHEL, TAHMINA MUJTABA PC	
		C12N5/06, C12N5/08	
		CC Strandedness: Single;	
		CC Topology: Linear;	
		FH Key	Location/Qualifiers.
FEATURES		Location/Qualifiers	
source		1. .22	
		/organism="Staphylococcus aureus"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:1280"	
Query Match		0.5%; Score 18.8; DB 1; Length 23;	
Best Local Similarity		90.9%; Pred. No. 3.8e+02;	
Matches		20; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy		2315 GTCTGTGTGTGTGTGTGCT 2336	
Db		2 GTATGTGTGTGTGTGTGTGT 23	
RESULT 181			
AX486835/c		22 bp	DNA linear PAT 16-AUG-2002
LOCUS		AX486835	
DEFINITION		Sequence 4135 from Patent WO02053728.	
ACCESSION		AX486835	
VERSION		AX486835.1	GI:22320983
KEYWORDS		Candida albicans	
SOURCE		Candida albicans	
ORGANISM		Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.	
REFERENCE		1	
AUTHORS		Rosmer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.	
TITLE		Gene disruption methodologies for drug target discovery	
JOURNAL		Patent: WO 02053728-A 4135 11-JUL-2002;	
Elitra Pharmaceuticals, Inc. (US)			
FEATURES		Location/Qualifiers	
source		1. .22	
		/organism="Candida albicans"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:5476"	
Query Match		0.5%; Score 18.8; DB 1; Length 22;	
Best Local Similarity		90.9%; Pred. No. 3.6e+02;	
Matches		20; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy		2322 TGTGTGTGTGTGTGTGTGTG 2343	
Db		22 TGTACGTGTGTGTGTGTGTGTG 1	
RESULT 182			
AX926722		23 bp	DNA linear PAT 19-DEC-2003
LOCUS		AX926722	
DEFINITION		Sequence 5 from Patent WO03085133.	
ACCESSION		AX926722	
VERSION		AX926722.1	GI:40247008
KEYWORDS		synthetic construct	
SOURCE		synthetic construct	
ORGANISM		artificial sequences.	
REFERENCE		1	
AUTHORS		Nagaraju, J.G.	
TITLE		Novel flier-PCR primers and method of identifying genotyping diverse genomes of plant and animal systems including rice varieties, a kit thereof	
JOURNAL		Patent: WO 03085133-A 5 16-OCT-2003;	
		Centre for DNA Fingerprinting and Diagnostics, Centre for; the Department of Biotechnology, Ministry of Science & Technology (IN)	
FEATURES		Location/Qualifiers	
source		1. .23	
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		/mol_type="unassigned DNA"	
		/db_xref="taxon:32630"	
		/note="A novel FISSR-PCR primer for genotyping eukaryotes"	
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Best Local Similarity		90.9%; Pred. No. 3.8e+02;	
Matches		20; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Qy		2315 GTCTGTGTGTGTGTGTGCT 2336	
Db		2 GTATGTGTGTGTGTGTGTGT 23	


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RESULT 183
AR058875/c
LOCUS          AR058875          24 bp      DNA          linear      PAT 29-SEP-1999
DEFINITION     Sequence 7 from patent US 5837835.
ACCESSION      AR058875
VERSION        AR058875.1 GI:5984452
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE         Oligonucleotide N3'-P5' phosphoramidates: hybridization and
              nuclease resistance properties
JOURNAL        Patent: US 5837835-A 7 17-NOV-1998;
FEATURES       Location/Qualifiers
               source
               0.5%; Score 18.8; DB 1; Length 24;
               Best Local Similarity 90.9%; Pred.No.3.9e+02;
               Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match
Best Local Similarity 90.9%; Score 18.8; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 22 TATATATAAAATATATATA 1

RESULT 186
AR079582/c
LOCUS          AR079582          24 bp      DNA          linear      PAT 31-AUG-2000
DEFINITION     Sequence 9 from patent US 5965720.
ACCESSION      AR079582
VERSION        AR079582.1 GI:10006326
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE         Oligonucleotide N3' .fwdarw.P5' phosphoramidates
JOURNAL        Patent: US 5965720-A 9 12-OCT-1999;
FEATURES       Location/Qualifiers
               source
               0.5%; Score 18.8; DB 1; Length 24;
               Best Local Similarity 90.9%; Pred.No.3.9e+02;
               Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match
Best Local Similarity 90.9%; Score 18.8; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 22 TATATATAAAATATATATA 1

RESULT 187
AR123289/c
LOCUS          AR123289          24 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION     Sequence 7 from patent US 6169170.
ACCESSION      AR123289
VERSION        AR123289.1 GI:14108255
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE         Oligonucleotide N3' .fwdarw.N5' phosphoramidate Duplexes
JOURNAL        Patent: US 6169170-A 7 02-JAN-2001;
FEATURES       Location/Qualifiers
               source
               0.5%; Score 18.8; DB 1; Length 24;
               Best Local Similarity 90.9%; Pred.No.3.9e+02;
               Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match
Best Local Similarity 90.9%; Score 18.8; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 22 TATATATAAAATATATATA 1

RESULT 188
AR123291/c
LOCUS          AR123291          24 bp      DNA          linear      PAT 31-AUG-2000
DEFINITION     Sequence 7 from patent US 5965720.
ACCESSION      AR079580
VERSION        AR079580.1 GI:10006324
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE         Oligonucleotide N3' .fwdarw.P5' phosphoramidates
```

PN	JP 2003012688-A/7
PD	15-JAN-2003
PF	12-JUN-2002 JP 2002171743
PI	18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI
SERBGI	M GRAYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02, C12Q1/68	
CC	Strandedness: Both;
CC	Topology: Linear;
CC	Oligonucleotide N3' to P5' phosphoramidate: synthesis and CC compound;
CC	hybridization and nuclease tolerant characteristics FH Key
FT	source Location/Qualifiers
FT	1..24 /organism='Unidentified'. Location/Qualifiers 1..24
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source	/organism='unidentified' /mol_type='genomic DNA' /db_xref='taxon:32644'
Query Match	0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity	90.9%; Pred. No. 3.9e+02;
Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	2823 TATATATACATATATATATA 2844
Db	22 TATATATAAATATATATA 1
RESULT 191	
BD188893/c	
LOCUS	BD188893 24 bp DNA linear PAT 17-JUL-2003
DEFINITION	Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;
ACCESSION	BD188893
VERSION	BD188893.1 GI:32998632
KEYWORDS	JP 2003012688-A/9.
SOURCE	unidentified
ORGANISM	unclassified
REFERENCE	1 (bases 1 to 24)
AUTHORS	Gryaznov,S.M., Schultz,R.G. and Chen,J
TITLE	Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
JOURNAL	hybridization and nuclease tolerant characteristics Patent: JP 2003012688-A 9 15-JAN-2003; LYNX THERAPEUTICS INC
COMMENT	OS Unidentified PN JP 2003012688-A/9 PD 15-JAN-2003 PF 12-JUN-2002 JP 2002171743 PI 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI SERBGI M GRAYZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC C07H19/16//C12Q1/02, C12Q1/68 CC Strandedness: Both; CC Topology: Linear; CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' CC /note= 'where the intersubunit bond is 'np'' 'where the intersubunit bond is 'np'' FH Key Location/Qualifiers FT misc feature 1..2 FT misc feature 3..4 FT misc feature 5..6 FT misc feature 7..8 FT misc feature 9..10 FT misc feature 15..16 FT misc feature 17..18

TITLE Oligonucleotide N3', fwardw.p5', phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5631135-A 7 20-MAY-1997;
FEATURES Location/Qualifiers
source 1..24
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Query Match 0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
|||||
Db 22 TATATATAAAATATATATATA 1

RESULT 197
I43129/c
LOCUS 24 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 9 from patent US 5631135.
ACCESSION I43129
VERSION I43129.1 GI:2468373
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligonucleotide N3', fwardw.p5', phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5631135-A 9 20-MAY-1997;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
|||||
Db 22 TATATATAAAATATATATATA 1

RESULT 198
I43129/c
LOCUS 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 7 from patent US 5726297.
ACCESSION I43129
VERSION I43129.1 GI:3936475
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3', P5', phosphoramidates
JOURNAL Patent: US 5726297-A 7 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
|||||
Db 22 TATATATAAAATATATATATA 1

RESULT 199
I43129/c
LOCUS 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 9 from patent US 5726297.
ACCESSION I43129
VERSION I43129.1 GI:3936477
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3', P5', phosphoramidates
JOURNAL Patent: US 5726297-A 9 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.8; DB 1; Length 24;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
|||||
Db 22 TATATATAAAATATATATATA 1

RESULT 200
AR177699
LOCUS 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 39 from patent US 6312949.
ACCESSION AR177699
VERSION AR177699.1 GI:17920054
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Sakurada,K., Palmer,T. and Gage,F.H.
TITLE Regulation of tyrosine hydroxylase expression
JOURNAL Patent: US 6312949-A 39 06-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.6; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1345 TCTGAGATCGAGATGATGAA 1364
|||||
Db 1 TCNGAGATGAGTGTGAA 20

RESULT 201
AR028293
LOCUS 25 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5858662.
ACCESSION AR028293
VERSION AR028293.1 GI:5940266
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Keating,M.T. and Morris,C.A.
TITLE Diagnosis of Williams syndrome and Williams syndrome cognitive
profile by analysis of the presence or absence of a LIM-kinase gene
JOURNAL Patent: US 5858662-A 3 12-JAN-1999;
FEATURES Location/Qualifiers

source 1. .25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1678 GACTTCGGGCTGCCCGGACGCTG 1702
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Db 1 GACTTTGGGCTGGCTGACATGC 25

RESULT 202
AR434784
LOCUS AR434784 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1207 from patent US 6656700.
ACCESSION AR434784
VERSION AR434784.1 GI:40197627
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 25)
AUTHORS Gu, Y. and Shannon, M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 1207 02-DEC-2003;
FEATURES Location/Qualifiers
source 1. .25
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.5%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2321 GTGTGTGTGTGTCGTCGTGTGTG 2345
|||||
Db 1 GTGTGTGTGTGTGAGTGTGTATTG 25

RESULT 203
A63570
LOCUS A63570 20 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 11 from Patent WO9720924.
ACCESSION A63570
VERSION A63570.1 GI:3717225
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1
AUTHORS Scaggiante, B. and Quadrioglio, F.
TITLE A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL AGENTS
JOURNAL Patent: WO 9720924-A 11 12-JUN-1997;
SAICOM S R L (IT)
COMMENT Other publication IT M1952539 19970604
Other publication AU 1175497 19970627.
FEATURES Location/Qualifiers
source 1. .20
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/db_xref="taxon:32644"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
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Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTCGTGT 2338
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/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTCGTG 2337
|||||
Db 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 206
AR129684/c
LOCUS AR129684 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 88 from patent US 6187545.
ACCESSION AR129684
VERSION AR129684.1 GI:14117581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J. and Cowse, L.M.
TITLE Antisense modulation of pepck-cycosolic expression
JOURNAL Patent: US 6187545-A 88 13-FEB-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTCGTGT 2338
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Db 1 GTGTGTGTGTGTGTGTGTGT 20

source 1. .20
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Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTCGTG 2337
|||||
Db 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 205
AR123339/c
LOCUS AR123339 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6169176.
ACCESSION AR123339
VERSION AR123339.1 GI:14108305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Bruice, T.C. and Dev, A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 5 02-JAN-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTCGTGT 2338
|||||
Db 20 GTGTGTGTGTGTGTGTGTGT 1

source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTCGTG 2337
|||||
Db 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 206
AR129684/c
LOCUS AR129684 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 88 from patent US 6187545.
ACCESSION AR129684
VERSION AR129684.1 GI:14117581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J. and Cowse, L.M.
TITLE Antisense modulation of pepck-cycosolic expression
JOURNAL Patent: US 6187545-A 88 13-FEB-2001;
FEATURES Location/Qualifiers
source 1. .20
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/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTCGTGT 2338
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

source 1. .20
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Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTCGTG 2337
|||||
Db 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 205
AR123339/c
LOCUS AR123339 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6169176.
ACCESSION AR123339
VERSION AR123339.1 GI:14108305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Bruice, T.C. and Dev, A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 5 02-JAN-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTCGTGT 2338
|||||
Db 20 GTGTGTGTGTGTGTGTGTGT 1

source 1. .20
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/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTCGTG 2337
|||||
Db 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 206
AR129684/c
LOCUS AR129684 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 88 from patent US 6187545.
ACCESSION AR129684
VERSION AR129684.1 GI:14117581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J. and Cowse, L.M.
TITLE Antisense modulation of pepck-cycosolic expression
JOURNAL Patent: US 6187545-A 88 13-FEB-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTCGTGT 2338
|||||
Db 1 GTGTGTGTGTGTGTGTGTGT 20

source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTCGTG 2337
|||||
Db 20 TGTGTGTGTGTGTGTGTGTG 1

RESULT 205
AR123339/c
LOCUS AR123339 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6169176.
ACCESSION AR123339
VERSION AR123339.1 GI:14108305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Bruice, T.C. and Dev, A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 5 02-JAN-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
DB 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 207
E36173      20 bp DNA linear PAT 31-JAN-2002
LOCUS      Upstream regulatory sequence of melanocortin-1 receptor gene and
DEFINITION utilization thereof.
ACCESSION  E36173
VERSION     E36173.1 GI:18626400
KEYWORDS   JP 2000166563-A/15.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Moro,O., Ifuku,O. and Ideta,T.
TITLE     Upstream regulatory sequence of melanocortin-1 receptor gene and
JOURNAL   utilization thereof
PATENT    Patent: JP 2000166563-A 15 20-JUN-2000;
COMMENT   SHISEIDO CO LTD
OS        JP 2000166563-A/15
PD        20-JUN-2000
PF        04-DEC-1998 JP 1998345881
PR        OSAMU MORO, OJI IFUKU, TATSURO IDETA
PI        C12N15/09, C12N5/10, C12Q1/66, C12Q1/68//C07K14/705, (C12N15/09,
PC        C12R1:91),
PC        C12N15/00, C12N5/00, (C12N15/00, C12R1:91)
CC        Key source
FH        Location/Qualifiers
FT        1..20
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2842
DB 20 TATATATATATATATATATA 1

RESULT 209
AX179298      20 bp DNA linear PAT 03-JUL-2001
LOCUS      Sequence 1 from Patent WO0141813.
DEFINITION  AX179298
ACCESSION   AX179298
VERSION     AX179298.1 GI:14598969
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE  1
AUTHORS     Linnik,M.D. and Mcnealy,P.A.
TITLE       Methods of treating lupus based on antibody affinity and screening
            methods and compositions for use thereof
JOURNAL     Patent: WO 0141813-A 1 14-JUN-2001;
            LA JOLLA PHARMACEUTICAL COMPANY (CA)
FEATURES   source
            1..20
            Location/Qualifiers
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
DB 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 210
AX179299/c      20 bp DNA linear PAT 03-JUL-2001
LOCUS      Sequence 2 from Patent WO0141813.
DEFINITION  AX179299
ACCESSION   AX179299
VERSION     AX179299.1 GI:14598970
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE  1

```


Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATAT 2843
 ||||| ||||| ||||| ||||| |||||
 Db 20 ATATATATATATATAT 1

RESULT 214
 BD097545
 LOCUS 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Method for regulating telomeric length.
 ACCESSION BD097545
 VERSION WO 0160996-A/9.
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Ota,K. and Shibata,T.
 TITLE Method for regulating telomeric length
 JOURNAL Patent: WO 0160996-A 9 23-AUG-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, JAPAN SCIENCE AND
 TECHNOLOGY CORP, KUNIHIO OTA, TAKEHIKO SHIBATA

COMMENT
 OS Artificial Sequence
 FN WO 0160996-A/9
 PD 23-AUG-2001
 PF 14-FEB-2001 WO 2001JP001024
 PR 18-FEB-2000 JP OOP 41929
 PI KUNIHIO OTA, TAKEHIKO SHIBATA
 PC C12N15/09,A61K35/76,A61K38/00,A61K48/00,A61P35/00,A61P43/00,
 PC C07H21/00,
 PC C07K14/395,C12N9/16
 CC Description of Artificial Sequence:synthetic DNA FH Key
 FT source 1..20
 PT Location/Qualifiers

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 source
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
 ||||| ||||| ||||| ||||| |||||
 Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 215
 BD105781/C
 LOCUS 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION Conjugates of biologically stable polymers and polynucleotides for
 treating systemic lupus erythematosus.
 ACCESSION BD105781
 VERSION BD105781.1 GI:22651355
 KEYWORDS JP 2001354569-A/6
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Conrad,M.J. and Coutts,S.
 TITLE Conjugates of biologically stable polymers and polynucleotides for
 treating systemic lupus erythematosus
 JOURNAL Patent: JP 2001354569-A 6 25-DEC-2001;
 LA JOLLA PHARMACEUTICAL CO
 COMMENT
 OS Artificial Sequence
 FN JP 2001354569-A/6
 PD 25-DEC-2001
 PF 04-APR-2001 JP 2001106534
 PR 16-JAN-1990 US 466138,13-MAR-1990 US 494118 PI

MICHAEL J CONRAD,STEPHEN COUTTS
 PC A61K31/7088,A61K47/48,A61P37/02,C07K14/00,C12N15/00,C12N15/00
 CC Synthetic Construct
 FH Key Location/Qualifiers
 FT source 1..20
 PT /organism="Artificial Sequence".

FEATURES
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.5%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
 ||||| ||||| ||||| ||||| |||||
 Db 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 216
 AX398276/C
 LOCUS 21 bp DNA linear PAT 27-MAY-2002
 DEFINITION Sequence 1 from Patent WO0220543.
 ACCESSION AX398276
 VERSION AX398276.1 GI:21261077
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Sinha,N.
 TITLE Synthesis for oligonucleotide synthesis
 JOURNAL Patent: WO 0220543-A 1 14-MAR-2002;
 Avecia Biotechnology, Inc. (US)

FEATURES
 source
 1..21
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Sequence prepared in Example 4"

Query Match 0.5%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 3.9e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
 ||||| ||||| ||||| ||||| |||||
 Db 20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 217
 AX398277
 LOCUS 21 bp DNA linear PAT 27-MAY-2002
 DEFINITION Sequence 2 from Patent WO0220543.
 ACCESSION AX398277
 VERSION AX398277.1 GI:21261078
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Sinha,N.
 TITLE Synthesis for oligonucleotide synthesis
 JOURNAL Patent: WO 0220543-A 2 14-MAR-2002;
 Avecia Biotechnology, Inc. (US)

FEATURES
 source
 1..21
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Sequence prepared in Example 4"


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Query Match      0.5%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
Db 1 GTGTGTGTGTGTGTGTGTGT 20

RESULT 218
LOCUS AX926721/c 24 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 4 from Patent WO03085133.
ACCESSION AX926721
VERSION AX926721.1 GI:40247005
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Nagai, J.G.
TITLE Novel fssr-pcr primers and method of identifying genotyping
diverse genomes of plant and animal systems including rice
varieties, a kit thereof
JOURNAL Patent: WO 03085133-A 4 16-OCT-2003;
Centre for DNA Fingerprinting and Diagnostics, Centre for; the
Department of Biotechnology, Ministry of Science & Technology (IN)
FEATURES
source
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="A novel FISSR-PCR primer for genotyping eukaryotes"

Query Match      0.5%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTGTGT 2354
Db 24 GTGTGTGTGTGTGTGTGTGT 5

RESULT 219
LOCUS AB086601 25 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for Japanese flounder
microsatellite sequence Pol1189TUF.
ACCESSION AB086601
VERSION AB086601.1 GI:28804453
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Coimbra, M.R.M., Kobayashi, K., Koretsugu, S., Hasegawa, O., Ohara, E.,
Ozaki, A., Sakamoto, T., Naruse, K. and Okamoto, N.
TITLE A genetic linkage map of the Japanese Flounder, (Paralichthys
olivaceus)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 25)
AUTHORS Coimbra, M.R.M., Kobayashi, K., Koretsugu, S., Hasegawa, O., Ohara, E.,
Ozaki, A., Sakamoto, T., Naruse, K. and Okamoto, N.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-2002) Nobuaki Okamoto, Tokyo University of
Fisheries, Department of Aquatic Biosciences; 4-5-7 Konan,
Minato-Ku, Tokyo 108-8477, Japan
(E-mail: nokamoto@tokyo-u-fish.ac.jp, Tel: 81-3-5463-0547,
Fax: 81-3-5463-0552)
FEATURES
source
Location/Qualifiers
1. .25
/organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="forward primer for Japanese flounder microsatellite
sequence Pol1189TUF"

misc_feature
1. .25

Query Match      0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 4.8e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2331 GTGCGTGTGTGTGTGTGTGTGCA 2353
Db 2 GTGTGTGTGTGTGTGTGTGTGCA 24

RESULT 220
LOCUS AR071800/c 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 29 from patent US 5912147.
ACCESSION AR071800
VERSION AR071800.1 GI:7222688
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler, D., Basik, M. and Anderson, G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 29 15-JUN-1999;
Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTGTGTG 2333
Db 18 TCTGTGTGTGTGTGTGTGTG 1

RESULT 221
LOCUS AX482165/c 18 bp DNA linear PAT 17-AUG-2002
DEFINITION Sequence 142 from Patent EP125233.
ACCESSION AX482165
VERSION AX482165.1 GI:22316987
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van der Kuy, A.C. and Cornelissen, M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 125233-A 142 24-JUL-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3'TAG019GENE-2"

Query Match      0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 AAGCTGCTGAAGGAGGCGC 1905
Db 18 AAGCTGCTGAAGGAGGCGC 1

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RESULT 222
AX511404/c
LOCUS AX511404 18 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 142 from Patent WO02059558.
ACCESSION AX511404
VERSION AX511404.1 GI:23392281
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1. von Kuhl, A.C. and Cornelissen, M.
AUTHORS Means and methods for treatment evaluation.
TITLE Patent: WO 02059558-A 142 01-AUG-2002;
JOURNAL Amsterdam Support Diagnostics B.V. (NL)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3'TAG019GENE-2"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 AAGCTGCTGAAGGAGGCG 1905
|||||
Db 18 AAGCTGCTGAAGGAGGCG 1

RESULT 223
AX721765/c
LOCUS AX721765 18 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 144 from Patent EPI298221.
ACCESSION AX721765
VERSION AX721765.1 GI:30422356
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1. von Kuhl, A.C. and Cornelissen, M.
AUTHORS Means and methods for treatment evaluation
TITLE Patent: EP 1298221-A 144 02-APR-2003;
JOURNAL Primagene Holding B.V. (NL)
FEATURES
source
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer 3'TAG019GENE-2"
Query Match 0.5%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1888 AAGCTGCTGAAGGAGGCG 1905
|||||
Db 18 AAGCTGCTGAAGGAGGCG 1

RESULT 224
E05497
LOCUS E05497 20 bp DNA linear PAT 29-SEP-1997
DEFINITION PCR primer for detecting polymorphism of Oryza sativa and Zea
maize.
ACCESSION E05497
VERSION E05497.1 GI:2173685
KEYWORDS JP 1993244995-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct

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artificial sequences.
1 (bases 1 to 20)
AUTHORS Komatsu, Y. and Kikuchi, Y.
TITLE NEW PRIMER
JOURNAL Patent: JP 1993244995-A 7 24-SEP-1993;
COMMENT KYOWA HAKKO KOGYO CO LTD
OC Artificial gene
OS Zea mays
PN JP 1993244995-A/7
PD 24-SEP-1993
PF 24-SEP-1991 JP 1991243122
PI KOMATSU YUKI, KIKUCHI YASUHIRO
PC C12Q1/68, C12N15/11;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.5%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGC 2352
|||||
Db 2 GTGTGTGTGTGTGTGC 19

RESULT 225
BD192794
LOCUS BD192794 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor.
ACCESSION BD192794
VERSION BD192794.1 GI:33002533
KEYWORDS JP 2002513291-A/21.
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
REFERENCE
1 (bases 1 to 22)
AUTHORS Rao, M.S., Proschel, M.M. and Mujtaba, T.
TITLE Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor
JOURNAL Patent: JP 2002513291-A 21 08-MAY-2002;
COMMENT UNIVERSITY OF UTAH RESEARCH FOUNDATION
PN JP 2002513291-A/21
PD 08-MAY-2002
PF 07-MAY-1998 JP 1998548581
PR 07-MAY-1997 US 08/852744 06-MAY-1998 US 09/073881 PI
MAHENDRA S RAO, MARGOT MAYER PROSCHEL, TAHMINA MUJTABA PC
C12N5/06, C12N5/08
CC Strandedness: Single;
CC Topology: Linear;
CC Key Location/Qualifiers.
FEATURES
source
Location/Qualifiers
1. .22
/organism="Staphylococcus aureus"
/mol_type="genomic DNA"
/db_xref="taxon:1280"
Query Match 0.5%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1347 TGAGATGGAGATGATGAA 1364
|||||
Db 5 TGAGATGGAGATGATGAA 22

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```
RESULT 226
LOCUS I30547
DEFINITION Sequence 10 from patent US 5580969.
ACCESSION I30547
VERSION I30547.1 GI:1821338
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.-H.
TITLE Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL Patent: US 5580969-A 10 03-DEC-1996;
FEATURES
source
1..21
/mol_type="unassigned DNA"
/organism="unknown"
Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTCGCGTGT 2338
| | | | | | | | | | | | | | | | | | | |
Db 21 TGTGTGTGTGTGTGTGTGTGT 1

RESULT 227
LOCUS AX020772/c
DEFINITION Sequence 272 from Patent W0934016.
ACCESSION AX020772
VERSION AX020772.1 GI:10044471
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Vider,B.Z.
JOURNAL A method for identifying and characterizing cells and tissues
PATENT: WO 9934016-A 272 08-JUL-1999;
GENENA LTD (IL); VIDIR BEN ZION (IL)
FEATURES
source
1..21
/mol_type="unassigned DNA"
/organism="Homo sapiens"
Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1798 AGTGACGCTGTCGTCCTTGGG 1818
| | | | | | | | | | | | | | | | | | | |
Db 21 AGTGATGTCGTGTCCTATGGG 1

RESULT 228
LOCUS AX116107
DEFINITION Sequence 1230 from Patent W00129262.
ACCESSION AX116107
VERSION AX116107.1 GI:14033049
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE Picoult-Newburg,L. and Pohl,M.
AUTHORS Genotyping reagents, kits and methods of use thereof
TITLE
```

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JOURNAL Patent: WO 0129262-A 1230 26-APR-2001;
FEATURES Orchid Biosciences, Inc. (US)
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2320 TGTGTGTGTGTGTCGCGTGT 2340
| | | | | | | | | | | | | | | | | | | |
Db 1 TCTGTGTGTGTGTGCTGTGT 21

RESULT 229
LOCUS AX556883/c
DEFINITION Sequence 10 from Patent W002058723.
ACCESSION AX556883
VERSION AX556883.1 GI:25899981
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Vicari,A.P., Caux,C. and Laface,D.
TITLE Chemokines as adjuvants of immune response
JOURNAL Patent: WO 02058723-A 10 01-AUG-2002;
Schering Corporation (US)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTCGCGTGT 2339
| | | | | | | | | | | | | | | | | | | |
Db 21 GTGTGTGTGAGTGTGAGTGTG 1

RESULT 230
LOCUS BD089174
DEFINITION A method of arraying genome clone.
ACCESSION BD089174
VERSION BD089174.1 GI:22634784
KEYWORDS JP 2001321190-A/1418.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1418 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
COMMENT OS Artificial Sequence
PN JP 2001321190-A/1418
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
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CC      Description of Artificial Sequence:Synthetic DNA.FH      Key
FT      Location/Qualifiers
FT      source
FT      1..21
FT      /organism='Artificial Sequence'.
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    1..21
    Location/Qualifiers
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
Query Match
    0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity
    90.5%; Pred.No.4.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY      2332 TCGGTGTGTGTGTGTGTGC 2352
Db      1 TGTGTGTGTGTGTGTGTCC 21

RESULT 231
LOCUS      AB068223
DEFINITION      Synthetic construct DNA, reverse primer for human STS sts-R12616F
at 1p36.
ACCESSION      AB068223
VERSION        AB068223.1 GI:15129027
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS      Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Chira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
TITLE      A BAC-based STS-content map spanning a 35-Mb region of human
Chromosome 1p35-p36
JOURNAL      Genomics 74 (1), 55-70 (2001)
MEDLINE      21269192
PUBMED      11374902
REFERENCE
2 (bases 1 to 21)
AUTHORS      Horii,A.
DIRECT SUBMISSION
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan [E-mail:horii@mail.cc.tohoku.ac.jp.
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
    source
    1..21
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
misc_feature
    1..21
    /note="reverse primer for human STS sts-R12616F at 1p36
sts-R12616F obtained from clones B12616, B156A20,
B141M15, B137L6, B157A17, B157P23, Human BAC library
RPC1-11"
Query Match
    0.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity
    90.5%; Pred.No.4.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY      2332 TCGGTGTGTGTGTGTGTGC 2352
Db      1 TGTGTGTGTGTGTGTGTCC 21

RESULT 232
LOCUS      A57514
DEFINITION      Sequence 6 from Patent WO9632483.
ACCESSION      A57514
VERSION        A57514.1 GI:3713372

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KEYWORDS      unidentified
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
1
AUTHORS      Masucci,M.G.
TITLE      IMMUNE-EVADING PROTEINS
JOURNAL      Patent: WO 9632483-A 6 17-OCT-1996;
MASUCCI MARIA GRAZIA (SE)
COMMENT      Other publication AU 5284296 961030.
FEATURES
    source
    1..24
    Location/Qualifiers
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"
Query Match
    0.5%; Score 17.8; DB 1; Length 24;
Best Local Similarity
    90.5%; Pred.No.5.1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY      2103 CACCCCGAGCTCCAGCTCTC 2123
Db      4 CACCCCGAGCTCCAGCTCTC 24

RESULT 233
LOCUS      AR052980
DEFINITION      Sequence 10 from patent US 5833991.
ACCESSION      AR052980
VERSION        AR052980.1 GI:5977842
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 24)
AUTHORS      Masucci,M.G.
TITLE      Glycine-containing sequences conferring invisibility to the immune
system
JOURNAL      Patent: US 5833991-A 10 10-NOV-1998;
FEATURES
    source
    1..24
    Location/Qualifiers
    /organism="unknown"
    /mol_type="unassigned DNA"
Query Match
    0.5%; Score 17.8; DB 1; Length 24;
Best Local Similarity
    90.5%; Pred.No.5.1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY      2103 CACCCCGAGCTCCAGCTCTC 2123
Db      4 CACCCCGAGCTCCAGCTCTC 24

RESULT 234
LOCUS      AX117030
DEFINITION      Sequence 2153 from Patent WO0129262.
ACCESSION      AX117030
VERSION        AX117030.1 GI:14033972
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS      Picoult-Newburg,L. and Pohl,M.
TITLE      Genotyping reagents, kits and methods of use thereof
JOURNAL      Patent: WO 0129262-A 2153 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
    source
    1..24
    Location/Qualifiers
    /organism="synthetic construct"
    /mol_type="unassigned DNA"

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/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 0.5%; Score 17.8; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2338
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 21

RESULT 235
BD249753/c
LOCUS BD249753 PTHR and PTHR3 receptors. 24 bp DNA linear PAT 17-JUL-2003
DEFINITION BD249753
ACCESSION BD249753
VERSION BD249753.1 GI:33059523
KEYWORDS JP 2002531091-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Jueppner,H. and Rubin,D.A.
TITLES PTHR and PTHR3 receptors
JOURNAL Patent: JP 2002531091-A 14 24-SEP-2002;
COMMENT THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002531091-A/14
PD 24-SEP-2002
PF 30-NOV-1999 JP 2000585406
PR 30-NOV-1998 US 60/110467
PI HARALD JUEPPNER,DAVID A RUBIN
PC C12N15/09,A61K38/00,A61K45/00,A61P5/18,C07K14/705,C07K16/28,
PC C12N1/15
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,G01N33/15,G01N33/50,PC
G01N33/53,
PC G01N33/566/C12Q1/68,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: DNA Primer FH Key
Location/Qualifiers
FT source 1..24
FT /organism="Artificial Sequence".

FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.5%; Score 17.6; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1344 GTCTGAGTGGAGATCATGAAGAT 1367
DB 24 GTCTGAGAGAAGGTTCATGAAGAT 1

RESULT 236
AR302333/c
LOCUS AR302333 Sequence 17 from patent US 6541220. 24 bp DNA linear PAT 12-JUN-2003
DEFINITION AR302333
ACCESSION AR302333
VERSION AR302333.1 GI:31690581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Jueppner,H. and Rubin,D.A.
TITLES Nucleic acid encoding PTHR receptor
JOURNAL Patent: US 6541220-A 17 01-APR-2003;
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.5%; Score 17.6; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1945 TACATGATCATCGGGAGTGTCTGG 1968
DB 1 TACATGATCATGGTCAAGTGTCTGG 24

RESULT 237
AX740251
LOCUS AX740251 Sequence 7 from Patent EP1300146. 24 bp DNA linear PAT 10-MAY-2003
DEFINITION AX740251
ACCESSION AX740251
VERSION AX740251.1 GI:30523425
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hilberg,F., Brandstetter,I., van Meel,J., Bette,P. and Kleemann,R.
TITLES Pharmaceutical composition for the treatment of animal mammary tumors
JOURNAL Patent: EP 1300146-A 7 09-APR-2003;
COMMENT Boehringer Ingelheim International GmbH (DE)
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 0.5%; Score 17.6; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1945 TACATGATCATCGGGAGTGTCTGG 1968
DB 1 TACATGATCATGGTCAAGTGTCTGG 24

RESULT 238
AX743827
LOCUS AX743827 Sequence 7 from Patent WO03030910. 24 bp DNA linear PAT 14-MAY-2003
DEFINITION AX743827
ACCESSION AX743827
VERSION AX743827.1 GI:30722579
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hilberg,F., Brandstetter,I., Bette,P., Kleemann,R. and van Meel,J.
TITLES Pharmaceutical composition for the treatment of disorders of non-human mammals
JOURNAL Patent: WO 03030910-A 7 17-APR-2003;
COMMENT Boehringer Ingelheim International GmbH (DE)
FEATURES
source
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match
Best Local Similarity 0.5%; Score 17.6; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1945 TACATGATCATCGGGAGTGTCTGG 1968
DB 1 TACATGATCATGGTCAAGTGTCTGG 24
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LOCUS       BD174952                19 bp    DNA             linear     PAT 18-MAR-2003
DEFINITION   Method for examining flat epithelial cell.
ACCESSION    BD174952
VERSION      BD174952.1  GI:29120646
KEYWORDS     JP 2002272474-A/3.
SOURCE       synthetic construct
            artificial sequences.
ORGANISM     Okamoto,T.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Belotserkovskii,B., Reddy,G. and Zarling,D.
TITLE        Locked nucleic acid hybrids and methods of use
JOURNAL      Patent: WO 0063365-A 7 26-OCT-2000;
            Pangene Corporation (US)
COMMENT      ZERIA PHARMACEUTICALS CO LTD
            OS Artificial Sequence
            PN JP 2002272474-A/3
            PD 24-SEP-2002
            PF 22-MAR-2001 JP 2001083352
            PI TETSUJI OKAMOTO
            PC C12N15/09,A61K45/00,A61P35/00,C12Q1/68,C12Q1/68,G01N33/15, PC
            GOIN33/50,
            CC FGPR3 mutagenic oligonucleotide
            FH Key Location/Qualifiers
            FT source 1..19
            /organism='Artificial Sequence'.
FEATURES     source
            1..19
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1855 CCGTACCCCGCATCCCTG 1873
Db 1 CCGTACCCCTGCATCCCTG 19
RESULT 245
I31530/c
LOCUS       I31530                19 bp    DNA             linear     PAT 06-FEB-1997
DEFINITION   Sequence 442 from patent US 5582979.
ACCESSION    I31530
VERSION      I31530.1  GI:1822321
KEYWORDS     Unknown.
SOURCE       Unclassified.
ORGANISM     Weber,J.L.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
TITLE        method of using the same
JOURNAL      Patent: US 5582979-A 442 10-DEC-1996;
FEATURES     Location/Qualifiers
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGTGCGT 2336
Db 19 TGTGTGTGTGTGTGTGTGT 1
RESULT 246
AX040467/c
LOCUS       AX040467                19 bp    DNA             linear     PAT 18-NOV-2000
DEFINITION   Sequence 7 from Patent WO0063365.

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ACCESSION    AX040467.1  GI:11230259
VERSION      AX040467.1
KEYWORDS     synthetic construct
SOURCE       synthetic construct
            artificial sequences.
ORGANISM     Belotserkovskii,B., Reddy,G. and Zarling,D.
REFERENCE    1
            Locked nucleic acid hybrids and methods of use
            Patent: WO 0063365-A 7 26-OCT-2000;
            Pangene Corporation (US)
FEATURES     Location/Qualifiers
            1..19
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Z-DNA"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGTGCGT 2336
Db 19 TGTGTGTGTGTGTGTGTGT 1
RESULT 247
AX040468
LOCUS       AX040468                19 bp    DNA             linear     PAT 18-NOV-2000
DEFINITION   Sequence 8 from Patent WO0063365.
ACCESSION    AX040468
VERSION      AX040468.1  GI:11230260
KEYWORDS     synthetic construct
SOURCE       synthetic construct
            artificial sequences.
ORGANISM     Belotserkovskii,B., Reddy,G. and Zarling,D.
REFERENCE    1
            Locked nucleic acid hybrids and methods of use
            Patent: WO 0063365-A 8 26-OCT-2000;
            Pangene Corporation (US)
FEATURES     Location/Qualifiers
            1..19
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Z-DNA"
Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2318 TGTGTGTGTGTGTGTGCGT 2336
Db 1 TGTGTGTGTGTGTGTGTGT 19
RESULT 248
AX132174
LOCUS       AX132174                19 bp    DNA             linear     PAT 15-MAY-2001
DEFINITION   Sequence 3392 from Patent WO0130362.
ACCESSION    AX132174
VERSION      AX132174.1  GI:14138479
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
            Robbins,J.M. and Tritz,R.
            Ribozyme therapy for the treatment of proliferative skin and eye
            diseases

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JOURNAL Patent: WO 0130362-A 3392 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source

LOCUS 133568
DEFINITION Sequence 7 from patent US 5593834.
ACCESSION I33568
VERSION I33568.1 GI:1824359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lane,M.J., Benight,A.S. and Faldasz,B.D.
TITLE Method of preparing DNA sequences with known ligand binding characteristics
JOURNAL Patent: US 5593834-A 7 14-JAN-1997;
FEATURES Location/Qualifiers
source

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.7e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2550 TCGGCTCTGCTTTCAC 2568
|||||
Db 1 TCGGCTCTACCTTTCAC 19

RESULT 249
AR129716
LOCUS AR129716 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 120 from patent US 6187545.
ACCESSION AR129716
VERSION AR129716.1 GI:14117613
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Butler,M.M., Wyatt,J. and Cowsert,L.M.
TITLE Antisense modulation of pepck-cytosolic expression
JOURNAL Patent: US 6187545-A 120 13-FEB-2001;
FEATURES Location/Qualifiers
source

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2325 GTGTGTGTGCTGTGTG 2343
|||||
Db 1 GTGTGTGTGAGTGTGTG 19

RESULT 250
I33568
LOCUS I33568 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5593834.
ACCESSION I33568
VERSION I33568.1 GI:1824359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lane,M.J., Benight,A.S. and Faldasz,B.D.
TITLE Method of preparing DNA sequences with known ligand binding characteristics
JOURNAL Patent: US 5593834-A 7 14-JAN-1997;
FEATURES Location/Qualifiers
source

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3463 TATATATCTATATATAT 3481
|||||
Db 2 TATATATAGCTATATATAT 20

RESULT 251
I33568/c
LOCUS I33568 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 7 from patent US 5593834.
ACCESSION I33568
VERSION I33568.1 GI:1824359
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lane,M.J., Benight,A.S. and Faldasz,B.D.
TITLE Method of preparing DNA sequences with known ligand binding characteristics
JOURNAL Patent: US 5593834-A 7 14-JAN-1997;
FEATURES Location/Qualifiers
source

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3463 TATATATCTATATATAT 3481
|||||
Db 19 TATATATAGCTATATATAT 1

RESULT 252
AX462693
LOCUS AX462693 20 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 437 from Patent EP1217079.
ACCESSION AX462693
VERSION AX462693.1 GI:21885906
KEYWORDS
SOURCE Aegilops tauschii
ORGANISM Aegilops tauschii
REFERENCE 1
AUTHORS Bernard,M., Sourdis,P. and Guyomarch,H.
TITLE Microsatellite markers from Triticum tauschii
JOURNAL Patent: EP 1217079-A 437 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES Location/Qualifiers
source

Query Match 0.5%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2330 TGTGCGTGTGTGTGTGT 2348
|||||
Db 1 TGTGCGTGTGTGTGTGT 19

RESULT 253
AR126570
LOCUS AR126570 21 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6180349.
ACCESSION AR126570
VERSION AR126570.1 GI:14113163
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.


```
REFERENCE 1 (bases 1 to 21)
AUTHORS  Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
TITLE     Quantitative PCR method to enumerate DNA copy number
JOURNAL   Patent: US 6180349-A 1 30-JAN-2001;
FEATURES  Location/Qualifiers
source    1..21
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTG 2333
Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 254
AR126571
LOCUS     AR126571
DEFINITION Sequence 2 from patent US 6180349.
ACCESSION AR126571
VERSION   AR126571.1 GI:14113164
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS  Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
TITLE     Quantitative PCR method to enumerate DNA copy number
JOURNAL   Patent: US 6180349-A 2 30-JAN-2001;
FEATURES  Location/Qualifiers
source    1..21
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTG 2333
Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 255
AX203572/c
LOCUS     AX203572
DEFINITION Sequence 202 from Patent WO0153520.
ACCESSION AX203572
VERSION   AX203572.1 GI:15392997
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS  Cullen,P. and Seedorf,U.
TITLE     Gene chip for neonate screening
JOURNAL   Patent: WO 0153520-A 202 26-JUL-2001;
          Cullen, Paul (DE) ; Seedorf, Udo (DE)
FEATURES  Location/Qualifiers
source    1..21
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3667 GCCATGGCTCAGGGTGGTC 3685
Db 2 GTGTGTGTGTGTGTGTG 20

REFERENCE 1 (bases 1 to 21)
AUTHORS  Ginzinger,D.G., Godfrey,T.E., Jensen,R.H. and Gray,J.W.
TITLE     Quantitative PCR method to enumerate DNA copy number
JOURNAL   Patent: US 6180349-A 1 30-JAN-2001;
FEATURES  Location/Qualifiers
source    1..21
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTG 2333
Db 2 GTGTGTGTGTGTGTGTG 20

RESULT 256
AX613777/c
LOCUS     AX613777
DEFINITION Sequence 4802 from Patent WO02072882.
ACCESSION AX613777
VERSION   AX613777.1 GI:28409206
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1
AUTHORS  Cullen,P. and Seedorf,U.
TITLE     Coronary chip
JOURNAL   Patent: WO 02072882-A 4802 19-SEP-2002;
          OGHAM GmbH (DE)
FEATURES  Location/Qualifiers
source    1..21
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.5%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3667 GCCATGGCTCAGGGTGGTC 3685
Db 21 GCCATGGCTCAGGGTGGTC 3

RESULT 257
AR264920
LOCUS     AR264920
DEFINITION Sequence 4 from patent US 6492121.
ACCESSION AR264920
VERSION   AR264920.1 GI:29693307
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS  Kurane,R., Kanagawa,T., Kanagata,Y., Kurata,S., Yamada,K.,
          Yokomaki,T., Koyama,O. and Furusho,K.
TITLE     Method for determining a concentration of target nucleic acid
          molecules, nucleic acid probes for the method, and method for
          analyzing data obtained by the method
          Patent: US 6492121-A 4 10-DEC-2002;
FEATURES  Location/Qualifiers
source    1..30
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match      0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTGCTTCTGCTCTTTT 3285
Db 3 ATATATTTTTTTGTTTTTTTTTTTTT 29

RESULT 258
AR264926
LOCUS     AR264926
DEFINITION Sequence 10 from patent US 6492121.
ACCESSION AR264926
VERSION   AR264926.1 GI:29693313
KEYWORDS
```



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and method for analyzing data obtained by that method.
BD072871
VERSION BD072871.1 GI:22618474
KEYWORDS JP 2001286300-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 9 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/9
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12N15/00,C12M1/00,C12N15/09,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
CC Key Location/Qualifiers
FH source 1..30
FT /organism='synthetic construct'
/mb_type='genomic DNA'
/db_xref='taxon:32630'

FEATURES
source
Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
Db | ||||| ||||| ||||| ||||| |||||
3 ATATATTTTTCCTTTTCTTTTCTTTT 29

RESULT 264
BD107498
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION BD107498
ACCESSION BD107498
VERSION BD107498.1 GI:23202316
KEYWORDS JP 2002000275-A/7.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 7 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/7
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12N15/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC acid.
CC Key Location/Qualifiers
FH source 1..30
FT /organism='synthetic construct'
/mb_type='genomic DNA'
/db_xref='taxon:32630'

FEATURES
source
Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
Db | ||||| ||||| ||||| ||||| |||||
3 ATATATTTTTCCTTTTCTTTTCTTTT 29

RESULT 263
BD107492
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION BD107492
ACCESSION BD107492
VERSION BD107492.1 GI:23202310
KEYWORDS JP 2002000275-A/1.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 1 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT OS Artificial Sequence
PN JP 2002000275-A/1
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133

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Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
Db 3 ATATATTTTCTTTTCTTTTCTTTT 29

RESULT 265
BD145024 30 bp DNA linear PAT 17-JAN-2003
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145024
VERSION BD145024.1 GI:27850782
KEYWORDS JP 2002119291-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
JOURNAL and method for analyzing data obtained by that method
PATENT: JP 2002119291-A 5 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/5
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.

FEATURES
source
1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3285
Db 3 ATATATTTTCTTTTCTTTTCTTTT 29

RESULT 267
BD166025 30 bp DNA linear PAT 17-JAN-2003
LOCUS Novel nucleic acid probes, method for determining concentrations of
DEFINITION nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166025
VERSION BD166025.1 GI:27871837
KEYWORDS JP 2002191372-A/5.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
TITLE Novel nucleic acid probes, method for determining concentrations of
JOURNAL nucleic acid by using the probes, and method for analyzing data
PATENT: JP 2002191372-A 5 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/5
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC

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C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examine the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..30
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
Db 3 ATATATTTTATTTGCTTTCCTTTT 29

RESULT 268
B166030
LOCUS 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION B166030
VERSION JP 2002191372-A/10.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 10 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/10
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examine the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..30
/organism='unidentified'
/mol_type='genomic DNA'

Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
Db 3 ATATATTTTATTTGCTTTCCTTTT 29

RESULT 268
B166030
LOCUS 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION B166030
VERSION JP 2002191372-A/10.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 10 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/10
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examine the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..30
/organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..30
/organism='unidentified'
/mol_type='genomic DNA'

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/db_xref='taxon:32644'

Query Match 0.5%; Score 17.4; DB 1; Length 30;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
Db 3 ATATATTTTATTTGCTTTCCTTTT 29

RESULT 269
AX248881/C
LOCUS 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 960 from Patent WO0166800.
ACCESSION AX248881
VERSION AX248881.1 GI:15863504
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 960 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source
Location/Qualifiers
1..31
/organism='Homo sapiens'
/mol_type='unassigned DNA'
/db_xref='taxon:9606'

Query Match 0.5%; Score 17.4; DB 1; Length 31;
Best Local Similarity 85.7%; Pred. No. 7e+02;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3414 AGGGGCGCGCCCTGTGTGCAG 3434
Db 21 AGGGGCGCGCCCTGTGTGCAG 1

RESULT 270
A38159
LOCUS 22 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 3 from Patent WO9408008.
ACCESSION A38159
VERSION A38159.1 GI:2294765
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hawkins,R.E., Russell,S.J., Stevenson,F.K. and Winter,G.P.
TITLE IMPROVEMENTS IN OR RELATING TO IMMUNE RESPONSE MODIFICATION
JOURNAL Patent: WO 9408008-A 3 14-APR-1994;
MEDICAL RES COUNCIL (GB)
COMMENT Other publication CA 2145064 940414
Other publication AU 4832493 940426
Other publication JP 8501699T 960227.
FEATURES
source
Location/Qualifiers
1..22
/organism='unidentified'
/mol_type='unassigned DNA'
/db_xref='taxon:32644'

Query Match 0.5%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGACGTGGTGAGGCTG 874
Db 1 GAGGTGACGCTGGTGAGTCTG 22

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RESULT 271	AR173686	Sequence 3 from patent US 6306591.	22 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR173686					
DEFINITION	Sequence 3 from patent US 6306591.					
ACCESSION	AR173686					
VERSION	AR173686.1	GI:17914006				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 22)					
AUTHORS	Cockett,N.E. and Beever,J.E.					
TITLE	Screening for the molecular defect causing spider lamb syndrome in sheep					
JOURNAL	Patent: US 6306591-A 3 23-OCT-2001;					
FEATURES	Location/Qualifiers					
source	1..22					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	0.5%;	Score 17.2;	DB 1;	Length 22;		
Best Local Similarity	86.4%;	Pred. No. 5.6e+02;				
Matches	19;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
QY	1852	TCCCGTACCCGGCATCCCTG 1873				
Db	1	TCGCCGTACCCGTGCATCCCGC 22				
RESULT 272	A27197	Oligonucleotide primer for human heavy chain HuVH3aBACK.	23 bp	DNA	linear	PAT 23-MAY-1995
LOCUS	A27197					
DEFINITION	Oligonucleotide primer for human heavy chain HuVH3aBACK.					
ACCESSION	A27197					
VERSION	A27197.1	GI:905127				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1 (bases 1 to 23)					
AUTHORS	Jespers,L.S.A., Winter,G.P., Baier,M. and Hoogenboom,H.R.J.					
TITLE	Production of chimeric antibodies - a combinatorial approach					
JOURNAL	Patent: WO 9306213-A 32 01-APR-1993;					
FEATURES	CAMBRIDGE ANTIBODY TECH (GB); MEDICAL RES COUNCIL (GB)					
source	Location/Qualifiers					
1..23						
/organism="synthetic construct"						
/mol_type="unassigned DNA"						
/db_xref="taxon:32630"						
Query Match	0.5%;	Score 17.2;	DB 1;	Length 23;		
Best Local Similarity	86.4%;	Pred. No. 5.8e+02;				
Matches	19;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
QY	853	GAGGAGGAGCTGTTGGAGGCTG 874				
Db	1	GAGTGCAGCTGTTGGAGTCTG 22				
RESULT 275	AR077343	Sequence 58 from patent US 5962255.	23 bp	DNA	linear	PAT 31-AUG-2000
LOCUS	AR077343					
DEFINITION	Sequence 58 from patent US 5962255.					
ACCESSION	AR077343					
VERSION	AR077343.1	GI:10004089				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 23)					
AUTHORS	Griffiths,A.David., Williams,S.Cameron., Waterhouse,P.Michael., Nissim,A., Winter,G.Paul., Johnson,K.Stuart. and Smith,A.John.Hammond.					
TITLE	Methods for producing recombinant vectors					
JOURNAL	Patent: US 5962255-A 58 05-OCT-1999;					
FEATURES	Location/Qualifiers					
source	1..23					
	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	0.5%;	Score 17.2;	DB 1;	Length 23;		
Best Local Similarity	86.4%;	Pred. No. 5.8e+02;				
Matches	19;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
QY	853	GAGGAGGAGCTGTTGGAGGCTG 874				
Db	1	GAGTGCAGCTGTTGGAGTCTG 22				
RESULT 273	A32939	Synthetic PCR primer HuVII3aBACK.	23 bp	DNA	linear	PAT 11-DEC-1996
LOCUS	A32939					
DEFINITION	Synthetic PCR primer HuVII3aBACK.					
ACCESSION	A32939					
VERSION	A32939.1	GI:1926588				
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	artificial sequences.					
REFERENCE	1 (bases 1 to 23)					
AUTHORS						
TITLE	METHODS FOR PRODUCING MEMBERS OF SPECIFIC BINDING PAIRS					

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Db      1  GAGGTGCAGCTGCTGGAGTCTG 22
          23 bp  DNA
          linear  PAT 16-MAY-2001
RESULT 276
AR117963
LOCUS      AR117963
DEFINITION Sequence 12 from patent US 6140471.
ACCESSION AR117963
VERSION    AR117963.1 GI:14098869
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 23)
AUTHORS    Johnson,K.Stuart., Winter,G.Paul., Griffiths,A.David.,
           Smith,A.John.Hammond, and Waterhouse,P.Michael.
TITLE      Methods for producing members of specific binding pairs
JOURNAL    Patent: US 6140471-A 12 31-OCT-2000;
FEATURES   Location/Qualifiers
            1..23
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      853  GAGGAGGAGCTGCTGGAGGCTG 874
          |||||
          1  GAGGTGCAGCTGCTGGAGTCTG 22

Db      1  GAGGTGCAGCTGCTGGAGTCTG 22
          |||||
          1  GAGGTGCAGCTGCTGGAGTCTG 22

RESULT 278
CQ802102
LOCUS      CQ802102
DEFINITION Sequence 87 from Patent WO2004007717.
ACCESSION CQ802102
VERSION    CQ802102.1 GI:47058632
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Unger,C.M., Beste,G., Jensen,K.H., Zehetmeier,C., Knauer,R.,
           Quelbenzu,B.L., Torella,C. and Ilag,L.L.
TITLE      Proteomic screen to identify disease-related biological
           molecules and inhibitors thereto
JOURNAL    Patent: WO 2004007717-A 87 22-JAN-2004;
           Xerion Pharmaceuticals AG (DE)
FEATURES   Location/Qualifiers
            1..23
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: primer"
Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      853  GAGGAGGAGCTGCTGGAGGCTG 874
          |||||
          1  GAGGTGCAGCTGCTGGAGTCTG 22

Db      1  GAGGTGCAGCTGCTGGAGTCTG 22
          |||||
          1  GAGGTGCAGCTGCTGGAGTCTG 22

RESULT 279
CQ846562
LOCUS      CQ846562
DEFINITION Sequence 83 from Patent EP1433846.
ACCESSION CQ846562
VERSION    CQ846562.1 GI:50895792
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    McCafferty,J., Pope,A.R., Johnson,K.S., Hoogenboom,H.R.,
           Griffiths,A.D., Jackson,R.H., Holliger,K.P., Marks,J.D.,
           Clackson,T.P., Chiswell,D.J., Winter,G.P. and Bonnett,T.P.
TITLE      Phagemid-based method of producing filamentous bacteriophage
           particles displaying antibody molecules and the corresponding
           bacteriophage particles
JOURNAL    Patent: EP 1433846-A 83 30-JUN-2004;
           Cambridge Antibody Technology LTD (GB); Medical Research Council
           (GB)
FEATURES   Location/Qualifiers
            1..23
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="PCR Primer"
Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      853  GAGGAGGAGCTGCTGGAGGCTG 874
          |||||
          1  GAGGTGCAGCTGCTGGAGTCTG 22

Db      1  GAGGTGCAGCTGCTGGAGTCTG 22
          |||||
          1  GAGGTGCAGCTGCTGGAGTCTG 22

RESULT 277
BD231857
LOCUS      BD231857
DEFINITION Methods for diagnosis and treatment of hemophilia A patients with
           an inhibitor.
ACCESSION BD231857
VERSION    BD231857.1 GI:33041627
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 23)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Voorberg,J.J., Brink,E.N.V.D. and Turenhout,E.A.M.
           Methods for diagnosis and treatment of hemophilia A patients with
           an inhibitor
JOURNAL    Patent: JP 2002514422-A 5 21-MAY-2002;
           STICHTING SANQUIN BLOEDVOORZIENING
COMMENT    OS Homo sapiens (human)
           PN JP 2002514422-A/5
           PD 21-MAY-2002
           PF 2000548471
           PR 07-MAY-1999 JP 2000548471
           PI 08-MAY-1998 EP 98201543.0
           PI JOHANNES JACOBUS VOORBERG, EDWARD NORBERT VAN DEN BRINK, PI
           ELLEN ANNE MARIA TURENHOUT
           PC C12N15/09,A61K38/36,A61K39/395,A61K39/395,A61P7/04,A61P43/00,
           PC C07K16/36,
           PC C07K16/42,C12Q1/68,C12N15/00,A61K37/46
           CC Note = 'primer huV3aback'
           FH Key Location/Qualifiers
           FT primer bind (1)..(23).
           Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
Query Match      0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 280
E09110 LOCUS 23 bp DNA linear PAT 29-SEP-1997
DEFINITION Synthetic oligonucleotides for primer.
ACCESSION E09110
VERSION E09110.1 GI:22025736
KEYWORDS JP 1995115978-A/5.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Katou,T., Yamamoto,K., Nishioka,K. and Mizushima,Y.
TITLE METHOD FOR DETECTING AND CLONING ANTIBODY GENE
JOURNAL Patent: JP 1995115978-A 5 09-MAY-1995;
L T T KENKUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995115978-A/5
PD 09-MAY-1995
PF 22-OCT-1993 JP 1993287628
PI KATOU TOMOHIRO, YAMAMOTO KAZUHIKO, NISHIOKA KUZUKI, PI
PC C12N15/09.C12Q1/68.G01N33/53;
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..23
FT misc_feature 1..23 /organism='Artificial sequences' FT
FT /note='Synthetic oligonucleotide for primer of
5'-side'.
FEATURES
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Location/Qualifiers
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGGAGCTG 874
DB 1 GAGGTGCAGCTGGTGGAGCTG 22
RESULT 281
I27518 LOCUS 23 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 32 from patent US 5565332.
ACCESSION I27518
VERSION I27518.1 GI:1818294
KEYWORDS Unknow.
SOURCE Unknow.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hoogenboom,H.R.J.M., Baier,M., Jespers,L.S.A.T. and Winter,G.P.
TITLE Production of chimeric antibodies - a combinatorial approach
JOURNAL Patent: US 5565332-A 32 15-OCT-1996;
FEATURES
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Location/Qualifiers
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/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGGAGCTG 874
DB 1 GAGGTGCAGCTGGTGGAGCTG 22

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Db 1 GAGGTGCAGCTGGTGGAGCTG 22
RESULT 282
I44506 LOCUS 23 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 2 from patent US 5635177.
ACCESSION I44506
VERSION I44506.1 GI:2469219
KEYWORDS Unknow.
SOURCE Unknow.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett,B.D., Goeddel,D. and Matthews,W.
TITLE Protein tyrosine kinase agonist antibodies
JOURNAL Patent: US 5635177-A 2 03-JUN-1997;
FEATURES
source
Location/Qualifiers
1..23
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1801 GACGTCTGCTCTTTGGGGTCC 1822
DB 23 GACGTCTGCTCTTTGGGAATTC 2
RESULT 283
I95684 LOCUS 23 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 12 from patent US 5733743.
ACCESSION I95684
VERSION I95684.1 GI:3940154
KEYWORDS Unknow.
SOURCE Unknow.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Johnson,K.Stuart., Winter,G.Paul., Griffiths,A.David.,
Smith,A.John.Hammond, and Waterhouse,P.Michael.
TITLE Methods for producing members of specific binding pairs
JOURNAL Patent: US 5733743-A 12 31-MAR-1998;
FEATURES
source
Location/Qualifiers
1..23
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGGAGCTG 874
DB 1 GAGGTGCAGCTGGTGGAGCTG 22
RESULT 284
AR262782 LOCUS 23 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 2 from patent US 6331302.
ACCESSION AR262782
VERSION AR262782.1 GI:28074466
KEYWORDS Unknow.
SOURCE Unknow.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Bennett,B.D., Goeddel,D., Lee,J.M., Matthews,W., Tsai,S.P. and
Wood,W.I.

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TITLE      Protein tyrosine kinase agonist antibodies
JOURNAL    Patent: US 6331302-A 2 18-DEC-2001;
FEATURES   Location/Qualifiers
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           1..23
           /organism="unknown"
           /mol_type="genomic DNA"

Query Match
Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
Matches 19; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1801 GAGCTCTGCTCTTTGGGTCC 1822
Db 23 GAGCTCTGCTCTTTGGAATTC 2

RESULT 285
AR265406
LOCUS      AR265406                23 bp      DNA          linear      PAT 10-APR-2003
DEFINITION Sequence 58 from patent US 6492160.
ACCESSION AR265406
VERSION   AR265406.1 GI:29693938
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS   Griffiths,A.D., Williams,S.C., Waterhouse,P.M., Nissim,A.,
           Winter,G.P., Johnson,K.S. and Smith,A.J.H.
TITLE     Methods for producing members of specific binding pairs
JOURNAL   Patent: US 6492160-A 58 10-DEC-2002;
FEATURES   Location/Qualifiers
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           /organism="unknown"
           /mol_type="genomic DNA"

Query Match
Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

RESULT 286
AR301927
LOCUS      AR301927                23 bp      DNA          linear      PAT 12-JUN-2003
DEFINITION Sequence 8 from patent US 6538938.
ACCESSION AR301927
VERSION   AR301927.1 GI:31689807
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS   Fisher,W.E.
TITLE     Method for generating memory addresses for accessing memory-cell
           arrays in memory devices
JOURNAL   Patent: US 6538938-A 8 25-MAR-2003;
FEATURES   Location/Qualifiers
           1..23
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Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

TITLE      Protein tyrosine kinase agonist antibodies
JOURNAL    Patent: US 6642041-A 35 04-NOV-2003;
FEATURES   Location/Qualifiers
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           /mol_type="genomic DNA"

Query Match
Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

RESULT 287
AR428817
LOCUS      AR428817                23 bp      DNA          linear      PAT 18-DEC-2003
DEFINITION Sequence 35 from patent US 6642041.
ACCESSION AR428817
VERSION   AR428817.1 GI:40188603
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS   Chen,J., Feder,J.N., Nelson,T.C., Krystek,S.R. and Duclos,F.
TITLE     Polynucleotides encoding a novel metalloprotease, MP-1
JOURNAL   Patent: US 6642041-A 35 04-NOV-2003;
FEATURES   Location/Qualifiers
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           /organism="unknown"
           /mol_type="genomic DNA"

Query Match
Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

RESULT 288
AR438219
LOCUS      AR438219                23 bp      DNA          linear      PAT 20-FEB-2004
DEFINITION Sequence 35 from patent US 6663485.
ACCESSION AR438219
VERSION   AR438219.1 GI:42662835
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS   Niermann,M.
TITLE     Combine having a feeding device for transferring and an outlet zone
           for discharging materials
JOURNAL   Patent: US 6663485-A 35 16-DEC-2003;
FEATURES   Location/Qualifiers
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           /organism="unknown"
           /mol_type="genomic DNA"

Query Match
Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

RESULT 289
AR447097/C
LOCUS      AR447097                23 bp      DNA          linear      PAT 20-FEB-2004
DEFINITION Sequence 2 from patent US 6673343.
ACCESSION AR447097
VERSION   AR447097.1 GI:42674995
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS   Bennett,B.D., Goeddel,D.V., Lee,J.M., Matthews,W., Tsai,S.P. and
           Wood,W.I.
TITLE     SAL-S1 receptor protein tyrosine kinase agonist antibodies
JOURNAL   Patent: US 6673343-A 2 06-JAN-2004;
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FEATURES
  source
    Location/Qualifiers
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        /organism="unknown"
        /mol_type="genomic DNA"

Query Match
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  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1801 GAGCTGTGTCCTTTGGGTCC 1822
Db 23 GAGCTGTGTCCTTTGGAATTC 2

RESULT 290
AX010545
LOCUS AX010545 23 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 5 from Patent WO9958680.
ACCESSION AX010545
VERSION AX010545.1 GI:9997375
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1
  AUTHORS Voorberg,J.J., Turenhout,E.A. and Van Den Brink,E.N.
  TITLE Method for diagnosis and treatment of haemophilia a patients with
  an inhibitor
  JOURNAL Patent: WO 9958680-A 5 18-NOV-1999;
  VOORBERG JOHANNES JACOBUS (NL); DEN BRINK EDWARD NORBERT VAN (NL);
  STICHTING SANQUIN BLOEDVOORZIE (NL); TURENHOUT ELLEN ANNE MARIA
  (NL)
FEATURES
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        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
      primer_bind
        1..23
          /note="primer huVH3aback"

Query Match
  Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

RESULT 291
AX03707
LOCUS AX03707 23 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 42 from Patent WO0152904.
ACCESSION AX03707
VERSION AX03707.1 GI:15393156
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Gill,P.S. and Masood,R.
  TITLE Methods and compositions for antisense vegf oligonucleotides
  JOURNAL Patent: WO 0152904-A 42 26-JUL-2001;
  Gill, Parkash, S. (US)
FEATURES
  source
    Location/Qualifiers
      1..23
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="VEGFR-1 gene specific primers for RT-PCR"

Query Match
  Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 CAGGTGGCCCGGGCATGGAGT 1594
Db 1 CAAGTGGCCAGAGGCATGGAGT 22

RESULT 293
AX357138
LOCUS AX357138 23 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 14 from Patent WO20834.
ACCESSION AX357138
VERSION AX357138.1 GI:18674311
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Ault-Riche,D. and Kassner,P.D.
  TITLE Collections of binding proteins and tags and uses thereof for
  nested sorting and high throughput screening
  JOURNAL Patent: WO 0206834-A 14 24-JAN-2002;
  Pointilliste, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..23
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer:HuVH3aBACK"

Query Match
  Best Local Similarity 86.4%; Score 17.2; DB 1; Length 23;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

RESULT 294
AR058875
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Best Local Similarity 86.4%; Pred. No. 5.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 CAGGTGGCCCGGGCATGGAGT 1594
Db 1 CAAGTGGCCAGAGGCATGGAGT 22

RESULT 292
AX203708
LOCUS AX203708 23 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 43 from Patent WO0152904.
ACCESSION AX203708
VERSION AX203708.1 GI:15393157
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Gill,P.S. and Masood,R.
  TITLE Methods and compositions for antisense vegf oligonucleotides
  JOURNAL Patent: WO 0152904-A 43 26-JUL-2001;
  Gill, Parkash, S. (US)
FEATURES
  source
    Location/Qualifiers
      1..23
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="VEGFR-1 gene specific primers for RT-PCR"

Query Match
  Best Local Similarity 86.4%; Pred. No. 5.8e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1573 CAGGTGGCCCGGGCATGGAGT 1594
Db 1 CAAGTGGCCAGAGGCATGGAGT 22

RESULT 293
AX357138
LOCUS AX357138 23 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 14 from Patent WO20834.
ACCESSION AX357138
VERSION AX357138.1 GI:18674311
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
  REFERENCE 1
  AUTHORS Ault-Riche,D. and Kassner,P.D.
  TITLE Collections of binding proteins and tags and uses thereof for
  nested sorting and high throughput screening
  JOURNAL Patent: WO 0206834-A 14 24-JAN-2002;
  Pointilliste, Inc. (US)
FEATURES
  source
    Location/Qualifiers
      1..23
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
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        /note="Primer:HuVH3aBACK"

Query Match
  Best Local Similarity 86.4%; Pred. No. 5.8e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGAGCTGTGGAGGCTG 874
Db 1 GAGGTGCAGCTGTGGAGTCTG 22

RESULT 294
AR058875
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LOCUS AR058875 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5837835.
ACCESSION AR058875
VERSION AR058875.1 GI:5984452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 7 17-NOV-1998;
FEATURES
source
Location/Qualifiers
1..24
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Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24
RESULT 295
LOCUS AR058877 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5837835.
ACCESSION AR058877
VERSION AR058877.1 GI:5984454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates: hybridization and
nuclease resistance properties
JOURNAL Patent: US 5837835-A 9 17-NOV-1998;
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24
RESULT 296
LOCUS AR079580 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5965720.
ACCESSION AR079580
VERSION AR079580.1 GI:10006324
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 7 12-OCT-1999;
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Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24
RESULT 297
LOCUS AR079582 24 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5965720.
ACCESSION AR079582
VERSION AR079582.1 GI:10006326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidates
JOURNAL Patent: US 5965720-A 9 12-OCT-1999;
FEATURES
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Location/Qualifiers
1..24
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Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24
RESULT 298
LOCUS AR123289 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 7 from patent US 6169170.
ACCESSION AR123289
VERSION AR123289.1 GI:14108255
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE Oligonucleotide N3'-p5' phosphoramidate Duplexes
JOURNAL Patent: US 6169170-A 7 02-JAN-2001;
FEATURES
source
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24
RESULT 299
LOCUS AR123291 24 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6169170.
ACCESSION AR123291
VERSION AR123291.1 GI:14108257

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KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE          Oligonucleotide N3' to P5' phosphoramidate Duplexes
JOURNAL        Patent: US 6169170-A 9 02-JAN-2001;
FEATURES       Location/Qualifiers
source         1..24
               /organism="unknown"
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Query Match    0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
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Db 3 TATATATATTTTATATATATA 24

RESULT 300
LOCUS          24 bp DNA linear PAT 17-JUL-2003
DEFINITION    Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;
               hybridization and nuclease tolerant characteristics.
ACCESSION     BD188891
VERSION       BD188891.1 GI:32998630
KEYWORDS      JP 2003012688-A/7.
SOURCE        Unidentified
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE          Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
               hybridization and nuclease tolerant characteristics
JOURNAL        Patent: JP 2003012688-A 7 15-JAN-2003;
FEATURES       Location/Qualifiers
source         1..24
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               /db_xref="taxon:32644"

Query Match    0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
|||||
Db 3 TATATATATTTTATATATATA 24

RESULT 301
LOCUS          24 bp DNA linear PAT 17-JUL-2003
DEFINITION    Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;
               hybridization and nuclease tolerant characteristics.
ACCESSION     BD188891
VERSION       BD188891.1 GI:32998630
KEYWORDS      JP 2003012688-A/7.
SOURCE        Unidentified
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE          Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
               hybridization and nuclease tolerant characteristics
JOURNAL        Patent: JP 2003012688-A 7 15-JAN-2003;
FEATURES       Location/Qualifiers
source         1..24
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Query Match    0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
|||||
Db 3 TATATATATTTTATATATATA 24

RESULT 302
LOCUS          24 bp DNA linear PAT 06-FEB-1997
DEFINITION    Sequence 7 from patent US 5591607.
ACCESSION     I33252
VERSION       I33252.1 GI:1824043
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE          Oligonucleotide N3.fwdarw.P5' phosphoramidates: triplex DNA
               information
JOURNAL        Patent: US 5591607-A 7 07-JAN-1997;

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hybridization and nuclease tolerant characteristics.

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BD188891
BD188891.1 GI:32998632
JP 2003012688-A/9.
SOURCE        Unidentified
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE          Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
               hybridization and nuclease tolerant characteristics
JOURNAL        Patent: JP 2003012688-A 9 15-JAN-2003;
FEATURES       Location/Qualifiers
source         1..24
               /organism="unidentified"
               /mol_type="genomic DNA"
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Query Match    0.5%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
|||||
Db 3 TATATATATTTTATATATATA 24

RESULT 302
LOCUS          24 bp DNA linear PAT 06-FEB-1997
DEFINITION    Sequence 7 from patent US 5591607.
ACCESSION     I33252
VERSION       I33252.1 GI:1824043
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS        Gryaznov,S.M., Schultz,R.G. and Chen,J.-k.
TITLE          Oligonucleotide N3.fwdarw.P5' phosphoramidates: triplex DNA
               information
JOURNAL        Patent: US 5591607-A 7 07-JAN-1997;

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FEATURES
  source
    Location/Qualifiers
    1..24
    /organism="unknown"
    /mol_type="unassigned DNA"

  Query Match
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  Best Local Similarity 86.4%; Pred. No. 6e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 303
I33254
LOCUS
  DEFINITION
    Sequence 9 from patent US 5591607.
  ACCESSION
    I33254
  VERSION
    I33254.1 GI:1824045
  KEYWORDS
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 24)
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  AUTHORS
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  TITLE
    Oligonucleotide N3.fwdarw.P5' phosphoramidates: triplex DNA
    formation
  JOURNAL
    Patent: US 5591607-A 9 07-JAN-1997;
  FEATURES
    source
      Location/Qualifiers
      1..24
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
    0.5%; Score 17.2; DB 1; Length 24;
  Best Local Similarity 86.4%; Pred. No. 6e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 304
I35117
LOCUS
  DEFINITION
    Sequence 7 from patent US 5599922.
  ACCESSION
    I35117
  VERSION
    I35117.1 GI:2088485
  KEYWORDS
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 24)
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  AUTHORS
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  TITLE
    Oligonucleotide N3'-P5' phosphoramidates: hybridization and
    nuclease resistance properties
  JOURNAL
    Patent: US 5599922-A 7 04-FEB-1997;
  FEATURES
    source
      Location/Qualifiers
      1..24
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
    0.5%; Score 17.2; DB 1; Length 24;
  Best Local Similarity 86.4%; Pred. No. 6e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 305
I35519
LOCUS
  DEFINITION
    Sequence 9 from patent US 5599922.
  ACCESSION
    I35519
  VERSION
    I35519.1 GI:2088487
  KEYWORDS
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 24)
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  AUTHORS
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  TITLE
    Oligonucleotide N3'-P5' phosphoramidates: hybridization and
    nuclease resistance properties
  JOURNAL
    Patent: US 5599922-A 9 04-FEB-1997;
  FEATURES
    source
      Location/Qualifiers
      1..24
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
    0.5%; Score 17.2; DB 1; Length 24;
  Best Local Similarity 86.4%; Pred. No. 6e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 306
I43127
LOCUS
  DEFINITION
    Sequence 7 from patent US 5631135.
  ACCESSION
    I43127
  VERSION
    I43127.1 GI:2468371
  KEYWORDS
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 24)
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  AUTHORS
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  TITLE
    Oligonucleotide N3'.fwdarw.P5' phosphoramidates: hybridization and
    nuclease resistance properties
  JOURNAL
    Patent: US 5631135-A 7 20-MAY-1997;
  FEATURES
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      Location/Qualifiers
      1..24
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      /mol_type="unassigned DNA"

  Query Match
    0.5%; Score 17.2; DB 1; Length 24;
  Best Local Similarity 86.4%; Pred. No. 6e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 307
I43129
LOCUS
  DEFINITION
    Sequence 9 from patent US 5631135.
  ACCESSION
    I43129
  VERSION
    I43129.1 GI:2468373
  KEYWORDS
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 24)
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  AUTHORS
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  TITLE
    Oligonucleotide N3'.fwdarw.P5' phosphoramidates: hybridization and
    nuclease resistance properties
  JOURNAL
    Patent: US 5631135-A 9 20-MAY-1997;
  FEATURES
    source
      Location/Qualifiers
      1..24
      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
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  Best Local Similarity 86.4%; Pred. No. 6e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 308
I43129
LOCUS
  DEFINITION
    Sequence 9 from patent US 5631135.
  ACCESSION
    I43129
  VERSION
    I43129.1 GI:2468373
  KEYWORDS
    Unknown.
  ORGANISM
    Unknown.
  REFERENCE
    1 (bases 1 to 24)
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  AUTHORS
    Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
  TITLE
    Oligonucleotide N3'.fwdarw.P5' phosphoramidates: hybridization and
    nuclease resistance properties
  JOURNAL
    Patent: US 5631135-A 9 20-MAY-1997;
  FEATURES
    source
      Location/Qualifiers
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      /organism="unknown"
      /mol_type="unassigned DNA"

  Query Match
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  Best Local Similarity 86.4%; Pred. No. 6e+02;
  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

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source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.5%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 308
LOCUS 192005 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 7 from patent US 5726297.
ACCESSION 192005
VERSION 192005.1 GI:3936475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3, P5, phosphoramidates
JOURNAL Patent: US 5726297-A 7 10-MAR-1998;
FEATURES
source 1. .24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.5%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 309
LOCUS 192007 24 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 9 from patent US 5726297.
ACCESSION 192007
VERSION 192007.1 GI:3936477
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.-K.
TITLE Oligodeoxyribonucleotide N3, P5, phosphoramidates
JOURNAL Patent: US 5726297-A 9 10-MAR-1998;
FEATURES
source 1. .24
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.5%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 3 TATATATATTTTATATATATA 24

RESULT 310
LOCUS 192007 17 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for gaining probe which is for screening human Tie gene.

ACCESSION E11484
VERSION 1
KEYWORDS JP 1996143598-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Yasunaga,K., Suda,T., Iwama,A., Kurozumi,K., Shimizu,Y., Nakada,S.
TITLE ANTI-TIE MONOCLONAL ANTIBODY AND HYBRIDOMA
JOURNAL Patent: JP 1996143598-A 2 04-JUN-1996;
COMMENT YAMANOUCHI PHARMACEUT CO LTD
OS None
OC Artificial sequences.
PN JP 1996143598-A/2
PD 04-JUN-1996
PF 17-NOV-1994 JP 1994308249
PI YASUNAGA KUNIO, SUDA TOSHIO, IWAMA ATSUSHI, KUROZUMI KOICHI,
PI SHIMIZU YASUAKI, NAKADA SUSUMU, MASUYASU YASUHIKO PC
C07K16/28, C12N5/10, C12P21/08, G01N33/53, G01N33/53, PC
G01N33/577//C12N15/02,
PC (C12P21/08, C12R1:91);
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH Key Location/Qualifiers
FT source 1. .17
FT /organism="Artificial sequences".
FEATURES
source 1. .17
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1765 GAGGCGCTTGTGTGACCG 1781
Db 17 GAGGCGCTTGTGTGACCG 1

RESULT 311
LOCUS AR455908 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 18 from patent US 6686160.
ACCESSION AR455908
VERSION AR455908.1 GI:42690802
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 18 03-FEB-2004;
FEATURES
source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTG 2333
Db 1 CTGTGTGTGTGTGTGTG 17
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RESULT 312
LOCUS AR455910/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 20 from patent US 686160.
ACCESSION AR455910
VERSION AR455910.1 GI:42690804
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: US 686160-A 20 03-FEB-2004;
FEATURES
    source
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTC 2334
Db 17 TGTGTGTGTGTGTGTC 1

RESULT 313
LOCUS AX239678 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 18 from Patent WO0164948.
ACCESSION AX239678
VERSION AX239678.1 GI:15797343
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 18 07-SEP-2001;
JOURNAL Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
    source
        1..17
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer"

Query Match
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 1 CTGTGTGTGTGTGTG 17

RESULT 314
LOCUS AX239680/c 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 20 from Patent WO0164948.
ACCESSION AX239680
VERSION AX239680.1 GI:15797345
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen,W.A. and van Haeringen,H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 20 07-SEP-2001;
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FEATURES
    source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer"

Dr. van Haeringen Laboratorium B.V. (NL)
Location/Qualifiers

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTC 2334
Db 17 TGTGTGTGTGTGTGTC 1

RESULT 315
LOCUS AR071773/c 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 2 from patent US 5912147.
ACCESSION AR071773
VERSION AR071773.1 GI:7222661
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 2 15-JUN-1999;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 316
LOCUS AR071777/c 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 6 from patent US 5912147.
ACCESSION AR071777
VERSION AR071777.1 GI:7222665
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 6 15-JUN-1999;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 317
LOCUS AR071777/c 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 6 from patent US 5912147.
ACCESSION AR071777
VERSION AR071777.1 GI:7222665
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 6 15-JUN-1999;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 17; DB 1; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1
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RESULT 317
AR071778/c
LOCUS AR071778 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 7 from patent US 5912147.
ACCESSION AR071778
VERSION AR071778.1 GI:7222666
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 7 15-JUN-1999;
FEATURES
1. .18
Location/Qualifiers
/mol_type="unassigned DNA"
source

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2317 CTGTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 318
AR071779/c
LOCUS AR071779 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 8 from patent US 5912147.
ACCESSION AR071779
VERSION AR071779.1 GI:7222667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 8 15-JUN-1999;
FEATURES
1. .18
Location/Qualifiers
/mol_type="unassigned DNA"
source

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2317 CTGTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 319
AR071801/c
LOCUS AR071801 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 30 from patent US 5912147.
ACCESSION AR071801
VERSION AR071801.1 GI:7222689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 30 15-JUN-1999;
FEATURES
1. .18
Location/Qualifiers
/mol_type="unassigned DNA"
source

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2317 CTGTGTGTGTGTGTGTG 2333
Db 17 CTGTGTGTGTGTGTG 1

RESULT 320
AR071802/c
LOCUS AR071802 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 31 from patent US 5912147.
ACCESSION AR071802
VERSION AR071802.1 GI:7222690
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 31 15-JUN-1999;
FEATURES
1. .18
Location/Qualifiers
/mol_type="unassigned DNA"
source

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1

RESULT 321
AR071803/c
LOCUS AR071803 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 32 from patent US 5912147.
ACCESSION AR071803
VERSION AR071803.1 GI:7222691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 32 15-JUN-1999;
FEATURES
1. .18
Location/Qualifiers
/mol_type="unassigned DNA"
source

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1

RESULT 322
AR178165/c
LOCUS AR178165 18 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 1 from patent US 6316186.
ACCESSION AR178165
VERSION AR178165.1 GI:17921058

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/mol_type="unassigned DNA"

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1

RESULT 320
AR071802/c
LOCUS AR071802 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 31 from patent US 5912147.
ACCESSION AR071802
VERSION AR071802.1 GI:7222690
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 31 15-JUN-1999;
FEATURES
1. .18
Location/Qualifiers
/mol_type="unassigned DNA"
source

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1

RESULT 321
AR071803/c
LOCUS AR071803 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 32 from patent US 5912147.
ACCESSION AR071803
VERSION AR071803.1 GI:7222691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 32 15-JUN-1999;
FEATURES
1. .18
Location/Qualifiers
/mol_type="unassigned DNA"
source

Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTG 1

RESULT 322
AR178165/c
LOCUS AR178165 18 bp DNA linear PAT 18-DEC-2001
DEFINITION Sequence 1 from patent US 6316186.
ACCESSION AR178165
VERSION AR178165.1 GI:17921058

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KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 18)
AUTHORS       Ekins,R.Philip.
TITLE         Binding assay using binding agents with tail groups
JOURNAL       Patent: US 6316186-A 1 13-NOV-2001;
FEATURES      Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 17 GTGTGTGTGTGTGTGTG 1

RESULT 323
AR178166
LOCUS      AR178166
DEFINITION Sequence 2 from patent US 6316186.
ACCESSION  AR178166
VERSION     AR178166.1 GI:17921059
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Ekins,R.Philip.
TITLE      Binding assay using binding agents with tail groups
JOURNAL    Patent: US 6316186-A 2 13-NOV-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AR178166
LOCUS      AR178166
DEFINITION Sequence 2 from patent US 6316186.
ACCESSION  AR178166
VERSION     AR178166.1 GI:17921059
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Ekins,R.Philip.
TITLE      Binding assay using binding agents with tail groups
JOURNAL    Patent: US 6316186-A 2 13-NOV-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 1 GTGTGTGTGTGTGTGTG 17

RESULT 324
AR182079
LOCUS      AR182079
DEFINITION Sequence 28 from patent US 6337188.
ACCESSION  AR182079
VERSION     AR182079.1 GI:20224995
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE      De novo or 'universal' sequencing array
JOURNAL    Patent: US 6337188-A 28 08-JAN-2002;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AR182079
LOCUS      AR182079
DEFINITION Sequence 28 from patent US 6337188.
ACCESSION  AR182079
VERSION     AR182079.1 GI:20224995
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE      De novo or 'universal' sequencing array
JOURNAL    Patent: US 6337188-A 28 08-JAN-2002;
FEATURES    Location/Qualifiers
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            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 1 GTGTGTGTGTGTGTGTG 17

RESULT 325
AR261503
LOCUS      AR261503
DEFINITION Sequence 28 from patent US 6322968.
ACCESSION  AR261503
VERSION     AR261503.1 GI:28072570
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Head,S.R., Golet,P., Karn,J. and Boyce-Jacino,M.
TITLE      De novo or 'universal' sequencing array
JOURNAL    Patent: US 6322968-A 28 27-NOV-2001;
FEATURES    Location/Qualifiers
            source
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            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGTG 2351
Db 2 GTGTGTGTGTGTGTGTG 18

RESULT 326
AX115187
LOCUS      AX115187
DEFINITION Sequence 310 from Patent WO0129262.
ACCESSION  AX115187
VERSION     AX115187.1 GI:14032129
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS    Picoult-Newburg,L. and Pohl,M.
TITLE      Genotyping reagents, kits and methods of use thereof
JOURNAL    Patent: WO 0129262-A 310 26-APR-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match      0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGCG 2335
Db 1 GTGTGTGTGTGTGTGCG 17

RESULT 327
AX175253
LOCUS      AX175253
DEFINITION Sequence 17 from Patent WO0144465.
ACCESSION  AX175253
VERSION     AX175253.1 GI:14598621
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
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artificial sequences.
1
REFERENCE
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 17 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GTGTGTGTGTGTGTGTG 2351
|||||
Db 2 GTGTGTGTGTGTGTGTG 18

RESULT 328
LOCUS AX175254 18 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 18 from Patent WO0144465.
ACCESSION AX175254
VERSION AX175254.1 GI:14598622
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 18 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GTGTGTGTGTGTGTGTG 2351
|||||
Db 2 GTGTGTGTGTGTGTGTG 18

RESULT 329
LOCUS BD087486 18 bp DNA linear PAT 27-AUG-2002
DEFINITION De novo or universal sequencing array.
ACCESSION BD087486
VERSION BD087486.1 GI:22633096
KEYWORDS JP 2001524319-A/28.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 18)
REFERENCE
AUTHORS Head,S.R., Golet,P., Karn,J. and Jacino,M.B.
TITLE De novo or universal sequencing array
JOURNAL Patent: JP 2001524319-A 28 04-DEC-2001;
ORCHID BIOSCIENCES INC
COMMENT
OS Artificial Sequence
PN JP 2001524319-A/28
PD 04-DEC-2001
PF 20-NOV-1998 JP 2000522278
PR 21-NOV-1997 US 08/976427
PI STEVEN R HEAD, PHILIP GOLETT, JONATHAN KARN, MICHAEL BOYCE JACINO
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/50, C12N15/00, PC

artificial sequences.
1
REFERENCE
AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 17 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GTGTGTGTGTGTGTGTG 2351
|||||
Db 2 GTGTGTGTGTGTGTGTG 18

RESULT 330
LOCUS CQ818365 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 7 from Patent WO2004044581.
ACCESSION CQ818365
VERSION CQ818365.1 GI:48427038
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE
AUTHORS Mackenzie,I., Rees,C.M., Nikitenko,L.L., Bicknell,R. and Smith,D.M.
TITLE Transcriptional regulation of crlr and uses thereof
JOURNAL Patent: WO 2004044581-A 7 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2333 GCGTGTGTGTGTGTGTG 2349
|||||
Db 17 GCGTGTGTGTGTGTGTG 1

RESULT 331
LOCUS CQ818387 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 29 from Patent WO2004044581.
ACCESSION CQ818387
VERSION CQ818387.1 GI:48427060
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Mackenzie,I., Rees,C.M., Nikitenko,L.L., Bicknell,R. and Smith,D.M.
TITLE Transcriptional regulation of crlr and uses thereof
JOURNAL Patent: WO 2004044581-A 29 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
source
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 17; DB 1; Length 20;
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[illegible]

JOURNAL Patent: US 6169170-A 8 02-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 5.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2842
 |||||
 20 TATATATAAAATATATATA 1

Db

RESULT 340
 ARI30163/c
 LOCUS ARI30163 20 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 66 from patent US 6187587.
 ACCESSION ARI30163
 VERSION ARI30163.1 GI:14118060
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Popoff, I., Brown-Driver, V.L. and Cowsert, L.M.
 TITLE Antisense inhibition of e2f transcription factor 1 expression
 JOURNAL Patent: US 6187587-A 66 13-FEB-2001;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 5.8e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2325 GTGTGTGCGTGTGTGTGT 2344
 |||||
 20 GTGTGTGAGCATGTGTGTGT 1

Db

RESULT 341
 ARI77700/c
 LOCUS ARI77700 20 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 40 from patent US 6312949.
 ACCESSION ARI77700
 VERSION ARI77700.1 GI:17920055
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Sakurada, K., Palmer, T. and Gage, F.H.
 TITLE Regulation of tyrosine hydroxylase expression
 JOURNAL Patent: US 6312949-A 40 06-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 5.8e+02;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1666 ATGAAGATCGACACTTCGG 1685
 |||||
 20 ATGAAGATHGCGACTTTGG 1

Db

RESULT 342
 BD18892

Journal	Patent	US	6169170-A	8	02-JAN-2001
FEATURES	LOCUS	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
LOCUS	DEFINITION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
DEFINITION	ACCESSION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
ACCESSION	VERSION	AR130163.1	GI:14118060		
VERSION	KEYWORDS	Unknown.			
KEYWORDS	SOURCE	Unknown.			
SOURCE	ORGANISM	Unknown.			
ORGANISM	REFERENCE	1 (bases 1 to 20)			
REFERENCE	AUTHORS	Popoff, I., Brown-Driver, V.L. and Cowert, L.M.			
AUTHORS	TITLE	Antisense inhibition of e2f transcription factor 1 expression			
TITLE	JOURNAL	Patent: US 6187587-A 66 13-FEB-2001			
JOURNAL	FEATURES	Location/Qualifiers			
FEATURES	source	1..20			
source	Db	20	TATATATATAATATATATA 1		
Db	Query Match	0.4%	Score 16.8; DB 1; Length 20;		
Query Match	Best Local Similarity	90.0%;	Pred. No. 5.8e+02;		
Best Local Similarity	Matches	18; Conservative	0; Mismatches 2; Indels	0; Gaps	0;
Matches	LOCUS	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
LOCUS	DEFINITION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
DEFINITION	ACCESSION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
ACCESSION	VERSION	AR130163.1	GI:14118060		
VERSION	KEYWORDS	Unknown.			
KEYWORDS	SOURCE	Unknown.			
SOURCE	ORGANISM	Unknown.			
ORGANISM	REFERENCE	1 (bases 1 to 20)			
REFERENCE	AUTHORS	Popoff, I., Brown-Driver, V.L. and Cowert, L.M.			
AUTHORS	TITLE	Antisense inhibition of e2f transcription factor 1 expression			
TITLE	JOURNAL	Patent: US 6187587-A 66 13-FEB-2001			
JOURNAL	FEATURES	Location/Qualifiers			
FEATURES	source	1..20			
source	Db	20	TATATATATAATATATATA 1		
Db	Query Match	0.4%	Score 16.8; DB 1; Length 20;		
Query Match	Best Local Similarity	90.0%;	Pred. No. 5.8e+02;		
Best Local Similarity	Matches	18; Conservative	0; Mismatches 2; Indels	0; Gaps	0;
Matches	LOCUS	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
LOCUS	DEFINITION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
DEFINITION	ACCESSION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
ACCESSION	VERSION	AR130163.1	GI:14118060		
VERSION	KEYWORDS	Unknown.			
KEYWORDS	SOURCE	Unknown.			
SOURCE	ORGANISM	Unknown.			
ORGANISM	REFERENCE	1 (bases 1 to 20)			
REFERENCE	AUTHORS	Popoff, I., Brown-Driver, V.L. and Cowert, L.M.			
AUTHORS	TITLE	Antisense inhibition of e2f transcription factor 1 expression			
TITLE	JOURNAL	Patent: US 6187587-A 66 13-FEB-2001			
JOURNAL	FEATURES	Location/Qualifiers			
FEATURES	source	1..20			
source	Db	20	TATATATATAATATATATA 1		
Db	Query Match	0.4%	Score 16.8; DB 1; Length 20;		
Query Match	Best Local Similarity	90.0%;	Pred. No. 5.8e+02;		
Best Local Similarity	Matches	18; Conservative	0; Mismatches 2; Indels	0; Gaps	0;
Matches	LOCUS	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
LOCUS	DEFINITION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
DEFINITION	ACCESSION	AR130163	Sequence 66 from patent US 6187587.	20 bp	DNA
ACCESSION	VERSION	AR130163.1	GI:14118060		
VERSION	KEYWORDS	Unknown.			
KEYWORDS	SOURCE	Unknown.			
SOURCE	ORGANISM	Unknown.			
ORGANISM	REFERENCE	1 (bases 1 to 20)			
REFERENCE	AUTHORS	Popoff, I., Brown-Driver, V.L. and Cowert, L.M.			
AUTHORS	TITLE	Antisense inhibition of e2f transcription factor 1 expression			
TITLE	JOURNAL	Patent: US 6187587-A 66 13-FEB-2001			
JOURNAL	FEATURES	Location/Qualifiers			
FEATURES	source	1..20			
source	Db	20	TATATATATAATATATATA 1		
Db	Query Match	0.4%	Score 16.8; DB 1; Length 20;		
Query Match	Best Local Similarity	90.0%;	Pred. No. 5.8e+02;		
Best Local Similarity	Matches	18; Conservative	0; Mismatches 2; Indels	0; Gaps	0;
Matches	LOCUS	AR1			

LOCUS BD188892 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;
hybridization and nuclease tolerant characteristics.
ACCESSION BD188892
VERSION BD188892.1 GI:32998631
KEYWORDS JP 2003012688-A/8.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
JOURNAL hybridization and nuclease tolerant characteristics
Patent: JP 2003012688-A 8 15-JAN-2003;
LYNX THERAPEUTICS INC
COMMENT OS Unidentified
PN JP 2003012688-A/8
PD 15-JAN-2003
PF 12-JUN-2002 JP 2002171743
PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI
SERGEI M GRYAZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02, C12Q1/68
CC Strandedness: Both;
CC Topology: Linear;
CC /note= 'where the intersubunit bond is 'np''
CC /note= 'where the intersubunit bond is 'np''
CC /note= 'where the intersubunit bond is 'np''
CC /note= 'where the intersubunit bond is 'np''
FH Key Location/Qualifiers
FT misc_feature 1..2
FT misc_feature 3..4
FT misc_feature 5..6
FT misc_feature 7..8.
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source
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3463 TATATATATCTATATATATA 3482
|||||
Db 1 TATATATATTTTATATATA 20

RESULT 343
BD188892/c
LOCUS
DEFINITION Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound;
hybridization and nuclease tolerant characteristics.
ACCESSION BD188892
VERSION BD188892.1 GI:32998631
KEYWORDS JP 2003012688-A/8.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gryaznov,S.M., Schultz,R.G. and Chen,J.
TITLE Oligonucleotide N3' to P5' phosphoramidate: synthesis and compound
JOURNAL hybridization and nuclease tolerant characteristics
Patent: JP 2003012688-A 8 15-JAN-2003;
LYNX THERAPEUTICS INC
COMMENT OS Unidentified
PN JP 2003012688-A/8
PD 15-JAN-2003
PF 12-JUN-2002 JP 2002171743
PR 18-MAR-1994 US 08/210505,18-MAR-1994 US 08/214599 PI
SERGEI M GRYAZNOV, RONALD G SCHULTZ, JER-KANG CHEN PC
C07H19/16//C12Q1/02, C12Q1/68
CC Strandedness: Both;

CC Topology: Linear;
CC /note= 'where the intersubunit bond is 'np''
CC /note= 'where the intersubunit bond is 'np''
CC /note= 'where the intersubunit bond is 'np''
CC /note= 'where the intersubunit bond is 'np''
FH Key Location/Qualifiers
FT misc_feature 1..2
FT misc_feature 3..4
FT misc_feature 5..6
FT misc_feature 7..8.
FEATURES
source
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATA 2842
|||||
Db 20 TATATATAAAATATATATA 1

RESULT 344
E32219/c
LOCUS
DEFINITION Method for isolating satellite sequence.
ACCESSION E32219
VERSION E32219.1 GI:13021841
KEYWORDS JP 2000060559-A/21.
SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hideaki,T. and Masashi,S.
TITLE Method for isolating satellite sequence
JOURNAL Patent: JP 2000060559-A 21 29-FEB-2000;
NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT OS Haliotis discus discus
PN JP 2000060559-A/21
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR HIDEAKI TAKAHASHI,MASASHI SEKINO
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
/organism='Haliotis discus discus'.
FEATURES
source
1..20
/organism="Haliotis discus discus"
/mol_type="genomic DNA"
/sub_species="discus"
/db_xref="taxon:91233"

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGT 2337
|||||
Db 20 TGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 345
124757/c
LOCUS
DEFINITION Sequence 20 from patent US 5545551.
ACCESSION 124757

Query Match 0.4%; score 16.8; DB 1; Length 20;

AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.

TITLE Polymorphic repeats in human genes

JOURNAL Patent: US 6472154-A 337 29-OCT-2002;

FEATURES Location/Qualifiers

source 1..20

/organism="unknown"

/mol_type="genomic DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2313 TGGTCTGTGTGTGTGTGT 2332

DB 20 TGGGGTGTGTGTGTGTGT 1

RESULT 356

AX956707/c

LOCUS 20 bp DNA linear PAT 08-JAN-2004

DEFINITION Sequence 257 from Patent WO03097869.

ACCESSION AX956707

VERSION AX956707.1 GI:40785216

KEYWORDS

SOURCE Rosa sp.

ORGANISM

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids 1; Rosales; Rosaceae; Rosoideae; Rosa.

1 Suess,K.H.

Microsatellite markers for genetic analyses and the differentiation

of roses

JOURNAL Patent: WO 03097869-A 257 27-NOV-2003;

Con/Cipio GmbH (DE)

FEATURES Location/Qualifiers

source 1..20

/organism="Rosa sp."

/mol_type="unassigned DNA"

/db_xref="taxon:36598"

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2337 GTGTGTGTGTGTGTGTGT 2356

DB 20 GTGTGTGTGTGTGTGTGT 1

RESULT 357

DOGKIT1A

LOCUS 20 bp DNA linear STS 11-APR-1996

DEFINITION Canis familiaris c-KIT Protooncogene (KIT1) STS DNA, 5' primer,

sequence tagged site.

ACCESSION L77376

VERSION L77376.1 GI:1261721

KEYWORDS STS; PCR identification; PCR primer; c-KIT Protooncogene; sequence

tagged site; universal mammalian STS.

SOURCE Canis familiaris (dog)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 20)

Venta,P.J., Brouillette,J.A., Yuzbasiyan-Gurkan,V. and Brewer,G.J.

Gene-specific universal mammalian sequence-tagged sites:

application to the canine genome

Unpublished (1996)

JOURNAL Original source text: Canis familiaris DNA.

COMMENT Gene-specific universal mammalian sequence-tagged site for KIT1.

Primer for the 5' end is in exon 18. Human product is 650 bp.

Canine product is 650 bp. PCR conditions: 1 min, 94 C, 2 min, 57 C,

3 min, 72 C, 35 cycles.

FEATURES Location/Qualifiers

source 1..20

/organism="Canis familiaris"

/mol_type="genomic DNA"

/db_xref="taxon:9615"

STS 1..20

primer_bind complement(1..20)

/note="PCR primer binding site"

/evidence=experimental

Query Match 0.4%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1744 CCCGTGAAGTGGATGGGCC 1763

DB 1 CCTGTGAAGTGGATGGCACC 20

RESULT 358

AR074234

LOCUS 21 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 42 from patent US 5952490.

ACCESSION AR074234

VERSION AR074234.1 GI:10000989

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)

AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,

Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and

Imbach,J.Louis.

Oligonucleotides having a conserved G4 core sequence

Patent: US 5952490-A 42 14-SEP-1999;

JOURNAL Location/Qualifiers

source 1..21

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 6e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2920 GGGCGGGCGGTGGGGGCG 2939

DB 2 GGGCGGGCGGGGGCGGGCG 21

RESULT 359

AR098876/c

LOCUS 21 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 11 from patent US 6077685.

ACCESSION AR098876

VERSION AR098876.1 GI:12808642

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)

AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.

Tumor suppressor merlin and antibodies thereof

Patent: US 6077685-A 11 20-JUN-2000;

JOURNAL Location/Qualifiers

source 1..21

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.4%; Score 16.8; DB 1; Length 21;

Best Local Similarity 90.0%; Pred. No. 6e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1614 CATCCACAGGGACCTGGCTG 1633


```
Db      21 CATCCATAGGAGCTGGCTG 2
||||| ||||| ||||| ||||| |||||
RESULT 360
179716/c
LOCUS      179716          21 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 11 from patent US 5707863.
ACCESSION  I79716
VERSION     I79716.1 GI:3208006
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE       Tumor suppressor gene merlin
JOURNAL     Patent: US 5707863-A 11 13-JAN-1998;
FEATURES    Location/Qualifiers
            source
            1..21
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1614 CATCCACAGGAGCTGGCTG 1633
||||| ||||| ||||| ||||| |||||
Db      21 CATCCATAGGAGCTGGCTG 2

RESULT 361
AR301331
LOCUS      AR301331          21 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 22 from patent US 6538126.
ACCESSION  AR301331
VERSION     AR301331.1 GI:31689115
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Cho,J.M., Lee,Y.B., Park,Y.W., Lim,K.J., Choi,D.Y., So,H.S.,
            Kim,C.H., Kim,S.T. and Yang,J.Y.
TITLE       Hepatitis C diagnostics and vaccines
JOURNAL     Patent: US 6538126-A 22 25-MAR-2003;
FEATURES    Location/Qualifiers
            source
            1..21
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2006 TGGTGGAGGACCTGGACCGT 2025
||||| ||||| ||||| ||||| |||||
Db      1 TGGTGGTGAACCTGGACCGT 20

RESULT 362
AX020545/c
LOCUS      AX020545          21 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 45 from Patent WO9934016.
ACCESSION  AX020545
VERSION     AX020545.1 GI:10044235
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1

AUTHORS     Jolly,D.J., Chang,S.M.W., Lee,W.T.L., Townsend,K. and O'Dea,J.
TITLE       Hepatitis therapeutics
JOURNAL     Patent: US 6297048-A 60 02-OCT-2001;
FEATURES    Location/Qualifiers
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              /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AUTHORS     Vider,B.Z.
TITLE       A method for identifying and characterizing cells and tissues
JOURNAL     Patent: WO 9934016-A 45 08-JUL-1999;
GENEVA LTD (IL); VIDER BEN ZION (IL)
FEATURES    Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1798 AGTGACGCTGCTGCTTTGG 1817
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Db      21 AGTGACGCTGCTGCTTTGG 2

RESULT 363
AX032596
LOCUS      AX032596          21 bp      DNA      linear      PAT 20-SEP-2000
DEFINITION Sequence 42 from Patent EP1016715.
ACCESSION  AX032596
VERSION     AX032596.1 GI:10279534
KEYWORDS    .
SOURCE      unidentified
            unidentified
            unclassified.
REFERENCE   1
AUTHORS     Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Becker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
TITLE       Oligonucleotides having a conserved g4 core sequence
JOURNAL     Patent: EP 1016715-A 42 05-JUL-2000;
            ISIS PHARMACEUTICALS INC (US)
FEATURES    Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      0.4%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2920 GGGCGGGGGCTGGGGGGCG 2939
||||| ||||| ||||| ||||| |||||
Db      2 GGGCGGGGGCTGGGGGGCG 21

RESULT 364
AR171534/c
LOCUS      AR171534          22 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 60 from patent US 6297048.
ACCESSION  AR171534
VERSION     AR171534.1 GI:17910484
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 22)
AUTHORS     Jolly,D.J., Chang,S.M.W., Lee,W.T.L., Townsend,K. and O'Dea,J.
TITLE       Hepatitis therapeutics
JOURNAL     Patent: US 6297048-A 60 02-OCT-2001;
FEATURES    Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Thu Oct 28 12:48:19 2004

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PC (C12N15/09,C12R1:01),(C12Q1/06,C12R1:01),(C12Q1/68,C12R1:01),
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CC Nucleic acid probe for detecting pectinatus, and method for
CC detecting
CC nucleic acid derived from the bacterium
CC Location/Qualifiers
FH Key 1..22
FT source
/organism='Pectinatus frisingensis'.
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source
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/organism='Pectinatus frisingensis'
/mol_type='genomic DNA'
/db_xref='taxon:865'
Query Match 0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1140 CGAGCTCGAGCTGCTGCCG 1159
Db 22 CGCGCTCGAGCTGCTGCTG 3
RESULT 367
LOCUS BD271420 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Fab fragment libraries and method of using the same.
ACCESSION BD271420
VERSION BD271420.1 GI:33081188
KEYWORDS JP 2002543830-A/12.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hoogenboom,H.R.J.M.
TITLE Novel Fab fragment libraries and method of using the same
JOURNAL Patent: JP 2002543830-A 12 24-DEC-2002;
COMMENT DYAX CORP
OS Artificial Sequence
PN JP 2002543830-A/12
PD 24-DEC-2002
PP 18-MAY-1999 EP 99201558.6
PR HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
PI C12N15/09,C07K16/34,G01N33/53,C12N15/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
FT source 1..23
/organism='Artificial Sequence'.
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/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGGTGGAGGCTG 874
Db 1 SAGGTGACAGCTGGTGGAGTCTG 22
RESULT 368
LOCUS BD271421 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Fab fragment libraries and method of using the same.
ACCESSION BD271421
VERSION BD271421.1 GI:33081189
KEYWORDS JP 2002543830-A/13.
SOURCE synthetic construct
PC (C12N15/09,C12R1:01),(C12Q1/06,C12R1:01),(C12Q1/68,C12R1:01),
PC C12N15/00,
PC (C12N15/00,C12R1:01)
CC Nucleic acid probe for detecting pectinatus, and method for
CC detecting
CC nucleic acid derived from the bacterium
CC Location/Qualifiers
FH Key 1..22
FT source
/organism='Pectinatus frisingensis'.
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/organism='Pectinatus frisingensis'
/mol_type='genomic DNA'
/db_xref='taxon:865'
Query Match 0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1820 TCCTGCTCGGAGATCTTC 1839
Db 20 TCTTGCTCTGGGAGATCTGC 1
RESULT 365
LOCUS BD005554/c 22 bp DNA linear PAT 31-JAN-2002
DEFINITION Compositions and methods for treating intracellular diseases.
ACCESSION BD005554
VERSION BD005554.1 GI:18633925
KEYWORDS JP 2001500738-A/60.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Salberg,M., Millich,D.R. and Lee,W.T.L.
TITLE Compositions and methods for treating intracellular diseases
JOURNAL Patent: JP 2001500738-A 60 23-JAN-2001;
COMMENT CHIRON CORP,THE SCRIPPS RESEARCH INSTITUTE
OS Unidentified
PN JP 2001500738-A/60
PD 23-JAN-2001
PP 16-SEP-1997 JP 1998514832
PR MATTI SALLBERG,DAVID R MILICH,WILLIAM T L LEE PC
PI C12N15/36,C12N15/19,A61K48/00,A61K39/12,A61K39/29 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..22
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source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1820 TCCTGCTCGGAGATCTTC 1839
Db 20 TCTTGCTCTGGGAGATCTGC 1
RESULT 366
LOCUS BD107557/c 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Nucleic acid probe for detecting pectinatus, and method for
detecting nucleic acid derived from the bacterium.
ACCESSION BD107557
VERSION BD107557.1 GI:23202375
KEYWORDS JP 2002017356-A/17.
SOURCE Pectinatus frisingensis
ORGANISM Pectinatus frisingensis
Bacteria; Firmicutes; Clostridia; Clostridiales;
Acidaminococaceae; Pectinatus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Motoyama,Y., Yasuhara,T. and Takahashi,K.
TITLE Nucleic acid probe for detecting pectinatus, and method for
detecting nucleic acid derived from the bacterium
JOURNAL Patent: JP 2002017356-A 17 22-JAN-2002;
COMMENT ASahi BREWERIES LTD
OS Pectinatus frisingensis
PN JP 2002017356-A/17
PD 22-JAN-2002
PP 03-JUL-2000 JP 2000201258
PR YASUO MOTOYAMA,TAKAOMI YASUHARA,KYOKO TAKAHASHI PC
PI C12N15/09,C12Q1/04,C12Q1/06,C12Q1/68,C12Q1/68,C12M1/00,C12M1/40,
40,

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ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hoogenboom,H.R.J.M.
TITLE Novel Rab fragment libraries and method of using the same
JOURNAL Patent: JP 2002543830-A 13 24-DEC-2002;
DIAX CORP
COMMENT OS Artificial Sequence
PN JP 2002543830-A/13
PD 24-DEC-2002
PF 18-MAY-2000 JP 2000618429
PR 18-MAY-1999 EP 99201558.6
PI HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
CI2N15/09,C07K16/34,G01N33/53,C12N15/00
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FH Key Location/Qualifiers
FT source 1..23
FT /organism='Artificial Sequence'.
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/db_xref="taxon:32630"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGAGCTGTGGAGGCTG 22
RESULT 369
AX074547
LOCUS AX074547 23 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 5 from Patent WO0104159.
ACCESSION AX074547
VERSION AX074547.1 GI:12710650
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Arepally,G., Kisiel,W., Kamei,K. and Kamei,S.
TITLE Compositions and methods useful for the diagnosis and treatment of
heparin induced thrombocytopenia/thrombosis
JOURNAL Patent: WO 0104159-A 5 18-JAN-2001;
Science & Technology Corporation UNM (US)
FEATURES
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1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 GAGGTGAAGCTGTGGAGGCTG 22
RESULT 370
AX455018
LOCUS AX455018 23 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 85 from Patent WO0208453.
ACCESSION AX455018
VERSION AX455018.1 GI:21714203
KEYWORDS
SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1
AUTHORS Farr,S.B., Pickett,G.G., Neft,R.E. and Dunn,R.T.
TITLE Canine toxicity genes
JOURNAL Patent: WO 0208453-A 85 31-JAN-2002;
Phase-1 Molecular Toxicology (US)
FEATURES
source
1..23
/organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1040 AGGTGTCCCTCGAGTCCAC 1059
Db 1 AGGTGTCCCTCGAGGCCAC 20
RESULT 371
AX785090
LOCUS AX785090 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 3 from Patent WO03050531.
ACCESSION AX785090
VERSION AX785090.1 GI:32952919
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Lasters,I., Pletinckx,J., Boutonnet,N., Lauwereys,M. and
Beirnaert,E.
TITLE Method for displaying loops from immunoglobulin domains in
different contexts
JOURNAL Patent: WO 03050531-A 3 19-JUN-2003;
AlgoNomics N.V. (BE); Ablynx N.V. (BE)
FEATURES
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="VH3B-Back primer"
Query Match 0.4%; Score 16.8; DB 1; Length 23;
Best Local Similarity 81.8%; Pred. No. 6.5e+02;
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGTGGAGGCTG 874
Db 1 SAGGTGCAGCTGTGGAGTCTG 22
RESULT 372
AX799210
LOCUS AX799210 23 bp DNA linear PAT 10-OCT-2003
DEFINITION Sequence 17 from Patent WO03054016.
ACCESSION AX799210
VERSION AX799210.1 GI:37605153
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Muyldermans,S.
TITLE Method for cloning of variable domain sequences
JOURNAL Patent: WO 03054016-A 17 03-JUL-2003;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
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/db_xref="taxon:32630"
/note="VH3B-Back primer"

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/organism="synthetic construct"
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Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGGAGGCTG 874
Db 1 SAGGTGCAGCTGGTGGAGTCTG 22

RESULT 373
A57513/c
LOCUS A57513 24 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 5 from Patent WO9632483.
ACCESSION A57513
VERSION A57513.1 GI:3713371
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Masucci,M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 5 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
FEATURES Other publication AU 5284296 961030.
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2104 ACCCGCACCTCCAGCTCCTC 2123
Db 24 ACCCGCACCTCCAGCTCCTC 5

RESULT 374
A57516
LOCUS A57516 24 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 8 from Patent WO9632483.
ACCESSION A57516
VERSION A57516.1 GI:3713374
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Masucci,M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 8 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
FEATURES Other publication AU 5284296 961030.
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2103 CACCCCGACCTCCAGCTCCT 2122
Db 4 CACCCCGACCTCCAGCTCCT 23

RESULT 377
CQ828722/c
LOCUS CQ828722 24 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 440 from Patent WO2004053120.
ACCESSION CQ828722
VERSION CQ828722.1 GI:49732205
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1

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AUTHORS Weihe, E., Bieller, A. and Schaefer, M.K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 440 24-JUN-2004;
Gruenthal GmbH (DE)
FEATURES
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Best Local Similarity 0.4%; Score 16.8; DB 1; Length 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3299 TTCTATAGGATTTTCTTT 3318
Db 21 TTCTCTAGGATTTTGTTT 2
RESULT 378
LOCUS E31758 24 bp DNA linear PAT 18-JUN-2001
DEFINITION DNA encoding protein regulating the expression of fibronectin gene.
ACCESSION E31758
VERSION E31758.1 GI:13018607
KEYWORDS JP 2000014385-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 24)
Takeshi, N. and Koichi, O.
AUTHORS DNA encoding protein regulating the expression of fibronectin gene
TITLE Patent: JP 2000014385-A 4 18-JAN-2000;
JOURNAL SUMITOMO ELECTRIC IND LTD
COMMENT
OS Unidentified
PN JP 2000014385-A/4
PD 18-JAN-2000
PF 06-JUL-1998 JP 1998190001
PR TAKESHI NAKAMURA, KOICHIRO ODA
PC C12N15/09, C07K14/47, C07K16/18, C12P21/08//C12N5/10, C12P21/02,
C12Q1/68,
PC C12N15/00, C12N5/00
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CC Topology: Linear;
PH Key Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2928 CGTGGGGGGCGTGAGGGA 2947
Db 3 CGTGGGGGGCGGGAAGGA 22
RESULT 379
LOCUS A48768 23 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 106 from Patent WO9604385.
ACCESSION A48768
VERSION A48768.1 GI:2302438
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
AUTHORS Ullrich, A., Bange, J. and Kuyazev, P.
TITLE Utilization of inhibitor for treating RTK hyperfunction-induced disorder, in particular, cancer.
JOURNAL Patent: JP 2002518292-A 4 25-JUN-2002;
MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV
COMMENT
OS Artificial Sequence
PN JP 2002518292-A/4
PD 25-JUN-2002
unclassified.
1 (bases 1 to 23)
Maertens, G., Bosman, F., De, M.G. and Buyse, M.
AUTHORS PURIFIED HEPATITIS C VIRUS ENVELOPE PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
JOURNAL Patent: WO 9604385-A 106 15-FEB-1996;
INNOGENETICS NV (BE)
COMMENT Other publication CA 2172273 960215
Other publication AU 3382495 960304.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2164 GCCCACCACGAGTGGGGGCTC 2186
Db 23 GCGCTACCCAGCAGCGGGAGCTC 1
RESULT 380
LOCUS AR157364 23 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 106 from patent US 6245503.
ACCESSION AR157364
VERSION AR157364.1 GI:16218298
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 23)
Maertens, G., Bosman, F., De Martynoff, G. and Buyse, M.-A.
AUTHORS Purified hepatitis C virus envelope proteins for diagnostic and therapeutic use
TITLE Patent: US 6245503-A 106 12-JUN-2001;
JOURNAL Location/Qualifiers
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Query Match
Best Local Similarity 0.4%; Score 16.6; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2164 GCCCACCACGAGTGGGGGCTC 2186
Db 23 GCGCTACCCAGCAGCGGGAGCTC 1
RESULT 381
LOCUS BD195029 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Utilization of inhibitor for treating RTK hyperfunction-induced disorder, in particular, cancer.
ACCESSION BD195029
VERSION BD195029.1 GI:33004785
KEYWORDS JP 2002518292-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 23)
Ullrich, A., Bange, J. and Kuyazev, P.
AUTHORS Utilization of inhibitor for treating RTK hyperfunction-induced disorder, in particular, cancer
TITLE Patent: JP 2002518292-A 4 25-JUN-2002;
JOURNAL MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV
COMMENT
OS Artificial Sequence
PN JP 2002518292-A/4
PD 25-JUN-2002
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TITLE      Rhesus her2/neu, nucleotides encoding same, and uses thereof
JOURNAL    Patent: WO 2004061105-A 34 22-JUL-2004;
            ISTITUTO DI RICERCA DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
FEATURES   (IT)
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="PCR Primer"

Query Match      0.4%;      Score 16.6;      DB 1;      Length 23;
Best Local Similarity 82.6%;      Pred. No. 6.8e+02;
Matches 19. Conservative
Mismatches 4;      Indels 0;      Gaps 0;

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QY		2144	CCCACGACTGTGCCCCCGGCC	2166
Dδ		23	CCCCGACCTGCAGCCCCCAGCC	1

LOCUS CBQ841340 23 bp
DEFINITION sequence 39 from Patent WO2004061105.
ACCESSION CBQ841340
VERSION CBQ841340.1 GI:50893132

SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
1
REFERENCE
1

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FEATURES
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    location/Qualifiers
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Query Match	0.4%	Score	16.6;	DB	1;	Length	23;
Best Local Similarity	82.6%	Pred. No.	6.8e+02;				
Matches	19;	Conservative	0;	Mismatches	4;	Indels	0;
						Gaps	0;

RESULT 385
AX020199/C

Accession	Sequence	Length	Source	Reference
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AF020199	ACCESSION			
AF020199	1			GI:100043988

SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1

AUTHORS Knyazev, P.; Bangs, J.; and Winkler, D.
TITLE Use of inhibitors for the treatment of disorders related to rtk
JOURNAL Patent: WO 9937259-A 6 29-JUL-1999;
Patent: WO 9937259-A 6 29-JUL-1999;

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer zur Amplifizierung der Transmembranomane
von FGFR-4 (Wildtyp und Mutante). Antisinn-Richtung."

Query Match      0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1009 CACAAGATCTCCCGCTTCCCGCT 1031
Db 23 CAGAAGCTCTCCCTCTTCCCTCT 1

RESULT 386
AX452855/c
LOCUS      23 bp      DNA      linear      PAT 06-JUL-2002
DEFINITION Sequence 106 from Patent EP1211315.
ACCESSION  AX452855
VERSION     AX452855.1 GI:21712497
KEYWORDS   Hepatitis C virus
SOURCE      Hepatitis C virus
ORGANISM    Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE 1
AUTHORS    Maertens,G., Bosman,F., de Martynoff,G. and Buyse,M.A.
TITLE      Recombinant vectors for producing hcv envelope proteins
JOURNAL    Patent: EP 1211315-A 106 05-JUN-2002;
            Innogenetics N.V. (BE)
FEATURES   Location/Qualifiers
            source
            1..23
            /organism="Hepatitis C virus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:11103"

Query Match      0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2164 GCCCACCACGAGTGGGGCTC 2186
Db 23 GCGCTACCCAGCAGCGGGAGCTC 1

RESULT 397
AX685107/c
LOCUS      23 bp      DNA      linear      PAT 29-MAR-2003
DEFINITION Sequence 106 from Patent WO2055548.
ACCESSION  AX685107
VERSION     AX685107.1 GI:29371469
KEYWORDS   Hepatitis C virus
SOURCE      Hepatitis C virus
ORGANISM    Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE 1
AUTHORS    Maertens,G., Bosman,F. and Buyse,M.A.
TITLE      Purified Hepatitis C virus envelope proteins for diagnostic and
            therapeutic use
JOURNAL    Patent: WO 0205548-A 106 18-JUL-2002;
            Innogenetics N.V. (BE)
FEATURES   Location/Qualifiers
            source
            1..23
            /organism="Hepatitis C virus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:11103"

Query Match      0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2164 GCCCACCACGAGTGGGGCTC 2186
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Db 23 GCGCTACCCAGCAGCGGGAGCTC 1

RESULT 388
AX794949/c
LOCUS      23 bp      DNA      linear      PAT 04-OCT-2003
DEFINITION Sequence 106 from Patent WO03051912.
ACCESSION  AX794949
VERSION     AX794949.1 GI:37515795
KEYWORDS   Hepatitis C virus
SOURCE      Hepatitis C virus
ORGANISM    Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE 1
AUTHORS    Maertens,G., Depla,E. and Bosman,F.
TITLE      Purified Hepatitis C virus envelope proteins for diagnostic and
            therapeutic use
JOURNAL    Patent: WO 03051912-A 106 26-JUN-2003;
            INNOGENETICS N.V. (BE)
FEATURES   Location/Qualifiers
            source
            1..23
            /organism="Hepatitis C virus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:11103"

Query Match      0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2164 GCCCACCACGAGTGGGGCTC 2186
Db 23 GCGCTACCCAGCAGCGGGAGCTC 1

RESULT 389
AX926751/c
LOCUS      23 bp      DNA      linear      PAT 19-DEC-2003
DEFINITION Sequence 34 from Patent WO03085133.
ACCESSION  AX926751
VERSION     AX926751.1 GI:40247107
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE 1
AUTHORS    Nagaraju,J.G.
TITLE      Novel fissr-pcr primers and method of identifying genotyping
            diverse genomes of plant and animal systems including rice
            varieties, a kit thereof
JOURNAL    Patent: WO 03085133-A 34 16-OCT-2003;
            Centre for DNA Fingerprinting and Diagnostics, Centre for; the
            Department of Biotechnology, Ministry of Science & Technology (IN)
FEATURES   Location/Qualifiers
            source
            1..23
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="A novel FISRR-PCR primer for genotyping eukaryotes"

Query Match      0.4%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 6.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2309 GCTTGGTCTGTGTGTGTGTG 2331
Db 23 GCTGTGCTATTGTGTGTGTGTG 1

RESULT 390
AR071772/c
LOCUS      18 bp      DNA      linear      PAT 18-FEB-2000
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Sequence 1 from patent US 5912147.
 DEFINITION AR071772
 ACCESSION AR071772.1 GI:7222660
 VERSION AR071772.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Stoler,D., Basik,M. and Anderson,G.
 TITLE Rapid means of quantitating genomic instability
 JOURNAL Patent: US 5912147-A 1 15-JUN-1999;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2334 CGTGTGTGTGTGTGTG 2351
 Db 18 CTTGTGTGTGTGTGTG 1
 RESULT 391
 LOCUS AR071799/c 18 bp DNA linear PAT 18-FEB-2000
 DEFINITION Sequence 28 from patent US 5912147.
 ACCESSION AR071799
 VERSION AR071799.1 GI:7222667
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Stoler,D., Basik,M. and Anderson,G.
 TITLE Rapid means of quantitating genomic instability
 JOURNAL Patent: US 5912147-A 28 15-JUN-1999;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2316 TCTGTGTGTGTGTGTG 2333
 Db 18 TTTGTGTGTGTGTGTG 1
 RESULT 392
 LOCUS E28534 18 bp DNA linear PAT 18-JUN-2001
 DEFINITION Method for labeling oligonucleotide and utilization thereof.
 ACCESSION E28534
 VERSION E28534.1 GI:13025386
 KEYWORDS JP 1999075880-A/1.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
 TITLE Method for labeling oligonucleotide and utilization thereof
 JOURNAL Patent: JP 1999075880-A 1 23-MAR-1999;
 COMMENT OS Unidentified
 PN JP 1999075880-A/1
 PD 23-MAR-1999
 PF 10-JUL-1998 JP 1998195719
 PR

PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
 C12N15/09,C12Q1/68,G01N33/58,C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..18
 /organism="Unidentified".
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2823 TATATATACATATATATA 2840
 Db 1 TATATATATATATATATA 18
 RESULT 393
 LOCUS E28534/c 18 bp DNA linear PAT 18-JUN-2001
 DEFINITION Method for labeling oligonucleotide and utilization thereof.
 ACCESSION E28534
 VERSION E28534.1 GI:13025386
 KEYWORDS JP 1999075880-A/1.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
 TITLE Method for labeling oligonucleotide and utilization thereof
 JOURNAL Patent: JP 1999075880-A 1 23-MAR-1999;
 COMMENT OS Unidentified
 PN JP 1999075880-A/1
 PD 23-MAR-1999
 PF 10-JUL-1998 JP 1998195719
 PR
 PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
 C12N15/09,C12Q1/68,G01N33/58,C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..18
 /organism="Unidentified".
 FEATURES Location/Qualifiers
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 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 Query Match 0.4%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 5.9e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2823 TATATATACATATATATA 2840
 Db 18 TATATATATATATATATA 1
 RESULT 394
 LOCUS AR241816 18 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 104 from patent US 6472154.
 ACCESSION AR241816
 VERSION AR241816.1 GI:27287628
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.


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Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 104 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2822 GTATATACATATATAT 2839
Db 1 GTATATATATATATAT 18

RESULT 395
LOCUS AX355057 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 85 from Patent WO0197843.
ACCESSION AX355057
VERSION AX355057.1 GI:18619724
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 85 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATAT 2841
Db 1 ATATATATATATATAT 18

RESULT 396
LOCUS AX355057/c 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 85 from Patent WO0197843.
ACCESSION AX355057
VERSION AX355057.1 GI:18619724
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 85 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

/Note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 0.4%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATAT 2841
Db 1 ATATATATATATATAT 18

RESULT 397
LOCUS AR338196 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 17 from patent US 6569618.
ACCESSION AR338196
VERSION AR338196.1 GI:33724947
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yasue,H. and Yoshimura,M.
TITLE Diagnosis of diseases associated with coronary twitching
JOURNAL Patent: US 6569618-A 17 27-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3064 TGTTCACACACCCCAACA 3081
Db 3 TGATCCACACACCCCAACA 20

RESULT 398
LOCUS AR393666 21 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 205 from patent US 6617122.
ACCESSION AR393666
VERSION AR393666.1 GI:40120447
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hayden,M.R., Brooks-Wilson,A.R. and Pimstone,S.N.
TITLE Process for identifying modulators of ABC1 activity
JOURNAL Patent: US 6617122-A 205 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 6.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 497 ACACGCTGGACGTGCTGG 514
Db 1 ACACGCTGGGCGTGCTGG 18

RESULT 399
LOCUS AX020767/c 21 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 267 from Patent WO9934016.
ACCESSION AX020767
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Nemeth, E.F. and Brown, E.M.
CALCIUM RECEPTOR-ACTIVE MOLECULES
Patent: WO 9418959-A 2 01-SEP-1994;
BRIGHAM & WOMEN'S HOSPITAL (US); NPS PHARMA INC (US)

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RESULT 404
A25416/c
LOCUS A25416 21 bp DNA linear PAT 23-JUN-1995
DEFINITION CE gene mutagenic primer.
ACCESSION A25416
VERSION A25416.1 GI:1248088
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS
JOURNAL
FEATURES
    Location/Qualifiers
    source
        neoplastic disease
        Patent: US 5866329-A 3 02-FEB-1999;
        Location/Qualifiers
        1..21
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16.2; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1807 TGGTCCTTTGGGCTCTGCTC 1827
Db 1 TGGTCCTTTGGGCTCTGCTC 21

RESULT 407
AR084555/c
LOCUS AR084555 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 44 from patent US 5981185.
ACCESSION AR084555
VERSION AR084555.1 GI:10011326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 44 09-NOV-1999;
FEATURES
    Location/Qualifiers
    source
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16.2; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGAGATGATGAAGATGAT 1370
Db 21 GATGATGATGATGATGAT 1

RESULT 408
AR084576
LOCUS AR084576 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 65 from patent US 5981185.
ACCESSION AR084576
VERSION AR084576.1 GI:10011347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 65 09-NOV-1999;
FEATURES
    Location/Qualifiers
    source
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16.2; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGAGATGATGAAGATGAT 1370
Db 1 GATGATGATGATGATGAT 21

RESULT 409
AR084576
LOCUS AR084576 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 65 from patent US 5981185.
ACCESSION AR084576
VERSION AR084576.1 GI:10011347
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 65 09-NOV-1999;
FEATURES
    Location/Qualifiers
    source
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16.2; DB 1; Length 21;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGAGATGATGAAGATGAT 1370
Db 1 GATGATGATGATGATGAT 21

RESULT 409
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AR121232/c
 LOCUS AR121232 21 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 12 from patent US 6159710.
 ACCESSION AR121232
 VERSION AR121232.1 GI:14104808
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 21)
 Fraser,N.W., Zabolotny,J.M. and Krummenacher,C.F.
 Method and compositions for stabilizing unstable gene transcripts
 Patent: US 6159710-A 12 12-DEC-2000;
 JOURNAL Location/Qualifiers
 FEATURES
 source
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 183 CGGGAGGACGAGGCTGAGGA 203
 Db 21 CGAGGAGGAGGAGGAGGA 1
 RESULT 410
 LOCUS I32944 21 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 5 from patent US 5589451.
 ACCESSION I32944
 VERSION I32944.1 GI:1823735
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 21)
 Wilson,S.E.
 Methods and treatments for corneal healing with hepatocyte and
 keratinocyte growth factors
 Patent: US 5589451-A 5 31-DEC-1996;
 JOURNAL Location/Qualifiers
 FEATURES
 source
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21
 RESULT 411
 LOCUS I87090 21 bp DNA linear PAT 10-JUN-1998
 DEFINITION Sequence 4 from patent US 5703047.
 ACCESSION I87090
 VERSION I87090.1 GI:3206808
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 21)
 Wilson,S.E.
 Methods and treatments for corneal healing with growth factors
 Patent: US 5703047-A 4 30-DEC-1997;
 JOURNAL Location/Qualifiers
 FEATURES
 source
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21

/mol_type="unassigned DNA"
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21
 RESULT 412
 LOCUS BD132045 21 bp DNA linear PAT 18-SEP-2002
 DEFINITION Gene associated with neoplastic disease or malignancy associated
 ACCESSION BD132045
 VERSION BD132045.1 GI:23226990
 KEYWORDS JP 2002503450-A/2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 21)
 Black,K., Ljubimova,J.Y. and Demetriou,A.A.
 Gene associated with neoplastic disease or malignancy associated
 Patent: JP 2002503450-A 2 05-FEB-2002;
 JOURNAL CEDARS SINAI MEDICAL CENTER
 COMMENT OS Homo sapiens (human)
 PN JP 2002503450-A/2
 PD 05-FEB-2002
 PF 11-DEC-1998 JP 2000524431
 PR 12-DEC-1997 US 08/989750
 PI KEITH BLACK,JULIA Y LJUBIMOVA,ACHILLES A DEMETRIOU PC
 C12N15/09,A61K38/00,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
 G01N33/566
 PC G01N33/574,C12N15/00,A61K37/02
 CC Gene associated with neoplastic disease or malignancy CC
 associated gene
 FH Key Location/Qualifiers
 FT source 1..21 /organism='Homo sapiens (human)'.
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 Location/Qualifiers
 1..21 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 Query Match 0.4%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 7.1e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1807 TGGTCCTTTGGGGTCTGCTC 1827
 Db 1 TGGTCCTTTGGGGTCTGCTC 21
 RESULT 413
 LOCUS BD140705 21 bp DNA linear PAT 18-SEP-2002
 DEFINITION Methods for the simultaneous identification of novel biological
 targets and lead structures for drug development..
 ACCESSION BD140705
 VERSION BD140705.1 GI:23235650
 KEYWORDS JP 2002508507-A/7.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 1 (bases 1 to 21)
 Heekner,D.L., Zepp,C.M., Gao,Y. and Jones,S.W.
 Methods for the simultaneous identification of novel biological
 targets and lead structures for drug development
 Patent: JP 2002508507-A 7 19-MAR-2002;
 JOURNAL

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SEPRACOR INC
OS Artificial Sequence
PN JP 2002508507-A/7
PD 19-MAR-2002
PF 18-DEC-1998 JP 2000539165
PR 18-DEC-1997 US 60/058035
PI DONALD L HEERER, CHARLES M ZEPPE, YUN GAO, STEVEN W JONES PC
G01N33/542, C12Q1/04, C12Q1/69, C12Q1/70, G01N21/00, G01N21/76, PC
G01N33/53,
PC G01N33/566//C12N15/09, C12N15/00
CC Description of Artificial Sequence: construct FH Key
FT Location/Qualifiers
FT source 1..22
/organism='Artificial Sequence'.

FEATURES
source
LOCUS AR074772 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 69 from patent US 5955276.
ACCESSION AR074772
VERSION AR074772.1 GI:10001525
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 69 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3463 TATATATATCTATATATATAA 3483
Db 21 TATATATACCTAGGTATATAA 1

RESULT 414
LOCUS AR074772/c 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 69 from patent US 5955276.
ACCESSION AR074772
VERSION AR074772.1 GI:10001525
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 69 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
Db 21 ACACACATATATATATA 1

RESULT 415
LOCUS AR074786/c 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 83 from patent US 5955276.
ACCESSION AR074786
VERSION AR074786.1 GI:10001539
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 83 21-SEP-1999;
FEATURES
source
LOCUS AR074772/c 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 69 from patent US 5955276.
ACCESSION AR074772
VERSION AR074772.1 GI:10001525
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 69 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3463 TATATATATCTATATATATAA 3483
Db 21 TATATATACCTAGGTATATAA 1

RESULT 414
LOCUS AR074772/c 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 69 from patent US 5955276.
ACCESSION AR074772
VERSION AR074772.1 GI:10001525
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 69 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
Db 21 ACACACATATATATATA 1

RESULT 415
LOCUS AR074786/c 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 83 from patent US 5955276.
ACCESSION AR074786
VERSION AR074786.1 GI:10001539
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 83 21-SEP-1999;
FEATURES
source
LOCUS AR074787/c 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 84 from patent US 5955276.
ACCESSION AR074787
VERSION AR074787.1 GI:10001540
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 84 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATAT 2843
Db 1 TATATATATATATATATGTGT 21

RESULT 417
LOCUS AR074787/c 22 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 84 from patent US 5955276.
ACCESSION AR074787
VERSION AR074787.1 GI:10001540
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 84 21-SEP-1999;
FEATURES
source
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
Db 21 ACACATATATATATATATA 1

RESULT 418
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CQ754864/c
LOCUS CQ754864 22 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 11 from Patent EP1375510.
ACCESSION CQ754864
VERSION CQ754864.1 GI:44845892
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS te Koppele,J.M. and Bank,R.A.
TITLE Modification of collagenous materials and medical treatment,
diagnosis and monitoring of fibrotic conditions
JOURNAL Patent: EP 1375510-A 11 02-JAN-2004;
Nederlandse Organisatie voor Toegepast-Natuurwetenschappelijk
Onderzoek TNO (NL)
FEATURES
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: forward primer
exon 7"
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2325 GTGTGTGTGCTGTGTGTGTG 2345
Db 21 GTGTGTGTGTGTGTGTGTG 1
RESULT 419
AX184223/c
LOCUS AX184223 22 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1976 from Patent WO0142511.
ACCESSION AX184223
VERSION AX184223.1 GI:15135567
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
TITLE Ibd-related polymorphisms
JOURNAL Patent: WO 0142511-A 1976 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
Biotherapeutics Corporation (CA)
FEATURES
source Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3469 TATCTATATATATATATTTTATTG 3490
Db 22 TATATATATATATANGTTGTTG 1
RESULT 420
BD140700/c
LOCUS BD140700 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods for the simultaneous identification of novel biological
targets and lead structures for drug development.
ACCESSION BD140700
VERSION BD140700.1 GI:23235645
KEYWORDS JP 2002508507-A/2.

synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 22)
Heefner,D.L., Zepp,C.M., Gao,Y. and Jones,S.W.
Methods for the simultaneous identification of novel biological
targets and lead structures for drug development
Patent: JP 2002508507-A 2 19-MAR-2002;
SEPRACOR INC
OS Artificial Sequence
PN JP 2002508507-A/2
PD 19-MAR-2002
PF 18-DEC-1998 JP 2000539165
PI 18-DEC-1997 US 60/068035
PR DONALD L. HEFNER, CHARLES M. ZEPF, YUN GAO, STEVEN W. JONES PC
GOIN33/542, CI2Q1/04, CI2Q1/68, CI2Q1/70, G01N21/00, G01N21/76, PC
GOIN33/53,
PC G01N33/566//CI2N15/09, CI2N15/00
CC Description of Artificial Sequence: construct FH Key
Location/Qualifiers
FT source 1..22
FT Location/Qualifiers
1..22
/organism="Artificial Sequence".
source
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 7.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3463 TATATATATCTATATATATAA 3483
Db 21 TATATATACCTAGGTATATAA 1
RESULT 421
AR233986/c
LOCUS AR233986 23 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 4 from patent US 6458551.
ACCESSION AR233986
VERSION AR233986.1 GI:27276620
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS Wilkison,H.
TITLE Estrogen receptor
JOURNAL Patent: US 6458551-A 4 01-OCT-2002;
FEATURES
source Location/Qualifiers
1..23
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 666 GGTGGGCGCGGACGCACACC 686
Db 23 GGTGGGCGCTGCTCGGACACC 3
RESULT 422
AR316862/c
LOCUS AR316862 23 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 4 from patent US 6562592.
ACCESSION AR316862
VERSION AR316862.1 GI:33695952
KEYWORDS
SOURCE Unknown.


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LOCUS       AX804134                      23 bp    DNA             linear      PAT 25-NOV-2003
DEFINITION   Sequence 302 from Patent WO03060160.
ACCESSION    AX804134
VERSION      AX804134.1  GI:38521269
KEYWORDS     Oreochromis niloticus (Nile tilapia)
SOURCE       Oreochromis niloticus
ORGANISM     Oreochromis niloticus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
              Labroidae; Cichlidae; Oreochromis.
REFERENCE    1
AUTHORS      Lie Y., Slettan, A., Hoeyum, M. and Lingaas, F.
TITLE        Verification of food origin based on nucleic acid pattern
              recognition
JOURNAL      Patent: WO 03060160-A 302 24-JUL-2003;
              Genomar ASA (NO)
FEATURES     Location/Qualifiers
              source
                1..23
                /organism="Oreochromis niloticus"
                /mol_type="unassigned DNA"
                /db_xref="taxon:8128"

Query Match      0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 730 AAGGAGCTAGAGTTCCTCC 750
      ||||| ||||| ||||| |||||
Db 2 AAGGAGATAGATGCTCTCC 22

RESULT 428
LOCUS       BD091393/c                      23 bp    DNA             linear      PAT 27-AUG-2002
DEFINITION   Estrogen receptor.
ACCESSION    BD091393
VERSION      BD091393.1  GI:22637004
KEYWORDS     JP 2001525319-A/3.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Wilkinson, H.
TITLE        Estrogen receptor
JOURNAL      Patent: JP 2001525319-A 3 11-DEC-2001;
              MERCK AND CO INC
COMMENT      OS Homo sapiens (human)
              PN JP 2001525319-A/3
              PD 11-DEC-2001
              PF 04-SEP-1998 JP 2000510766
              PR 08-SEP-1997 US 60/058271, 30-SEP-1997 US 60/060520 PR
              30-OCT-1997 GB 9722884.5, 20-MAR-1998 GB 9806032.0 PI HILARY
              WILKINSON
              PC C07K14/72, A61K45/00, A61P3/10, A61P5/32, A61P19/10, PC
              A61P25/28.
              PC A61P35/00, C12N15/09, G01N33/53, G01N33/566, C12N15/00 CC
              Estrogen receptor
              FH Key
              FT source
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                /organism="Homo sapiens (human)"
                /db_xref="taxon:9606"

FEATURES     Location/Qualifiers
              source
                1..23
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

Query Match      0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 666 GGTGGCCCGGACGCGACACC 686

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Db 23 GGTGGCGCTGTCGCGACACC 3
      ||||| ||||| ||||| ||||| |||||

RESULT 429
LOCUS       S61964                      23 bp    DNA             linear      PRI 07-MAY-1993
DEFINITION   (beta C)-beta-globin [5'region] [human, Genomic Mutant, 23 nt].
ACCESSION    S61964
VERSION      S61964.1  GI:236198
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Trabuchet, G., Elion, J., Dunda, O., Lapoumeroulie, C., Ducrocq, R.,
              Nadifi, S., Zohoun, I., Chaventre, A., Carnevale, P., Nagel, R.L., et, al.
              Nucleotide sequence evidence of the uniceentric origin of the beta C
              mutation in Africa
JOURNAL      Hum. Genet. 87 (5), 597-601 (1991)
MEDLINE      92009838
PUBMED       1680789
REMARK       GenBank staff at the National Library of Medicine created this
              entry [NCBI gibbsq 61964] from the original journal article.
FEATURES     Location/Qualifiers
              source
                1..23
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                1..23
                /gene="beta-globin"
                /allele="beta C"

Query Match      0.4%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3469 TATCTATATATATATATTTATT 3489
      ||||| ||||| ||||| ||||| |||||
Db 1 TATATATATATATATTTT 21

RESULT 430
LOCUS       A12053                      16 bp    DNA             linear      PAT 09-DEC-1993
DEFINITION   Oligonucleotide.
ACCESSION    A12053
VERSION      A12053.1  GI:491255
KEYWORDS     synthetic construct
              synthetic construct
              artificial sequences.
SOURCE       Epplen, J.T.
ORGANISM     Process for the detection of restriction fragment length
              polymorphisms in eukaryotic genomes
              Patent: EP 0266787-A 13 11-MAY-1988;
              Max-Planck-Gesellschaft zur Foerderung der Wissenschaften
              Location/Qualifiers
              source
                1..16
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGT 2350
      ||||| ||||| ||||| ||||| |||||
Db 1 GTGTGTGTGTGTGTGT 16

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RESULT 431
A12054/c
LOCUS      A12054      16 bp      DNA      linear      PAT 09-DEC-1993
DEFINITION Oligonucleotide.
ACCESSION  A12054
VERSION    A12054.1  GI:489449
KEYWORDS   synthetic construct
SOURCE     artificial sequences.
ORGANISM   1 (bases 1 to 16)
REFERENCE  Eppiten,J.T.
AUTHORS    Process for the detection of restriction fragment length
TITLE      polymorphisms in eukaryotic genomes
JOURNAL    Patent: EP 0266787-A 14 11-MAY-1988;
           Max-Planck-Gesellschaft zur Foerderung der Wissenschaften
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2335 GTGTGTGTGTGTGTGT 2350
        |||||
        16 GTGTGTGTGTGTGTGT 1
Db

RESULT 432
E32224/c
LOCUS      E32224      16 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION  E32224
VERSION    E32224.1  GI:13021854
KEYWORDS   JP 2000060559-A/26.
SOURCE     Hallotis discus discus
ORGANISM   Hallotis discus discus
           Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
           Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE  Hideaki,T. and Masashi,S.
AUTHORS    Method for isolating satellite sequence
TITLE      Patent: JP 2000060559-A 26 29-FEB-2000;
JOURNAL    NATL INST OF AGROBIOLOGICAL RESOURCES
COMMENT    OS Haliotis discus discus
           PN JP 2000060559-A/26
           PD 29-FEB-2000
           PF 18-AUG-1998 JP 1998232153
           PR HIDEAKI TAKAHASHI,MASASHI SEKINO
           PI C12N15/09,C12Q1/68,C12N15/00
           PC
           CC
           FH key Location/Qualifiers
           FT source 1..16
           FT /organism='Haliotis discus discus'.
FEATURES   Location/Qualifiers
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            /organism="Haliotis discus discus"
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            /sub_species="discus"
            /db_xref="taxon:91233"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2318 TGTGTGTGTGTGTGTG 2333
        |||||
        16 TGTGTGTGTGTGTGTG 1
Db

RESULT 433
A12054/c
LOCUS      A12054      16 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 439 from patent US 5582979.
ACCESSION  I31527
VERSION    I31527.1  GI:1822318
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
           1 (bases 1 to 16)
REFERENCE  Weber,J.L.
AUTHORS    Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
TITLE      method of using the same
JOURNAL    Patent: US 5582979-A 439 10-DEC-1996;
           Location/Qualifiers
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2318 TGTGTGTGTGTGTGTG 2333
        |||||
        16 TGTGTGTGTGTGTGTG 1
Db

RESULT 434
AR328666
LOCUS      AR328666      16 bp      RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 6068 from patent US 6566127.
ACCESSION  AR328666
VERSION    AR328666.1  GI:33714474
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
           1 (bases 1 to 16)
REFERENCE  Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
AUTHORS    Method and reagent for the treatment of diseases or conditions
TITLE      related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 6068 20-MAY-2003;
           Location/Qualifiers
FEATURES   Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned RNA"
Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      2317 CTGTGTGTGTGTGTGT 2332
        |||||
        1 CTGTGTGTGTGTGTGT 16
Db

RESULT 435
AR328667
LOCUS      AR328667      16 bp      RNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 6069 from patent US 6566127.
ACCESSION  AR328667
VERSION    AR328667.1  GI:33714475
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
           1 (bases 1 to 16)
REFERENCE  Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
AUTHORS    Method and reagent for the treatment of diseases or conditions
TITLE
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related to levels of vascular endothelial growth factor receptor
Patent: US 6566127-A 609 20-MAY-2003;
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match      0.4%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2335 GTGTGTGTGTGTGTG 2350
|||||
Db 1 GTGTGTGTGTGTGTG 16

RESULT 436
AR455906
LOCUS 131536 17 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 448 from patent US 5582979.
ACCESSION I31536
VERSION I31536.1 GI:1822327
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 448 10-DEC-1996;
FEATURES Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 437
AR455906
LOCUS 131536 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 16 from patent US 6686160.
ACCESSION AR455906
VERSION AR455906.1 GI:42690800
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 16 03-FEB-2004;
FEATURES Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 438
AR455907
LOCUS 131536 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 17 from patent US 6686160.
ACCESSION AR455907
VERSION AR455907.1 GI:42690801
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 17 03-FEB-2004;
FEATURES Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 439
AR455909/c
LOCUS 131536 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 19 from patent US 6686160.
ACCESSION AR455909
VERSION AR455909.1 GI:42690803
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 19 03-FEB-2004;
FEATURES Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 440
AR455911/c
LOCUS 131536 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6686160.
ACCESSION AR455911
VERSION AR455911.1 GI:42690805
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: US 6686160-A 21 03-FEB-2004;
FEATURES Location/Qualifiers
1. .17
source /organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||
Db 2 TGTGTGTGTGTGTGTG 17
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/mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 441
AX239676
LOCUS AX239676 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 16 from Patent WO0164948.
ACCESSION AX239676
VERSION AX239676.1 GI:15797341
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 16 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 442
AX239677
LOCUS AX239677 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 17 from Patent WO0164948.
ACCESSION AX239677
VERSION AX239677.1 GI:15797342
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 17 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 2 TGTGTGTGTGTGTGTG 17

RESULT 443
AX239679/c
LOCUS AX239679 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 19 from Patent WO0164948.
ACCESSION AX239679
VERSION AX239679.1 GI:15797344
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 19 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 444
AX239681/c
LOCUS AX239681 17 bp DNA linear PAT 26-SEP-2001
DEFINITION Sequence 21 from Patent WO0164948.
ACCESSION AX239681
VERSION AX239681.1 GI:15797346
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Haeringen, W.A. and van Haeringen, H.
TITLE Universal variable fragments
JOURNAL Patent: WO 0164948-A 21 07-SEP-2001;
Dr. van Haeringen Laboratorium B.V. (NL)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.4%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
      |||
Db 17 TGTGTGTGTGTGTGTG 2

RESULT 445
AR071774/c
LOCUS AR071774 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 3 from patent US 5912147.
ACCESSION AR071774
VERSION AR071774.1 GI:7222662
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
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AUTHORS      Stoler,D., Basik,M. and Anderson,G.
TITLE        Rapid means of quantitating genomic instability
JOURNAL      Patent: US 5912147-A 3 15-JUN-1999;
FEATURES     Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 446
AR071775/c
LOCUS      AR071775      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 4 from patent US 5912147.
ACCESSION  AR071775
VERSION     AR071775.1 GI:7222663
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 4 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 447
AR071776/c
LOCUS      AR071776      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 5 from patent US 5912147.
ACCESSION  AR071776
VERSION     AR071776.1 GI:7222664
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 5 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 448
AR071804/c
LOCUS      AR071804      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 33 from patent US 5912147.
ACCESSION  AR071804
VERSION     AR071804.1 GI:7222692
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 33 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 449
AR071805/c
LOCUS      AR071805      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 34 from patent US 5912147.
ACCESSION  AR071805
VERSION     AR071805.1 GI:7222693
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 34 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 450
AR071806/c
LOCUS      AR071806      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 35 from patent US 5912147.
ACCESSION  AR071806
VERSION     AR071806.1 GI:7222694
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 35 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1

RESULT 451
AR071807/c
LOCUS      AR071807      18 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION  AR071807
VERSION     AR071807.1 GI:7222695
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Stoler,D., Basik,M. and Anderson,G.
TITLE       Rapid means of quantitating genomic instability
JOURNAL     Patent: US 5912147-A 36 15-JUN-1999;
FEATURES    Location/Qualifiers
source
1. .18
/mol_type="unknown"
/organism="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2318 TGTGTGTGTGTGTGTG 2333
Db      16 TGTGTGTGTGTGTGTG 1
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/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 451
AR071807/c
LOCUS AR071807 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 36 from patent US 5912147.
ACCESSION AR071807
VERSION AR071807.1 GI:7222695
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 36 15-JUN-1999;
FEATURES Location/Qualifiers
1..18
source /organism="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 452
AR071808/c
LOCUS AR071808 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 37 from patent US 5912147.
ACCESSION AR071808
VERSION AR071808.1 GI:7222696
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 37 15-JUN-1999;
FEATURES Location/Qualifiers
1..18
source /organism="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 453
AR071809/c
LOCUS AR071809 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 38 from patent US 5912147.
ACCESSION AR071809
VERSION AR071809.1 GI:7222697

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 38 15-JUN-1999;
FEATURES Location/Qualifiers
1..18
source /organism="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2333
Db 16 TGTGTGTGTGTGTG 1

RESULT 454
AR082088
LOCUS AR082088 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Reagents and methods useful for detecting diseases of the prostate.
ACCESSION BD082088
VERSION BD082088.1 GI:22627698
KEYWORDS JP 2001523948-A/15.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,M., Friedman,P.N., Gordon,J., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: JP 2001523948-A 15 27-NOV-2001;
COMMENT ABBOTT LABORATORIES
PN JP 2001523948-A/15
PD 27-NOV-2001
PF 08-OCT-1997 JP 1998517758
PR 08-OCT-1996 US 08/727688
PI MAURICE COHEN,PAULA N FRIEDMAN,JULIAN GORDON,STEVEN C HODGES, PI MICHAEL R KLASS,JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C PI RUSSELL,
PI STEVEN D STROUPE
PC C12Q1/68,C07K14/47//C07K16/30,G01N33/574
CC Strandedness: Single;
CC Topology: Linear;
PH Key Location/Qualifiers.
1..18
source /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"

Query Match
Best Local Similarity 0.4%; Score 16; DB 1; Length 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 832 TGGCTGGTGGTGTGC 847
Db 3 TGGCTGGTGGTGTGC 18

RESULT 455
AR181773
LOCUS AR181773 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 235 from patent US 6335194.
ACCESSION AR181773
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VERSION      AR181773.1  GI:20223987
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Bennett,C.Frank., Ackermann,E.J., Swayze,E.E. and Cowseert,L.M.
TITLE        Antisense modulation of survivin expression
JOURNAL      Patent: US 6335194-A 235 01-JAN-2002;
FEATURES     Location/Qualifiers
             source
             1..20
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2830 ACATATATATATATA 2845
Db 1 ACATATATATATATA 16

RESULT 456
AR373540/c
LOCUS      AR373540      20 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 110 from patent US 6602713.
ACCESSION  AR373540
VERSION     AR373540.1  GI:40075669
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Wyatt,J.
TITLE        Antisense modulation of protein phosphatase 2 catalytic subunit
JOURNAL      Patent: US 6602713-A 110 05-AUG-2003;
FEATURES     Location/Qualifiers
             source
             1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2823 TATATATACATATATA 2838
Db 16 TATATATACATATATA 1

RESULT 457
AR926743
LOCUS      AR926743      20 bp      DNA      linear      PAT 19-DEC-2003
DEFINITION Sequence 26 from Patent WO03085133.
ACCESSION  AR926743
VERSION     AR926743.1  GI:40247078
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1
AUTHORS      Nagaraju,J.G.
TITLE        Novel fiber-pcr primers and method of identifying genotyping
JOURNAL      diverse genomes of plant and animal systems including rice
             varieties, a kit thereof
             Patent: WO 03085133-A 26 16-OCT-2003;
             Centre for DNA Fingerprinting and Diagnostics, Centre for; the
             Department of Biotechnology, Ministry of Science & Technology (IN)
FEATURES     Location/Qualifiers
             source
             1..20
             /organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="A novel FISSR-PCR primer for genotyping eukaryotes"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTGTGTGTGTGT 2350
Db 1 GTGTGTGTGTGTGTGT 16

RESULT 458
BD082093/c
LOCUS      BD082093      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Reagents and methods useful for detecting diseases of the
ACCESSION  BD082093
VERSION     BD082093.1  GI:22627703
KEYWORDS    JP 2001523948-A/20.
SOURCE      Zea mays
ORGANISM    Zea mays
REFERENCE    1 (bases 1 to 20)
AUTHORS      Cohen,M., Friedman,P.N., Gordon,J., Hodges,S.C., Klass,M.R.,
             Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
TITLE        Reagents and methods useful for detecting diseases of the prostate
JOURNAL      Patent: JP 2001523948-A 20 27-NOV-2001;
COMMENT      ABBOTT LABORATORIES
             PN JP 2001523948-A/20
             PD 27-NOV-2001
             PF 08-OCT-1997 JP 1998517758
             PR 08-OCT-1996 US 08/727688
             PI MAURICE COHEN,PAULA N FRIEDMAN,JULIAN GORDON,STEVEN C HODGES,
             PI MICHAEL R KLASS,JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C PI
             RUSSELL,
             PI STEVEN D STROUPE
             PC C1201/68, C07K14/47//C07K16/30, G01N33/574
             CC Strandedness: Single;
             CC topology: Linear;
             FH Key Location/Qualifiers.
             source
             1..20
             /organism="Zea mays"
             /mol_type="genomic DNA"
             /db_xref="taxon:4577"

Query Match      0.4%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 832 TGGCTGGTGTCTGCTGC 847
Db 16 TGGCTGGTGTCTGCTGC 1

RESULT 459
A33318
LOCUS      A33318
DEFINITION Synthetic APP gene exon 17 sequencing primer.
ACCESSION  A33318
VERSION     A33318.1  GI:1567858
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 22)
AUTHORS
TITLE        TEST AND MODEL FOR ALZHEIMER'S DISEASE
JOURNAL      Patent: WO 9213069-A 30 06-AUG-1992;

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Best Local Similarity 79.2%; Pred. No. 9.7e+02; Mismatches 5; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTT 24

RESULT 464
LOCUS AR478202
DEFINITION AR478202 30 bp DNA linear PAT 14-MAY-2004
ACCESSION Sequence 5 from patent US 6699661.
VERSION AR478202
KEYWORDS AR478202.1 GI:47236850
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanegawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 5 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..30
/mol_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTT 24

RESULT 465
LOCUS AR478205
DEFINITION AR478205 30 bp DNA linear PAT 14-MAY-2004
ACCESSION Sequence 8 from patent US 6699661.
VERSION AR478205
KEYWORDS AR478205.1 GI:47236853
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 8 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..30
/mol_type="genomic DNA"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTT 24

RESULT 466
LOCUS BD072866
DEFINITION BD072866 30 bp DNA linear PAT 27-AUG-2002
ACCESSION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
VERSION BD072866.1 GI:22618471
KEYWORDS JP 2001286300-A/6.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanegawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 6 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
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DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072866
VERSION BD072866.1 GI:22618469
KEYWORDS JP 2001286300-A/4.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanegawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 4 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/4
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEXAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the decrease in fluorescence emission of a nucleic acid probe CC
labeled with probe with a target nucleic.
CC acid.
FH Key Location/Qualifiers
FT source 1..30
FT /organism='Artificial Sequence'.

FEATURES
source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTT 24

RESULT 467
LOCUS BD072868
DEFINITION BD072868 30 bp DNA linear PAT 27-AUG-2002
ACCESSION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
VERSION BD072868.1 GI:22618471
KEYWORDS JP 2001286300-A/6.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanegawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 6 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
```


COMMENT OS Artificial Sequence
PN JP 2001286300-A/6
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53,G01N33/542,PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
FT /organism="synthetic construct"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32630"

FEATURES
source
1..30
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/mol_type="genomic DNA"
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Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
PAT 18-SEP-2002

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTTT 24

RESULT 468
BD107493
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION
ACCESSION BD107493
VERSION BD107493.1 GI:23202311
KEYWORDS JP 2002000275-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 4 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOLOGY

COMMENT OS Artificial Sequence
PN JP 2002000275-A/4
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12Q1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
FT /organism="synthetic construct"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32630"

FEATURES
source
1..30
/organism="synthetic construct"
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Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
PAT 17-JAN-2003

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTTT 24

RESULT 470
BD145025
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145025
VERSION BD145025.1 GI:27850783
KEYWORDS JP 2002119291-A/6.

source 1..30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
PAT 18-SEP-2002

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTTT 24

RESULT 469
BD107495
LOCUS Novel quantitative polymorphism analysis method.
DEFINITION
ACCESSION BD107495
VERSION BD107495.1 GI:23202313
KEYWORDS JP 2002000275-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 4 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOLOGY

COMMENT OS Artificial Sequence
PN JP 2002000275-A/4
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12Q1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
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FT /organism="synthetic construct"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32630"

FEATURES
source
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/organism="synthetic construct"
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Query Match 0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
PAT 17-JAN-2003

QY 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATTTTTTTTGTGTTTTT 24

RESULT 470
BD145025
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145025
VERSION BD145025.1 GI:27850783
KEYWORDS JP 2002119291-A/6.


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/mol_type="genomic DNA"
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Query Match      0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATATTTTATTGAGTTTT 3497
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Db 1 ATATATATTTTGTGTTTTT 24

RESULT 473
BD166028
LOCUS
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166028
VERSION 30 bp DNA linear PAT 17-JAN-2003
KEYWORDS Novel nucleic acid probes, method for determining concentrations of
SOURCE JP 2002191372-A/8.
ORGANISM unidentified
unidentified
unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane, R., Kanagawa, T., Kamagata, Y., Torimura, M., Kurata, S.,
Yamada, K. and Yokomaku, T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 8 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/8
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI
TORIMURA,
PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
C12N15/09, C12M1/00, C12Q1/68, G01N33/58//G01N33/53, G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
CC acid. Location/Qualifiers
FH Key 1..30
FT source /organism='Artificial Sequence'.
FEATURES
source
1..30
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATATTTTATTGAGTTTT 3497
||||| ||| ||| ||| |||
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 474
AR074777
LOCUS
DEFINITION Sequence 74 from patent US 5955276.
ACCESSION AR074777
SOURCE Homo sapiens (human)

/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 16; DB 1; Length 30;
Best Local Similarity 79.2%; Pred. No. 9.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3474 ATATATATATTTTATTGAGTTTT 3497
||||| ||| ||| ||| |||
Db 1 ATATATATTTTGTGTTTTT 24

RESULT 475
BD192775
LOCUS
DEFINITION Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor.
ACCESSION BD192775
VERSION 19 bp DNA linear PAT 17-JUL-2003
KEYWORDS Generation, characterization and isolation of neuroepithelial stem
SOURCE JP 2002513291-A/2.
ORGANISM Staphylococcus aureus
Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Rao, M.S., Proschel, M.M. and Mujtaba, T.
TITLE Generation, characterization and isolation of neuroepithelial stem
cells and lineage restricted intermediate precursor
JOURNAL Patent: JP 2002513291-A 2 08-MAY-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION
COMMENT PN JP 2002513291-A/2
PD 08-MAY-2002
PF 07-MAY-1998 JP 1998548581
PR 07-MAY-1997 US 08/852744, 06-MAY-1998 US 09/073881 PI
MAHENDRA S RAO, MARGOT MAYER PROSCHEL, TAHMINA MUJTABA PC
C12N5/06, C12N5/08
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Location/Qualifiers
/organism='Staphylococcus aureus'
/mol_type='genomic DNA'
/db_xref='taxon:1280'

Query Match      0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1210 GGGGAGGGCTGCTCGGCC 1228
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Db 19 GCGGAGGGCTGCTCGGCC 1

RESULT 476
AX132173
LOCUS
DEFINITION Sequence 3391 from patent WO0130362.
ACCESSION AX132173
VERSION AX132173.1 GI:14138478
KEYWORDS Homo sapiens (human)
SOURCE

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 3391 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES Location/Qualifiers
source 1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin B1 ribozyme binding site"

Query Match 0.4%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2548 GCTCGGCTCTGCTTTGC 2566
Db 1 GGTGGCCTCTACCTTTC 19

RESULT 477
A80994
LOCUS A80994 20 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 46 from Patent EP0918091.
ACCESSION A80994
VERSION A80994.1 GI:6731567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kahn, A. and Chelly, J.
TITLE A gene called XLIS and the XLIS gene product, called doublecortin and their applications
JOURNAL Patent: EP 0918091-A 46 26-MAY-1999;
INST NAT SANTE RECH MED (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2973 GCAGAGCACCGGCTTTT 2991
Db 1 GCATGAGCACCGGCTCTT 19

RESULT 478
A88143
LOCUS A88143 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 291 from Patent WO9833904.
ACCESSION A88143
VERSION A88143.1 GI:6736713
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 291 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers

source 1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1478 GGGCGCGCGCGCGCGG 1496
Db 1 GGGCGCGCGCGCGCGG 19

RESULT 479
A90110
LOCUS A90110 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 291 from Patent EP0856579.
ACCESSION A90110
VERSION A90110.1 GI:6738624
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Brysch, W.D. and Schlingensiepen, K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 291 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source 1..20
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1478 GGGCGCGCGCGCGCGG 1496
Db 1 GGGCGCGCGCGCGCGG 19

RESULT 480
A95373
LOCUS A95373 20 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 46 from Patent WO9927089.
ACCESSION A95373
VERSION A95373.1 GI:6779417
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 20)
AUTHORS Francis, F. and Kahn, A.
TITLE A GENE CALLED XLIS AND THE XLIS GENE PRODUCT, CALLED DOUBLECORTIN AND THEIR PREPARATIONS
JOURNAL Patent: WO 9927089-A 46 03-JUN-1999;
INST NAT SANTE RECH MED (FR); FRANCIS FIONA (FR)
FEATURES Location/Qualifiers
source 1..20
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2973 GCAGAGCACCGGCTTTT 2991
Db 1 GCATGAGCACCGGCTCTT 19

Db 1 GCATAGCACCAGGCTCTT 19

RESULT 481
AR070856/c
LOCUS 20 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5908830.
ACCESSION AR070856
VERSION AR070856.1 GI:7221744
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Smith,R.G., Cascieri,M.A., MacIntyre,E., MacNeil,D.J. and Menke,J.G.
TITLE Combination therapy for the treatment of diabetes and obesity
JOURNAL
FEATURES
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3685 CTCTTCTTGGGGCCAGTG 3703
Db 19 CTCTTCTTGGGGCTCACTG 1

RESULT 482
AR074792/c
LOCUS 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 89 from patent US 5955276.
ACCESSION AR074792
VERSION AR074792.1 GI:10001545
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL
FEATURES
source
1. .20
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Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2338 TGTGTGTGTGTGCACAT 2356
Db 20 TGTGTGTGTGTGTATAT 2

RESULT 483
AR117573/c
LOCUS 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 65 from patent US 6140124.
ACCESSION AR117573
VERSION AR117573.1 GI:14098479
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P.S. and McKay,R.

TITLE Antisense modulation of P38 mitogen activated protein kinase expression
JOURNAL
FEATURES
Location/Qualifiers
source
1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 43 GGGCCCCAGCGCTGCAGG 61
Db 20 GTGCCGACGCGCTGCAGG 2

RESULT 484
AR125552
LOCUS 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 53 from patent US 6177273.
ACCESSION AR125552
VERSION AR125552.1 GI:14111614
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Cowseert,L.M.
TITLE Antisense modulation of integrin-linked kinase expression
JOURNAL
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 856 GAGGAGCTGGTGAGGCTG 874
Db 2 GAGGAGCAGGTGAGACTG 20

RESULT 485
BD190536/c
LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Concurrent treatment for diabetes and obesity.
ACCESSION BD190536
VERSION BD190536.1 GI:33000275
KEYWORDS
SOURCE Rattus
ORGANISM Rattus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
AUTHORS Smith,R.G., Cascieri,M.A., MacIntyre,E., Mcneil,D.J. and Menke,J.G.
TITLE Concurrent treatment for diabetes and obesity
JOURNAL
COMMENT
PN JP 2002516605-A/1
PD 04-JUN-2002
PF 30-OCT-1997 JP 1998520803
PR 31-OCT-1996 US 60/029233 30-MAY-1997 GB 97/11042,3 PI
ROY G. SMITH,MARGARET A CASCIERI,EUAN MACINTYRE,DOUGLAS J PI
MCNEIL,
PI JOHN G MENKE
PC A61K45/00,A61K31/44,A61K38/00,A61P3/00,A61P3/10,A61K37/02 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers

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Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3685 CTCTTCTTGGGCCAGTG 3703
Db 19 CTCTTCTTGGGCTACTG 1

RESULT 486
BD250309/c
LOCUS BD250309 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of p38 mitogen activated protein kinase
ACCESSION BD250309
VERSION BD250309.1 GI:33060079
KEYWORDS JP 2002540781-A/61.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P.S., McKay,R. and Popoff,I.
TITLE Antisense modulation of p38 mitogen activated protein kinase
JOURNAL Patent: JP 2002540781-A 61 03-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002540781-A/61
PD 03-DEC-2002
PR 04-APR-2000 JP 2000609429
PF 06-APR-1999 US 09/286904
PI BRETT P MONIA, WILLIAM A GAARDE, PAMELA S NERO, ROBERT MCKAY, TAN
PI POPOFF
PC C12N15/09,A61K31/711,A61P19/02,A61P29/00,A61P37/06,
PC A61P43/00
PC C12N5/10,C12N9/99,C12N15/00,C12N5/00
CC Antisense modulation of p38 mitogen activated protein kinase
CC expression
KEY Location/Qualifiers
FT source 1. .20
FT /organism="Artificial Sequence".
FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 43 GGGCCCCAGCGGCTGCAGG 61
Db 20 GTGCCGCGAGCGGCTGCAGG 2

RESULT 487
E32215/c
LOCUS E32215 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32215
VERSION E32215.1 GI:13021826
KEYWORDS JP 2000060559-A/17.
SOURCE Haliotis discus discus
ORGANISM Haliotis discus discus
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Verigastropoda; Haliotoidea; Haliotidae; Haliotis.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hideaki,T. and Masashi,S.

TITLE Method for isolating satellite sequence
PATENT: JP 2000060559-A 17 29-FEB-2000;
OS Haliotis discus discus
PN JP 2000060559-A/17
PR 18-AUG-1998 JP 1998232153
PC C12N15/09,C12Q1/68,C12N15/00
CC
CC
FH Key 1. .20
FT source /organism="Haliotis discus discus".
FEATURES
source
1. .20
Location/Qualifiers
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/db_xref="taxon:91233"

Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2329 GTGTGCGTGTGTGTGTGTG 2347
Db 19 GCGCGCGTGTGTGTGTGTG 1

RESULT 488
AR228858/c
LOCUS AR228858 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 65 from patent US 6448079.
ACCESSION AR228858
VERSION AR228858.1 GI:27267997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P. and McKay,R.
TITLE Antisense modulation of p38 mitogen activated protein kinase
JOURNAL Patent: US 6448079-A 65 10-SEP-2002;
FEATURES
source
1. .20
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 15.8; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 43 GGGCCCCAGCGGCTGCAGG 61
Db 20 GTGCCGCGAGCGGCTGCAGG 2

RESULT 489
AR271190/c
LOCUS AR271190 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 133 from patent US 6503152.
ACCESSION AR271190
VERSION AR271190.1 GI:29702493
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pelz,D.T.
TITLE Putting trainer
JOURNAL Patent: US 6503152-A 133 07-JAN-2003;

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Query Match	0.4%	Score 15.8	DB 1	Length 20
Best Local Similarity	89.5%	Pred. No. 7.6e+02		
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ACCESSION	AX224884			
VERSION	AX224884.1	GI:15554957		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1			
AUTHORS	Gray, D.M. and Bollon, A.P.			
TITLE	Libraries of optimum subsequence regions of mrna and genomic dna for control of gene expression			
JOURNAL	Patent: WO 0161030-A 38 23-AUG-2001;			
FEATURES	Cytoclonal Pharmaceuticals, Inc. (US); University of Texas at Dallas, Dept. of Molecular and Cell Biology (US); Lab. of Experimental Carcinogenesis, National Cancer Institute/NIH (US)			
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RESULT 493				
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LOCUS	AX250713	20 bp	DNA	linear
DEFINITION	Sequence 5 from Patent WO0168670.			
ACCESSION	AX250713			
VERSION	AX250713.1	GI:15984451		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	1			
AUTHORS	Lazdunski, M., Lesage, F. and Maingret, F.			
TITLE	Novel family of mechanically sensitive human potassium channels activated by polyunsaturated fatty acids and use thereof			
JOURNAL	Patent: WO 0168670-A 5 20-SEP-2001;			
FEATURES	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)			
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						SOURCE	synthetic construct
						ORGANISM	synthetic construct
							artificial sequences.
						REFERENCE	1 (bases 1 to 20)
						AUTHORS	Bennett,F.C., Boggs,R.T. and Dean,N.M.
						TITLE	Oligonucleotide modulation of protein kinase C-epsilon
						JOURNAL	Patent: JP 2001224386-A 66 21-AUG-2001;
						COMMENT	ISIS PHARMACEUTICALS INC
							OS Artificial Sequence
							PN JP 2001224386-A/66
							PD 21-AUG-2001
							PF 13-DEC-2000 JP 2000379218
							PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
							FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
							C12N15/09,A61K48/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
							G01N33/53,
							PC G01N33/566,G01N33/573//A61K31/711,A61K31/712,A61K31/7125, PC
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						LOCUS	AX476807 20 bp DNA linear PAT 12-AUG-2002
						DEFINITION	Sequence 2028 from Patent WO0224750.
						ACCESSION	AX476807
						VERSION	AX476807.1 GI:22216092
						KEYWORDS	Homo sapiens (human)
						SOURCE	Homo sapiens
						ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
						REFERENCE	1
						AUTHORS	Zhang, J.
						TITLE	Human kidney tumor overexpressed membrane protein 1
						JOURNAL	Patent: WO 0224750-A 2028 28-MAR-2002;
							Aeomica, Inc. (US)
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						LOCUS	BD016057 20 bp DNA linear PAT 27-AUG-2002
						DEFINITION	Oligonucleotide modulation of protein kinase C-epsilon.


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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 323 CTCCTCCATCTCTGGCT 341
DB 2 CTCCTCCATCTCTGGCT 20

RESULT 498
BD017328
LOCUS      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-eta.
ACCESSION  BD017328
VERSION     BD017328.1 GI:22558504
KEYWORDS   JP 2001231579-A/66.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Bennett,F.C., Boggs,R.T. and Dean,N.M.
TITLE      Oligonucleotide modulation of protein kinase C-eta
JOURNAL    Patent: JP 2001231579-A 66 28-AUG-2001;
           ISIS PHARMACEUTICALS INC
COMMENT    OS Artificial Sequence
           PN JP 2001231579-A/66
           PD 28-AUG-2001
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           PR 09-JUL-1993 US 08/089996,22-FEB-1994 US 08/199779 PI
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           C12N15/09,A61K31/711,A61K31/712,A61K31/7125,A61K48/00,A61P29/ PC
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           PC A61P43/00,C07H21/00,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50, PC
           GO1N33/50,
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DB 2 CTCCTCCATCTCTGGCT 20

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BD065656
LOCUS      20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065656
VERSION     BD065656.1 GI:22611259
KEYWORDS   JP 2001511000-A/291.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Schlingensiefen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 291 07-AUG-2001;
           BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown

/mol_type="genomic DNA"
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PN JP 2001511000-A/291
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1478 GGGCGCGCGCGCGCGG 1496
DB 1 GGGCGCGCGCGCGCGG 19

RESULT 500
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LOCUS      20 bp      DNA      linear      PAT 18-FEB-2003
DEFINITION Transgenic animal having drug-metabolizing enzyme and
           utilization thereof.
ACCESSION  BD174235
VERSION     BD174235.1 GI:28415574
KEYWORDS   WO 02066635-A/5.
SOURCE     synthetic construct
ORGANISM   synthetic sequences.
           1 (bases 1 to 20)
REFERENCE  Katsuki,M., Kamataki,T., Teranishi,Y., Ishida,M. and Kato,M.
           Transgenic animal having drug-metabolizing enzyme gene and
           utilization thereof
           Patent: WO 02066635-A 5 29-AUG-2002;
           GENCOM CORP,MOTOYA KATSUKI,TETSUYA KAWATAKI,YUTAKA TERANISHI,
           MITSUYOSHI ISHIDA,MINORU KATO
           OS Artificial Sequence
           PN WO 02066635-A/5
           PD 29-AUG-2002
           PF 21-FEB-2002 WO 2002JP001555
           PR 23-FEB-2001 JP 01P 047735
           PI MOTOYA KATSUKI,TETSUYA KAWATAKI,YUTAKA TERANISHI,MITSUYOSHI
           PI ISHIDA,
           PI MINORU KATO
           PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,A01K67/
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           PC A01K67/027,A61K45/00,A61P1/00,A61P3/10,A61P5/00,A61P9/00, PC
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 842 TGCTGCCAGCCGAGGAGGA 860
DB 20 TGCTGCCAGCCGAGGAGGA 2
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RESULT 501
E14785 E14785 linear PAT 28-JUL-1999
LOCUS PCR primer.
DEFINITION
ACCESSION E14785
VERSION E14785.1 GI:5709468
KEYWORDS JP 1998014570-A/16.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Matsuda,M. and Kamei,M.
TITLE ANTIBODY DNA
JOURNAL
COMMENT
OS None
OC Artificial sequences.
PN JP 1998014570-A/16
PD 20-JAN-1998
PF 05-JUL-1996 JP 1996194095
PI MATSUDA MORIHIRO, KAMEI MASANORI
PC C12N15/02.C07H21/04.C07K16/12.G01N33/53.G01N33/569, PC
GOIN33/577//A61K39/395,
PC A61K39/395.C12N1/21.C12P21/08.C12Q1/68.(C12N15/02.C12R1:91),
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CC topology: Linear;
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FT /organism='Artificial sequences'.
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Best Local Similarity 81.1%; Pred. No. 7.9e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 853 GAGGAGGAGCTGCTGGAGGCT 873
DB 1 GAGGTGCAGCTGCTGGAGTCT 21
RESULT 502
BD056548/C
LOCUS 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Method to diagnose and treat pathological conditions resulting from
deficient ion transport.
ACCESSION BD056548
VERSION BD056548.1 GI:22602154
KEYWORDS JP 2001508291-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Lifton,R.P. and Simon,D.B.
TITLE Method to diagnose and treat pathological conditions resulting from
deficient ion transport
JOURNAL Patent: JP 2001508291-A 5 26-JUN-2001;
COMMENT YALE UNIVERSITY
OS Artificial Sequence
PN JP 2001508291-A/5
PD 26-JUN-2001
PF 19-DEC-1997 JP 1998530123
PR 31-DEC-1996 US 08/778052
PI RICHARD P LIFTON, DAVID B SIMON
PC C12N15/09.C07K14/435.C07K16/00.C12N1/15.C12N1/19.C12N1/21, PC
C12N5/10,
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for analysis of human TSC gene
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QY 3404 GTTTCACGAGGAGGCGCGG 3422
DB 21 GTGTCACGAGGAGGCGCCAG 3
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AR264925
LOCUS 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 9 from patent US 6492121.
ACCESSION AR264925
VERSION AR264925.1 GI:29693312
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 9 10-DEC-2002;
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QY 3259 ACATATTTTATTTGCTTGTCTCTTTT 3285
DB 3 ATATATTTTTCCTTTTCTTTTCTTTT 29
RESULT 504
AR478206
LOCUS 30 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 9 from patent US 6699661.
ACCESSION AR478206
VERSION AR478206.1 GI:47236854
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 9 02-MAR-2004;
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Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 30)	Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and Yokomaku,T.	Novel quantitative polymorphism analysis method	Patent: JP 2002000275-A 6 08-JAN-2002;	JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE & TECHNOL
OS	Artificial Sequence			
PN	JP 2002000275-A/6			
PD	08-JAN-2002			
PF	27-JUN-2000 JP 2000193133			
PI	RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI KURATA,			
PI	KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU			
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CC	decrease in fluorescence emission of a nucleic acid probe	labeled with		
CC	BODIBY FL/C6 upon the hybridization of the	probe with a target		
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DEFINITION	Method for assaying nucleic acid, nucleic acid probe used therefor,			
DEFINITION	and method for analyzing data obtained by that method.			
ACCESSION	BD145029			
VERSION	BD145029.1	GI:27850787		
KEYWORDS	JP 2002119291-A/10.			
SOURCE	synthetic construct			
ORGANISM	artificial construct			
REFERENCE	1 (bases 1 to 30)			
AUTHORS	Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.			
TITLE	Method for assaying nucleic acid, nucleic acid probe used therefor,			
JOURNAL	and method for analyzing data obtained by that method			
COMMENT	Patent: JP 2002119291-A 10 23-APR-2002;			
COMMENT	JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD			
OS	Artificial Sequence			
PN	JP 2002119291-A/10			
PD	23-APR-2002			
PF	27-APR-2001 JP 2001133529			
PI	RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI TORIMURA,			
PI	SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU			
PC	C12N15/09, C12N15/05, C12M1/00, C12Q1/68, G01N1/28, G01N33/53,			
PC	G01N33/566, G01N33/58, G01N37/00, G06F17/10, C12N15/00, C12N15/00,			
PC	G01N1/28			
PC	G01N1/28			

CC The base sequence was prepared synthetically on the aim of CC
 CC decrease in fluorescence emission of
 CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
 CC hybridization of
 CC the probe with a target nucleic acid.
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QY 3259 AGATATTTATTTGCTTTCCTTTT 3285
 Db 3 ATATATTTTTCCTTTTTCCTTTT 29

RESULT 508
 BD166029 30 bp DNA linear PAT 17-JAN-2003
 LOCUS Novel nucleic acid probes, method for determining concentrations of
 DEFINITION nucleic acid by using the probes, and method for analyzing data
 obtained by the method.
 ACCESSION BD166029
 VERSION BD166029.1 GI:27871841
 KEYWORDS JP 2002191372-A/9.
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Kurane, R., Kanagawa, T., Torimura, Y., Kurata, S.,
 Yamada, K., and Yokomaki, T.
 TITLE Novel nucleic acid probes, method for determining concentrations of
 nucleic acid by using the probes, and method for analyzing data
 obtained by the method
 JOURNAL Patent: JP 2002191372-A 9 09-JUL-2002;
 NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
 KANKYO ENGINEERING CO LTD
 COMMENT OS Artificial Sequence
 PN JP 2002191372-A/9
 PD 09-JUL-2002
 PF 26-SEP-2001 JP 2001295145
 PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KANAGATA, MASAKI PI
 TORIMURA,
 PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
 C12N15/09, C12M1/00, C12Q1/68, G01N33/58//G01N33/53, G01N33/566, PC
 C12N15/00
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 CC decrease in fluorescence emission of a nucleic acid probe CC
 CC labeled with
 CC BODIBY FL/C6 upon the hybridization of the
 CC probe with a target
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Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 3 ATATATTTTTCCTTTTTCCTTTT 29

RESULT 509
 AR309630 41 bp DNA linear PAT 12-JUN-2003
 LOCUS Sequence 9 from patent US 6555657.
 DEFINITION AR309630
 ACCESSION AR309630
 VERSION AR309630.1 GI:31701680
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 41)
 AUTHORS Christensen, T.
 TITLE Isolated transcription factor for an alpha-amylase promoter in
 filamentous fungi
 JOURNAL Patent: US 6555657-A 9 29-APR-2003;
 FEATURES Location/Qualifiers
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Query Match 0.4%; Score 15.8; DB 1; Length 41;
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QY 3300 TTCTATAGGATTTTCCTTTAGGAGATTTATTTT 3334
 Db 1 TTTTGAAGCTTTTTCCTTTTTCCTTTTTCCTTTT 35

RESULT 510
 BD238391/c 42 bp RNA linear PAT 17-JUL-2003
 LOCUS Sorting of proteins using RNA-protein fused body.
 DEFINITION BD238391
 ACCESSION BD238391.1 GI:33048161
 VERSION JP 2002536025-A/9.
 KEYWORDS synthetic construct
 SOURCE artificial sequences.
 ORGANISM 1 (bases 1 to 42)
 REFERENCE Szostak, J.W., Roberts, R.W. and Liu, R.
 AUTHORS Sorting of proteins using RNA-protein fused body
 TITLE Patent: JP 2002536025-A 9 29-OCT-2002;
 JOURNAL THE GENERAL HOSPITAL CORP
 COMMENT OS Artificial Sequence
 PN JP 2002536025-A/9
 PD 29-OCT-2002
 PF 01-FEB-2000 JP 2000598669
 PR 09-FEB-1999 US 09/247190
 PI JACK W SZOSTAK, RICHARD W ROBERTS, RIHE LIU
 PC C12N15/09, C07K14/00, C07K14/00, C12Q1/68, C12N15/00 CC
 Translation template
 FH Key Location/Qualifiers
 FT source 1..42
 FT /organism='Artificial Sequence'.
 FEATURES
 source 1..42
 Location/Qualifiers
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Query Match 0.4%; Score 15.8; DB 1; Length 42;
 Best Local Similarity 74.1%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3262 TATTTATTTGCTTTCCTTTTTCCTTTTTCCTTTT 3288

<p>TITLE NF2 isoforms</p> <p>JOURNAL Patent: US 5872214-A 12 16-FEB-1999;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>Db 1 CCCCACTCTCACCTATGTCCTCC 22</p> <p>RESULT 518</p> <p>LOCUS I29861/c</p> <p>DEFINITION I29861</p> <p>ACCESSION I29861</p> <p>VERSION I29861.1</p> <p>KEYWORDS GI:1820652</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 22)</p> <p>AUTHORS Seizinger,B.R., Kley,N.A. and Bianchi,A.B.</p> <p>TITLE NF2 isoforms</p> <p>JOURNAL Patent: US 5578462-A 12 26-NOV-1996;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 850 GCCGAGGAGGAGCTGTGGAGG 871</p> <p>Db 22 GCTGAAGAGGAGCTGTTCAGG 1</p> <p>RESULT 516</p> <p>LOCUS AR048932/c</p> <p>DEFINITION AR048932</p> <p>ACCESSION AR048932</p> <p>VERSION AR048932.1</p> <p>KEYWORDS GI:6004971</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 22)</p> <p>AUTHORS Nelson,N.C., Velarde,J. Jr. and Kacian,D.L.</p> <p>TITLE Oligonucleotide screening assay using DNA-altering agents and probes with protectable labels</p> <p>JOURNAL Patent: US 5824475-A 7 20-OCT-1998;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 1803 CBTCTGTCCTTTGGGTCCTG 1824</p> <p>Db 22 CTTGAGTCTCTTTGGGACCTG 1</p> <p>RESULT 517</p> <p>LOCUS CQ812601</p> <p>DEFINITION CQ812601</p> <p>ACCESSION CQ812601</p> <p>VERSION CQ812601.1</p> <p>KEYWORDS GI:47602071</p> <p>SOURCE synthetic construct</p> <p>ORGANISM synthetic construct</p> <p>REFERENCE 1</p> <p>AUTHORS Ozog,M.A., Bechberger,J. and Naus,C.</p> <p>TITLE Methods for neuroprotection</p> <p>JOURNAL Patent: WO 2004037281-A 5 06-MAY-2004;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="Primer"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 1119 CCCACGCTGGCCAAATGCTCC 1140</p>
<p>Db 1 CCCCACTCTCACCTATGTCCTCC 22</p> <p>RESULT 518</p> <p>LOCUS I29861/c</p> <p>DEFINITION I29861</p> <p>ACCESSION I29861</p> <p>VERSION I29861.1</p> <p>KEYWORDS GI:1820652</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 22)</p> <p>AUTHORS Seizinger,B.R., Kley,N.A. and Bianchi,A.B.</p> <p>TITLE NF2 isoforms</p> <p>JOURNAL Patent: US 5578462-A 12 26-NOV-1996;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 850 GCCGAGGAGGAGCTGTGGAGG 871</p> <p>Db 22 GCTGAAGAGGAGCTGTTCAGG 1</p> <p>RESULT 516</p> <p>LOCUS AR048932/c</p> <p>DEFINITION AR048932</p> <p>ACCESSION AR048932</p> <p>VERSION AR048932.1</p> <p>KEYWORDS GI:6004971</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unknown.</p> <p>REFERENCE 1 (bases 1 to 22)</p> <p>AUTHORS Nelson,N.C., Velarde,J. Jr. and Kacian,D.L.</p> <p>TITLE Oligonucleotide screening assay using DNA-altering agents and probes with protectable labels</p> <p>JOURNAL Patent: US 5824475-A 7 20-OCT-1998;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 1803 CBTCTGTCCTTTGGGTCCTG 1824</p> <p>Db 22 CTTGAGTCTCTTTGGGACCTG 1</p> <p>RESULT 517</p> <p>LOCUS CQ812601</p> <p>DEFINITION CQ812601</p> <p>ACCESSION CQ812601</p> <p>VERSION CQ812601.1</p> <p>KEYWORDS GI:47602071</p> <p>SOURCE synthetic construct</p> <p>ORGANISM synthetic construct</p> <p>REFERENCE 1</p> <p>AUTHORS Ozog,M.A., Bechberger,J. and Naus,C.</p> <p>TITLE Methods for neuroprotection</p> <p>JOURNAL Patent: WO 2004037281-A 5 06-MAY-2004;</p> <p>FEATURES Location/Qualifiers</p> <p>source</p> <p>1..22</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="Primer"</p> <p>Query Match 0.4%; Score 15.6; DB 1; Length 22;</p> <p>Best Local Similarity 81.8%; Pred. No. 8.6e+02;</p> <p>Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 1119 CCCACGCTGGCCAAATGCTCC 1140</p>	

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JOURNAL Patent: WO 0168900-A 6 20-SEP-2001;
FEATURES Vermicon AG (DE)
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kunstlichen Sequenz:
Oligonukleotidprimer"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2328 TGTGTCGTGTGTGTGTGTG 2349
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Db 1 TGTGTTCTGTGTGTATTGTG 22

RESULT 521
AX367061 22 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 20 from Patent WO0147959.
ACCESSION AX367061
VERSION AX367061.1 GI:18855281
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
AUTHORS Jager,D., Stockert,E., Scanlan,M., Knuth,A., Old,L., Gure,A. and
TITLE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
antigens, the antigens per se, and uses thereof
JOURNAL Patent: WO 0147959-A 20 05-JUL-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; MEMORIAL
SLOAN-KETTERING CANCER CENTER (US) ; Cornell Research Foundation
(US)
FEATURES Location/Qualifiers
source 1..22
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Query Match 0.4%; Score 15.6; DB 1; Length 22;
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Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2608 CAAAGCTGAGCTGCAGGGAAG 2629
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Db 1 CAAAGCAGAGCCTCCCGAAG 22

RESULT 522
AX740255 22 bp DNA linear PAT 10-MAY-2003
LOCUS
DEFINITION Sequence 11 from Patent EP1300146.
ACCESSION AX740255
VERSION AX740255.1 GI:30523429
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Hilberg,F., Brandstetter,I., van Meel,J., Bette,P. and Kleemann,R.
TITLE Pharmaceutical composition for the treatment of animal mammary
tumors
JOURNAL Patent: EP 1300146-A 11 09-APR-2003;
Boehringer Ingelheim International GmbH (DE)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"

JOURNAL Patent: WO 0168900-A 6 20-SEP-2001;
FEATURES Vermicon AG (DE)
source Location/Qualifiers
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Query Match 0.4%; Score 15.6; DB 1; Length 22;
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Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1748 TGAAGTGGATGGCGCTGAGGC 1769
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Db 1 TCAAGTGGATGGCGTGGAGTC 22

RESULT 523
AX743831 22 bp DNA linear PAT 14-MAY-2003
LOCUS
DEFINITION Sequence 11 from Patent WO03030910.
ACCESSION AX743831
VERSION AX743831.1 GI:30722583
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Hilberg,F., Brandstetter,I., Bette,P., Kleemann,R. and van Meel,J.
TITLE Pharmaceutical composition for the treatment of disorders of
non-human mammals
JOURNAL Patent: WO 03030910-A 11 17-APR-2003;
Boehringer Ingelheim International GmbH (DE)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1748 TGAAGTGGATGGCGCTGAGGC 1769
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Db 1 TCAAGTGGATGGCGTGGAGTC 22

RESULT 524
AX937575 22 bp DNA linear PAT 06-JAN-2004
LOCUS
DEFINITION Sequence 55 from Patent EP1361433.
ACCESSION AX937575
VERSION AX937575.1 GI:40713615
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Yanai,Y.C., Yamamoto,S.C., Yamamoto,K.C. and Ikegami,H.C.
TITLE Method for estimating therapeutic efficacy of tumor necrosis factor
(TNF)
JOURNAL Patent: EP 1361433-A 55 12-NOV-2003;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)
FEATURES Location/Qualifiers
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/note="Oligonucleotide used as primer for PCR detection of
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Query Match 0.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Thu Oct 28 12:48:19 2004

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QY      855 GGAGGAGCTGTGGAGGCTGAC 876
Db      1 GCAGGACCTGTGGAGGACTGAC 22

RESULT 525
LOCUS   A95626 17 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 28 from Patent WO9925815.
ACCESSION A95626
VERSION  A95626.1 GI:6779563
KEYWORDS
SOURCE   unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS  Herrmann, B. and Kispert, A.
TITLE    NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATIONS
JOURNAL  THEREOF
PATENT   WO 9925815-A 28 27-MAY-1999;
HERRMANN BERNHARD (DE); MAX PLANCK GESELLSCHAFT (DE)
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source   1..17
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/db_xref="taxon:32844"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1747 GTGAAGTGGATGGGCC 1763
Db      17 GTGAAGTGGATGGCACC 1

RESULT 526
LOCUS   AR023742 17 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 24 from patent US 5795726.
ACCESSION AR023742
VERSION  AR023742.1 GI:3977036
KEYWORDS
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Glucksmann, M. Alexandra.
TITLE    Methods for identifying compounds useful in treating type II
JOURNAL  diabetes
PATENT   US 5795726-A 24 18-AUG-1998;
LOCATION/Qualifiers
source   1..17
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Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      54 GCTGCAGGTGCTGAATG 70
Db      1 GCTGCAGGTGCTGGATG 17

RESULT 527
LOCUS   AR036967 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5800998.
ACCESSION AR036967
VERSION  AR036967.1 GI:5954823
KEYWORDS
SOURCE   Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS  Glucksmann, M. Alexandra.
TITLE    Assays for diagnosing type II diabetes in a subject
JOURNAL  Patent: US 5800998-A 21 01-SEP-1998;
FEATURES
source   1..17
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      54 GCTGCAGGTGCTGAATG 70
Db      1 GCTGCAGGTGCTGGATG 17

RESULT 528
LOCUS   BD199067 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION BD199067
VERSION  BD199067.1 GI:33008837
KEYWORDS JP 2002509721-A/2093.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS  Pavco, P. A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J. A.
TITLE    Method and reagent for treating diseases or conditions concerning
JOURNAL  molecule participating in vasculogenic response
PATENT   JP 2002509721-A 2093 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/2093
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PC JAMES A MCSWIGGEN
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions. CC
concerning molecule
CC participating in vasculogenic response
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Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1619 ACAGGACCTGGCTGCC 1635
Db      1 ACAGGATCTGGCTGCC 17

RESULT 529
BD226525/c

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LOCUS       BD226525               17 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION  Method and probes for the detection of chromosome aberrations.
ACCESSION   BD226525
VERSION     BD226525.1 GI:33036295
KEYWORDS    JP 2002513587-A/71.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM    1 (bases 1 to 17)
REFERENCE   1 (bases 1 to 17)
AUTHORS     Dongen,J.J.M.V., Pluzek,K.J., Nielsen,K.V. and Adelhorst,K.
TITLE       Method and probes for the detection of chromosome aberrations
JOURNAL     Patent: JP 2002513587-A 71 14-MAY-2002;
            DAKO AS
COMMENT     OS Artificial Sequence
            PN JP 2002513587-A/71
            PD 14-MAY-2002
            PE 04-MAY-1999 JP 2000547260
            PR 04-MAY-1998 DK 0615/98
            PI JACOBS JOHANNES MARIA VAN DONGEN, KARL JOHAN PLUZEK, KIRSTEN PI
            VANG NIELSEN,
            PI KIM ADELHORST
            PC C12N15/09,C07H21/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
            Description of Artificial Sequence:PNA probe, HER-2, position CC
            2776-2760
FH Key      Location/Qualifiers
FT source   1..17
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 AGACTTCGGGCTGGCCC 1693
Db 17 AGACTTCGGGCTGGCTC 1

RESULT 530
LOCUS       CQ623256               17 bp    DNA    linear    PAT 02-FEB-2004
DEFINITION  Sequence 7996 from Patent WO0192524.
ACCESSION   CQ623256
VERSION     CQ623256.1 GI:41673474
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Myosin-like gene expressed in human heart and muscle
JOURNAL     Patent: WO 0192524-A 7996 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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            /db_xref="taxon:9606"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1992 CACCTTCAGCAGCTGG 2008
Db 1 CACCATCAAGCAGCTGG 17

LOCUS       BD226525               17 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION  Method and probes for the detection of chromosome aberrations.
ACCESSION   BD226525
VERSION     BD226525.1 GI:33036295
KEYWORDS    JP 2002513587-A/71.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM    1 (bases 1 to 17)
REFERENCE   1 (bases 1 to 17)
AUTHORS     Dongen,J.J.M.V., Pluzek,K.J., Nielsen,K.V. and Adelhorst,K.
TITLE       Method and probes for the detection of chromosome aberrations
JOURNAL     Patent: JP 2002513587-A 71 14-MAY-2002;
            DAKO AS
COMMENT     OS Artificial Sequence
            PN JP 2002513587-A/71
            PD 14-MAY-2002
            PE 04-MAY-1999 JP 2000547260
            PR 04-MAY-1998 DK 0615/98
            PI JACOBS JOHANNES MARIA VAN DONGEN, KARL JOHAN PLUZEK, KIRSTEN PI
            VANG NIELSEN,
            PI KIM ADELHORST
            PC C12N15/09,C07H21/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
            Description of Artificial Sequence:PNA probe, HER-2, position CC
            2776-2760
FH Key      Location/Qualifiers
FT source   1..17
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1677 AGACTTCGGGCTGGCCC 1693
Db 17 AGACTTCGGGCTGGCTC 1

RESULT 530
LOCUS       CQ623256               17 bp    DNA    linear    PAT 02-FEB-2004
DEFINITION  Sequence 7996 from Patent WO0192524.
ACCESSION   CQ623256
VERSION     CQ623256.1 GI:41673474
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
            Shannon,M.E.
TITLE       Myosin-like gene expressed in human heart and muscle
JOURNAL     Patent: WO 0192524-A 7996 06-DEC-2001;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1992 CACCTTCAGCAGCTGG 2008
Db 1 CACCATCAAGCAGCTGG 17

LOCUS       AR188722               17 bp    DNA    linear    PAT 20-APR-2002
DEFINITION  Sequence 4210 from patent US 6346398.
ACCESSION   AR188722
VERSION     AR188722.1 GI:20234687
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 4210 12-FEB-2002;
            JOURNAL Location/Qualifiers
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Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1609 AAGTGCATCCACAGGGA 1625
Db 1 AAGTGTATCCACAGGGA 17

RESULT 532
LOCUS       AR188754               17 bp    DNA    linear    PAT 20-APR-2002
DEFINITION  Sequence 4242 from patent US 6346398.
ACCESSION   AR188754
VERSION     AR188754.1 GI:20234719
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 4242 12-FEB-2002;
            JOURNAL Location/Qualifiers
            FEATURES 1..17
            source /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1798 AGTGACGTCTGCTCCTT 1814
Db 1 AGTGACGTCTGCTCCTT 17

RESULT 533
LOCUS       AR190296               17 bp    DNA    linear    PAT 20-APR-2002
DEFINITION  Sequence 5784 from patent US 6346398.
ACCESSION   AR190296
VERSION     AR190296.1 GI:20236261
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 5784 12-FEB-2002;
            JOURNAL Location/Qualifiers
            FEATURES 1..17
            source /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1798 AGTGACGTCTGCTCCTT 1814
Db 1 AGTGACGTCTGCTCCTT 17

RESULT 533
LOCUS       AR190296               17 bp    DNA    linear    PAT 20-APR-2002
DEFINITION  Sequence 5784 from patent US 6346398.
ACCESSION   AR190296
VERSION     AR190296.1 GI:20236261
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 5784 12-FEB-2002;
            JOURNAL Location/Qualifiers
            FEATURES 1..17
            source /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1798 AGTGACGTCTGCTCCTT 1814
Db 1 AGTGACGTCTGCTCCTT 17

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JOURNAL Patent: US 6346398-A 5784 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1609 AAGTGCATCCACAGGGA 1625
Db 1 AAGTGTATCCACAGGGA 17

RESULT 534
AR286400 17 bp RNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 772 from patent US 6528640.
ACCESSION AR286400
VERSION AR286400.1 GI:29723996
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
TITLE Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
JOURNAL Synthetic ribonucleic acids with RNase activity
PATENT: US 6528640-A 772 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1678 GACTTCGGGCTGGCCG 1694
Db 1 GACTTCGGGCTGGCTCG 17

RESULT 535
AR324575 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 1977 from patent US 6566127.
ACCESSION AR324575
VERSION AR324575.1 GI:33710383
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1977 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1609 AAGTGCATCCACAGGGA 1625
Db 1 AAGTGTATCCACAGGGA 17

RESULT 536
AR324607 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 2009 from patent US 6566127.
ACCESSION AR324607
VERSION AR324607.1 GI:33710415
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2009 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1798 AGTGACGTCGTGCTCTT 1814
Db 1 AGTGACGTCGTGCTCTT 17

RESULT 537
AR329327 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 6729 from patent US 6566127.
ACCESSION AR329327
VERSION AR329327.1 GI:33715135
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6729 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1610 AGTGATCCACAGGGAC 1626
Db 1 AGTGATCCACAGGGAC 17

RESULT 538
AR329328 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 6730 from patent US 6566127.
ACCESSION AR329328
VERSION AR329328.1 GI:33715136
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6730 20-MAY-2003;
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FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1611 GTGATCCACAGGAC 1627
Db 1 GTGATCCACAGGAC 17

RESULT 539
AR329329
LOCUS AR329329 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6731 from patent US 6566127.
ACCESSION AR329329
VERSION AR329329.1 GI:33715137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6731 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1613 GCATCCACAGGACCTG 1629
Db 1 GTATCCACAGGACCTG 17

RESULT 540
AR329360
LOCUS AR329360 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6762 from patent US 6566127.
ACCESSION AR329360
VERSION AR329360.1 GI:33715168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6762 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1799 GTGACGCTGGTCTTT 1815
Db 1 GTGACGCTGGTCTTT 17

RESULT 541

AR398390
LOCUS AR398390 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 771 from patent US 6617438.
ACCESSION AR398390
VERSION AR398390.1 GI:40136163
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A., Matlic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 771 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCG 1694
Db 1 GACTTCGGCTGGCTG 17

RESULT 542
AR429225/c
LOCUS AR429225 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 28 from patent US 6642369.
ACCESSION AR429225
VERSION AR429225.1 GI:40189374
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Herrmann,B., Koschorz,B. and Kispert,A.
TITLE Nucleic acids involved in the responder phenotype and applications thereof
JOURNAL Patent: US 6642369-A 28 04-NOV-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1747 GTGAAGTGGATGCGCC 1763
Db 17 GTGAAGTGGATGCGCC 1

RESULT 543
AR464319
LOCUS AR464319 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7996 from patent US 6686188.
ACCESSION AR464319
VERSION AR464319.1 GI:42699376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7996 03-FEB-2004;

FEATURES	source	Location/Qualifiers	1. .17	Score 15.4; DB 1; Length 17;	Indels	Gaps	0;
Query Match		0.4%;	Score 15.4; DB 1; Length 17;				
Best Local Similarity		94.1%;	Pred. No. 7.4e+02;				
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	1992	CACCTTCAAGCAGCTGG	2008				
DB	1	CACCATCAAGCAGCTGG	17				
RESULT 544							
LOCUS	AX530933	Sequence 442 from Patent EP1239051.	17 bp	DNA	linear	PAT 22-NOV-2002	
DEFINITION	AX530933						
ACCESSION	AX530933	1	GI:25253656				
VERSION	AX530933.1						
KEYWORDS							
SOURCE		Homo sapiens (human)					
ORGANISM		Homo sapiens					
REFERENCE		Shannon,M.					
AUTHORS		Human posh-like protein 1					
TITLE		Patent: EP 1239051-A 442 11-SEP-2002;					
JOURNAL		Aeomica, Inc. (US)					
FEATURES		Location/Qualifiers					
source		1. .17					
Query Match		0.4%;	Score 15.4; DB 1; Length 17;				
Best Local Similarity		94.1%;	Pred. No. 7.4e+02;				
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	546	GGGCTGCCGGCAACC	562				
DB	1	GGGCTGCCGGCAACC	17				
RESULT 545							
LOCUS	AX734179	Sequence 5813 from Patent WO03025175.	17 bp	DNA	linear	PAT 08-MAY-2003	
DEFINITION	AX734179						
ACCESSION	AX734179						
VERSION	AX734179.1		GI:30513522				
KEYWORDS							
SOURCE		Homo sapiens (human)					
ORGANISM		Homo sapiens					
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS		Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.					
TITLE		Telerman,A., Anson,R. and Tuijnder,M.					
JOURNAL		Sequences involved in phenomena of tumour suppression, tumour					
FEATURES		reversion, apoptosis and/or virus resistance and their use as					
source		medicines					
Query Match		0.4%;	Score 15.4; DB 1; Length 17;				
Best Local Similarity		94.1%;	Pred. No. 7.4e+02;				
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	546	GGGCTGCCGGCAACC	562				
DB	1	GGGCTGCCGGCAACC	17				
RESULT 546							
LOCUS	AX738591	Sequence 4181 from Patent WO03025177.	17 bp	DNA	linear	PAT 08-MAY-2003	
DEFINITION	AX738591						
ACCESSION	AX738591						
VERSION	AX738591.1		GI:30517881				
KEYWORDS							
SOURCE		Homo sapiens (human)					
ORGANISM		Homo sapiens					
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS		Mammalia; Euthera; Primates; Catarhini; Hominidae; Homo.					
TITLE		Telerman,A., Anson,R. and Tuijnder,M.					
JOURNAL		Sequences involved in phenomena of tumour suppression, tumour					
FEATURES		reversion, apoptosis and/or resistance to viruses and the use					
source		thereof as medicaments					
Query Match		0.4%;	Score 15.4; DB 1; Length 17;				
Best Local Similarity		94.1%;	Pred. No. 7.4e+02;				
Matches	16;	Conservative	0;	Mismatches	1;	Indels	0;
QY	2206	GGTCCCAACAATGTGA	2222				
DB	1	GATCCCAACAATGTGA	17				
RESULT 547							
LOCUS	BD091430/c	Nucleic acids involved in the responder phenotype and applications	17 bp	DNA	linear	PAT 27-AUG-2002	
DEFINITION	BD091430	thereof.					
ACCESSION	BD091430						
VERSION	BD091430.1		GI:22637041				
KEYWORDS							
SOURCE		JP 2001523449-A/19.					
ORGANISM		synthetic construct					
REFERENCE		artificial sequences.					
AUTHORS		1 (bases 1 to 17)					
TITLE		Herrmann,B., Koschorz,B. and Kispert,A.					

RESULT 550


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QY 2316 TCTGTGTGTGTGTGTGT 2332
Db 17 TATGTGTGTGTGTGTGT 1

RESULT 557
AR103195/c
LOCUS AR103195 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 89 from patent US 6087160.
ACCESSION AR103195
VERSION AR103195.1 GI:12814783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yuan,J. and Miura,M.
TITLE Programmed cell death genes and proteins
JOURNAL Patent: US 6087160-A 89 11-JUL-2000;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1353 GGGATGATGACATGA 1369
Db 20 GGAGTTGATGACATGA 4

RESULT 558
AR199773/c
LOCUS AR199773 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 34 from patent US 6355482.
ACCESSION AR199773
VERSION AR199773.1 GI:20249847
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank, and Freier,S.M.
TITLE Antisense inhibition of integrin beta 4 binding protein expression
JOURNAL Patent: US 6355482-A 34 12-MAR-2002;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 721 ACCACCGACAGGAGCT 737
Db 20 ACCACCGACAGGAGCT 4

RESULT 559
AR214196/c
LOCUS AR214196 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 4 from patent US 6406890.
ACCESSION AR214196
VERSION AR214196.1 GI:23311726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mueller,M.W.

TITLE Process for the amplification of nucleic acid
JOURNAL Patent: US 6406890-A 4 18-JUN-2002;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2835 TATATATATAACATATA 2851
Db 19 TTTATATATAACATATA 3

RESULT 560
AR214200/c
LOCUS AR214200 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6406890.
ACCESSION AR214200
VERSION AR214200.1 GI:23311730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mueller,M.W.
TITLE Process for the amplification of nucleic acid
JOURNAL Patent: US 6406890-A 8 18-JUN-2002;
FEATURES
    Location/Qualifiers
    1..20
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2835 TATATATATAACATATA 2851
Db 19 TTTATATATAACATATA 3

RESULT 561
AR370498
LOCUS AR370498 20 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 17 from Patent WO0196371.
ACCESSION AR370498
VERSION AR370498.1 GI:18857540
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Broenner,G., Ciosek,T., Dohrmann,C., Haeder,T. and Rothe,M.
TITLE Adipose-related gene
JOURNAL Patent: WO 0196371-A 17 20-DEC-2001;
FEATURES
    Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"

Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 254 ACAAGAAGCTGCTGCC 270
Db 4 ACAAGAAGCTGCTGCC 20
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RESULT 562
AX527818
LOCUS AX527818.1 linear PAT 21-NOV-2002
DEFINITION Sequence 72 from Patent WO0230974.
ACCESSION AX527818
VERSION AX527818.1 GI:25172322
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Grose, W.M., Alsobrook, J.P., Lepley, D.M., Burgess, C.E., Mishra, V.,
Kekuda, R., Li, L., Padigaru, M., Shimkets, R.A., Zerhusen, B.D.,
Spytek, K.A., Edinger, S., Gerlach, V., Macdougall, J., Stone, D.,
Gunther, E., and Ellerman, K.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0230974-A 72 18-APR-2002;
Curagen Corporation (US)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 854 AGGAGGAGCTGTGGAG 870
DB 2 AGGAGGAGCTGTGGAG 18
RESULT 563
AX601143/c
LOCUS AX601143 linear PAT 17-FEB-2003
DEFINITION Sequence 238 from Patent WO02092851.
ACCESSION AX601143
VERSION AX601143.1 GI:28401216
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Binns, M.M., and Swinburne, J.E.
TITLE Genetic typing
JOURNAL Patent: WO 02092851-A 238 21-NOV-2002;
ANIMAL HEALTH TRUST (GB); The British Horseracing Board (GB)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 594 CCACTGCAAGGTGTACA 610
DB 20 CCACTGCAAGGTGTACA 4
RESULT 564
BD144226
LOCUS BD144226 linear PAT 17-JAN-2003
DEFINITION Method for examining allergic diseases.
ACCESSION BD144226
VERSION BD144226.1 GI:27849984
KEYWORDS JP 2002119281-A/14.

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Sugita, Y., Hashida, R., Ogawa, K., Fujishima, T. and Tsujimoto, K.
TITLE Method for examining allergic diseases
JOURNAL Patent: JP 2002119281-A 14 23-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
COMMENT
OS Artificial Sequence
PN JP 2002119281-A/14
PD 23-APR-2002
PF 11-OCT-2000 JP 2000311193
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, KOZO
TSUJIMOTO
PC C12N15/09, A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P37/08,
C12N5/10,
PC C12O1/02, C12O1/68, G01N33/15, G01N33/50// (C12N15/09, C12R1:91),
C12N5/10, C12R1:91), (C12O1/02, C12R1:91), C12N15/00, C12N5/00, PC
(C12N5/00, C12R1:91), (C12N5/00, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized
CC sequence primer
CC key Location/Qualifiers
FH key 1..20
FT source /organism='Artificial Sequence'.
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 8.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1874 TGGAGGAGCTCTCAAG 1890
DB 1 TGGAGGAGCTCTCAGG 17
RESULT 565
AR177588
LOCUS AR177588 21 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 28 from patent US 632934.
ACCESSION AR177588
VERSION AR177588.1 GI:17919943
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Johnson, G.L.
TITLE Human MEKK proteins, corresponding nucleic acid molecules, and uses
JOURNAL Patent: US 6312934-A 28 06-NOV-2001;
therefor
FEATURES
source
1..21
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2001 GCAGCTGGTGGAGACC 2017
DB 1 GGAGCTGGTGGAGACC 17
RESULT 566
CQ788487/c
LOCUS CQ788487 21 bp DNA linear PAT 24-MAR-2004


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DEFINITION      Sequence 64 from Patent WO2004020619.
ACCESSION       CQ788487
VERSION         CQ788487.1 GI:45723252
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1
AUTHORS         Constien,R., Muddle,G., Schroeder,A., Yu,P. and Hanke,P.
TITLE           Modified phospholipase c-gamma-2, expression products, and
                non-human animal models comprising said genes, and therapeutic uses
JOURNAL         Patent: WO 2004020619-A 64 11-MAR-2004;
                Ingenium Pharmaceuticals AG (DE)
FEATURES        Location/Qualifiers
                source
                1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="primer pic92-48"

Query Match      0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1559 TGTCTGTGCTACACAG 1575
DB 18 TGTCTGTGCTACACAG 2

RESULT 567
AX146144
LOCUS          AX146144 21 bp DNA linear PAT 31-MAY-2001
DEFINITION     Sequence 335 from Patent WO0134840.
ACCESSION      AX146144
VERSION        AX146144.1 GI:14284662
KEYWORDS       Homo sapiens (human)
SOURCE         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS        Au,K.G., Chen,J.G., Patil,N. and Thomas,D.
TITLE          Genetic compositions and methods
JOURNAL        Patent: WO 0134840-A 335 17-MAY-2001;
                GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES        Location/Qualifiers
                source
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                variation
                1..21
                /note="n' represents a polymorphic base"

Query Match      0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1820 TCCTGCTCTGGGAGATCT 1837
DB 4 TCCTCTNTGGGAGATCT 21

RESULT 568
AX539564
LOCUS          AX539564 21 bp DNA linear PAT 23-NOV-2002
DEFINITION     Sequence 351 from Patent WO02059142.
ACCESSION      AX539564
VERSION        AX539564.1 GI:25273096
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1

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AUTHORS         Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE           Polymorphisms in the human gene for the multidrug
                resistance-associated protein 1 (mrp-1) and their use in diagnostic
                and therapeutic applications
JOURNAL         Patent: WO 02059142-A 351 01-AUG-2002;
                Epidauros Biotechnologie AG (DE)
FEATURES        Location/Qualifiers
                source
                1..21
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="r = g or a"

Query Match      0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATGGCACAGGCTGGTG 21
DB 2 GGGTGGCACRGTGCTGGTG 20

RESULT 569
AX539565/c
LOCUS          AX539565 21 bp DNA linear PAT 23-NOV-2002
DEFINITION     Sequence 352 from Patent WO02059142.
ACCESSION      AX539565
VERSION        AX539565.1 GI:25273098
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1
AUTHORS        Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE           Polymorphisms in the human gene for the multidrug
                resistance-associated protein 1 (mrp-1) and their use in diagnostic
                and therapeutic applications
JOURNAL         Patent: WO 02059142-A 352 01-AUG-2002;
                Epidauros Biotechnologie AG (DE)
FEATURES        Location/Qualifiers
                source
                1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="y = c or t"

Query Match      0.4%; Score 15.4; DB 1; Length 21;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGATGGCACAGGCTGGTG 21
DB 20 GGGTGGCACRGTGCTGGTG 2

RESULT 570
AX955606
LOCUS          AX955606 21 bp DNA linear PAT 08-JAN-2004
DEFINITION     Sequence 5 from Patent WO03095491.
ACCESSION      AX955606
VERSION        AX955606.1 GI:40784264
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1
AUTHORS        Brekke,O.H., Stacy,J. and Kausmally,L.
TITLE          Product
JOURNAL        Patent: WO 03095491-A 5 20-NOV-2003;
                Affitech AS (NO) ; Brekke, Ole Henrik (NO)
FEATURES        Location/Qualifiers
                source
                1..21
                /organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 21;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 853 GAGGAGGACGTGGTGGAGCT 873
Db 1 GAGGTGACGTGKTGGAGWCY 21

RESULT 571
AX042549
LOCUS 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 115 from Patent WO0065088.
ACCESSION AX042549
VERSION AX042549.1 GI:11341157
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 115 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="DPBI Homozygote primer sequence"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3264 TTTTATTTGCTTGTCTCTTTTCCAG 3288
Db 1 TTTTATTTTGTCTTGTCTCTTTTCCAG 25

RESULT 572
AX043230
LOCUS 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 796 from Patent WO0065088.
ACCESSION AX043230
VERSION AX043230.1 GI:11341838
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 796 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="DPBI Heterozygote Primer Sequence"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3264 TTTTATTTGCTTGTCTCTTTTCCAG 3288
Db 1 TTTTATTTTGTCTTGTCTCTTTTCCAG 25

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RESULT 573
AX351715/c
LOCUS 30 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 11 from Patent WO0193902.
ACCESSION AX351715
VERSION AX351715.1 GI:18616998
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 11 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source
1. .30
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 30;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3310 TTTTCTTTTAGGAGATTATTTT 3334
Db 29 TTTTCTTTTAGGAGATTATTTT 5

RESULT 574
A08914/c
LOCUS 31 bp DNA linear PAT 02-SEP-1993
DEFINITION H.sapiens (haplotype 3, allele MS32, isolate Mormon, serial number
2) minisatellite sequence.
ACCESSION A08914
VERSION A08914.1 GI:411836
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 31)
AUTHORS Jeffreys, A.J.
TITLE Extended nucleotide sequences
JOURNAL Patent: EP 0370719-A 97 30-MAY-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES
source
1. .31
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 15.4; DB 1; Length 31;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3261 ATATTTTATTGCTTGTCTCTTTT 3285
Db 31 ATATTTTATTGCTTGTCTCTTTT 7

RESULT 575
AR029831
LOCUS 35 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861244.
ACCESSION AR029831
VERSION AR029831.1 GI:5943045
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 20 19-JAN-1999;
FEATURES Location/Qualifiers
source
1..35
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 35;
Best Local Similarity 76.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3262 TATTATTATGCTTCTCTTTTC 3286
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Db 2 TTTTCTTTTCTTTTCTTTTC 26
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RESULT 576
LOCUS I31440 41 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 352 from patent US 5582979.
ACCESSION I31440
VERSION I31440.1 GI:1822231
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 352 10-DEC-1996;
FEATURES Location/Qualifiers
source
1..41
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 41;
Best Local Similarity 61.0%; Pred. No. 1.3e+03;
Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3047 TGGGCCCCCTGGCACTCTTGTGCCACACCCCACTTCCA 3087
|||||
Db 1 TGAGACCTGGACACACACACACACACACACACACACACA 41
|||||

RESULT 577
LOCUS I31443 41 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 355 from patent US 5582979.
ACCESSION I31443
VERSION I31443.1 GI:1822234
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 355 10-DEC-1996;
FEATURES Location/Qualifiers
source
1..41
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.4; DB 1; Length 41;
Best Local Similarity 61.0%; Pred. No. 1.3e+03;
Matches 25; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3047 TGGGCCCCCTGGCACTCTTGTGCCACACCCCACTTCCA 3087
|||||

Db 1 TGAGACCTGGACACACACACACACACACACACACACACA 41
|||||

RESULT 578
LOCUS AR181773/c 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 235 from patent US 6335194.
ACCESSION AR181773
VERSION AR181773.1 GI:20223987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C. Frank., Ackermann, E.J., Swayze, E.E. and Cowsert, L.M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: US 6335194-A 235 01-JAN-2002;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3458 AAGTTTATATATCTATAT 3477
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Db 20 ATGTTTATATATATATCT 1
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RESULT 579
LOCUS A65910 20 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 23 from Patent WO9738114.
ACCESSION A65910
VERSION A65910.1 GI:4537911
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fontana, A., Constan, D.B., Tobler, A.R., Altmann, K. and Schlapbach, R.
TITLE PUROMYCIN-SENSITIVE AMINOPEPTIDASES
JOURNAL Patent: WO 9738114-A 23 16-OCT-1997;
COMMENT CIBA GEIGY AG (CH)
FEATURES Location/Qualifiers
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3275 TTGTCTCTTTTCAGGAGAT 3294
|||||
Db 1 TTTTCTCTTTTCAATAGAT 20
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RESULT 580
LOCUS AR050627 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5827726.
ACCESSION AR050627
VERSION AR050627.1 GI:5973352
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

[illegible]

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JOURNAL Patent: US 6271030-A 197 07-AUG-2001;
FEATURES
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  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1478 GGCGCGGGCGGGCCCGGGC 1497
Db 20 GGCGCGGGCGGGCCCGGGC 1
RESULT 586
LOCUS AR170760 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6291742.
ACCESSION AR170760
VERSION AR170760.1 GI:17908719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Somerville,C., Broun,P. and van de Loo,F.
TITLE Production of hydroxylated fatty acids in genetically modified
  Plants
JOURNAL Patent: US 6291742-A 13 18-SEP-2001;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
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Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2982 CAGGGCTTTTCTGGCACCG 3001
Db 20 CAAGGGCTTTTCTGGTACCG 1
RESULT 587
LOCUS AR176139 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6310194.
ACCESSION AR176139
VERSION AR176139.1 GI:17917438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Somerville,C., Broun,P. and van de Loo,F.
TITLE Plant fatty acid hydroxylases
JOURNAL Patent: US 6310194-A 13 30-OCT-2001;
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2982 CAGGGCTTTTCTGGCACCG 3001
Db 20 CAAGGGCTTTTCTGGTACCG 1
RESULT 588
LOCUS BD250269 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of p38 mitogen activated protein kinase
  expression.
ACCESSION BD250269
VERSION BD250269.1 GI:33060039
KEYWORDS JP 2002540781-A/21.
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Gaarde,W.A., Nero,P.S., Mckay,R. and Popoff,I.
TITLE Antisense modulation of p38 mitogen activated protein kinase
JOURNAL Patent: JP 2002540781-A 21 03-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
  OS Artificial Sequence
  PN JP 2002540781-A/21
  PD 03-DEC-2002
  PF 04-APR-2000 JP 2000609429
  PR 06-APR-1999 US 09/286904
  PI BRETT P MONIA,WILLIAM A GAARDE,PAMELA S NERO,ROBERT MCKAY,IAN
  PO POPOFF
  PC C12N15/09,A61K31/711,A61P19/02,A61P29/00,A61P37/06,
  A61P43/00,
  C12N5/10,C12N9/99,C12N15/00,C12N5/00
  PC Antisense modulation of p38 mitogen activated protein kinase
  CC expression
  FT Key
  FT source
  FT Location/Qualifiers
  FT /organism="Artificial Sequence".
FEATURES
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Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2321 GTGTGTGTGTGTGCGTGCT 2340
Db 20 GTTAGTGTGTGTGCTGTGT 1
RESULT 589
LOCUS CQ754256 20 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 6 from Patent WO2004001367.
ACCESSION CQ754256
VERSION CQ754256.1 GI:44845518
KEYWORDS
SOURCE synthetic construct
  ORGANISM synthetic construct
    artificial sequences.
REFERENCE 1
AUTHORS Rapp,U.R. and Sedlacek,H.H.
TITLE Test system for identifying cancerous diseases
JOURNAL Patent: WO 2004001367-A 6 31-DEC-2003;
  Medinova Gesellschaft fuer medizinische Innovationen aus;
  akademischer Forschung mbH (DE)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
      misc_feature
        1..20
          /note="primer"
Query Match
  Best Local Similarity 0.4%; Score 15.2; DB 1; Length 20;
  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1013 AGATCTCCGCTTCCGCTC 1032
Db 1 ACATCTCCGCGATCCCACTC 20

RESULT 590
CQ759158/c
LOCUS CQ759158 20 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 70 from Patent WO2003106681.
ACCESSION CQ759158
VERSION CQ759158.1 GI:44849149
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1
AUTHORS Altan,O., Kurreck,J., Grueneweller,A. and Erdmann,V.
TITLE Antisense oligonucleotides against pml
JOURNAL Patent: WO 2003106681-A 70 24-DEC-2003;
Gruenenthal GmbH (DE)
FEATURES
source
1..20
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1809 GTCCCTTGGGCTCTGCTCT 1828
Db 20 GTCCCTGGGATCTGCTCT 1

RESULT 591
CQ762434
LOCUS CQ762434 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 1052 from Patent WO2004003201.
ACCESSION CQ762434
VERSION CQ762434.1 GI:44905670
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrlh expression
JOURNAL Patent: WO 2004003201-A 1052 08-JAN-2004;
Pharmacia Corporation (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Human LRH1 antisense"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3558 CTGGACTGCTACCTTTCAAA 3577
Db 1 CTGCACAGCTACCTTTTAAA 20

RESULT 592
CQ762603/c
LOCUS CQ762603 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 1221 from Patent WO2004003201.
ACCESSION CQ762603

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CQ762603.1 GI:44905839
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrlh expression
JOURNAL Patent: WO 2004003201-A 1221 08-JAN-2004;
Pharmacia Corporation (US)
FEATURES
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Human LRH1 antisense"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2306 AGAGCTTTGGTCTGTGTGTG 2325
Db 20 AGAGCTTTGTCCTGCTGTGTG 1

RESULT 593
CQ763381
LOCUS CQ763381 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 1999 from Patent WO2004003201.
ACCESSION CQ763381
VERSION CQ763381.1 GI:44906617
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane,C.D.
TITLE Antisense modulation of lrlh expression
JOURNAL Patent: WO 2004003201-A 1999 08-JAN-2004;
Pharmacia Corporation (US)
FEATURES
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Human LRH1 antisense"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 318 CCCCACCTCCCTCCATCTCTCT 337
Db 1 CCCCACCTCCCAATCTCTT 20

RESULT 594
E12301
LOCUS E12301 20 bp DNA linear PAT 27-APR-1998
DEFINITION Primer.
ACCESSION E12301
VERSION E12301.1 GI:3251135
KEYWORDS JP 1996308586-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nezu,J.
TITLE CODING PROTEIN KINASE
JOURNAL Patent: JP 1996308586-A 2 26-NOV-1996;
CHUGAI PHARMACEUT CO LTD
COMMENT OS None

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[illegible]

QY 3715 GAGGTGTACCCAAACGGC 3734
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Db 20 GAGGTGTACCCAAACGAGC 1

RESULT 604
AR225997/c 20 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 60 from patent US 644465.
ACCESSION AR225997
VERSION AR225997.1 GI:27264151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt, J. and Freier, S.M.
TITLE Antisense modulation of Her-1 expression
JOURNAL Patent: US 644465-A 60 03-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1671 GATCGCAGACTTCGGGCTGG 1690
|||||
Db 20 GATCACAGATTTTGGGCTGG 1

RESULT 605
AR228818/c 20 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 22 from patent US 6448079.
ACCESSION AR228818
VERSION AR228818.1 GI:27267957
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P., Gaarde, W.A., Nero, P., and McKay, R.
TITLE Antisense modulation of p38 mitogen activated protein kinase
expression
JOURNAL Patent: US 6448079-A 22 10-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGTCGTGTGT 2340
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Db 20 GTTAGTGTGTGTGATGTGT 1

RESULT 606
AR264939 20 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 23 from patent US 6492121.
ACCESSION AR264939
VERSION AR264939.1 GI:29693326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

AUTHORS Kurane, R., Kanagawa, T., Kamagata, Y., Kurata, S., Yamada, K.,
Yokomaki, T., Koyama, O. and Furusho, K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 23 10-DEC-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATAATTTATTGAG 3492
|||||
Db 1 TATATATATAATTTTTTGGG 20

RESULT 607
AR304132 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 6 from patent US 6544768.
ACCESSION AR304132
VERSION AR304132.1 GI:31693046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buck, J. and Levin, L.R.
TITLE Mammalian soluble adenylyl cyclase
JOURNAL Patent: US 6544768-A 6 08-APR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1998 CAAGCAGCTGTGGAGGACC 2017
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Db 1 CGAGCAGCTGTGGAGATCC 20

RESULT 608
AR305121/c 20 bp DNA linear PAT 12-JUN-2003
LOCUS Sequence 75 from patent US 6545137.
ACCESSION AR305121
VERSION AR305121.1 GI:31694431
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
TITLE Receptor
JOURNAL Patent: US 6545137-A 75 08-APR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 157 GCTCCATCTCTGGAGATGA 176
Db 20 GCTGCATCTCTGGAGAGA 1

RESULT 609
LOCUS AR309225/c 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 75 from patent US 6555654.
ACCESSION AR309225
VERSION AR309225.1 GI:31701230
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
TITLE LDL-receptor
JOURNAL Patent: US 6555654-A 75 29-APR-2003;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 157 GCTCCATCTCTGGAGATGA 176
Db 20 GCTGCATCTCTGGAGAGA 1

RESULT 610
LOCUS AR399605 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 52 from patent US 6620623.
ACCESSION AR399605
VERSION AR399605.1 GI:40141777
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Yershov, G., Alferov, O. and Kukhtin, A.
TITLE Biochip reader with enhanced illumination and bioarray positioning
apparatus
JOURNAL Patent: US 6620623-A 52 16-SEP-2003;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGAGATGATGAAGATGA 1369
Db 1 GATGATGATGATGATGA 20

RESULT 611
LOCUS AR399627 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 74 from patent US 6620623.
ACCESSION AR399627
VERSION AR399627.1 GI:40141812
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of vascular endothelial growth factor
receptor-1 expression
JOURNAL Patent: US 6710174-A 72 23-MAR-2004;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGAGATGATGAAGATGA 1369
Db 1 GATGATGATGATGATGA 20

RESULT 612
LOCUS AR478220 20 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 23 from patent US 6699661.
ACCESSION AR478220
VERSION AR478220.1 GI:47236868
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurane, R., Kanagawa, T., Kamagata, Y., Kurata, S., Yamada, K.,
Yokomaku, T., Koyama, O. and Furusho, K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
Patent: US 6699661-A 23 02-MAR-2004;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATATTTTGGG 20
Db 1 TATATATATATTTTGGG 20

RESULT 613
LOCUS AR489949/c 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 72 from patent US 6710174.
ACCESSION AR489949
VERSION AR489949.1 GI:47257062
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of vascular endothelial growth factor
receptor-1 expression
JOURNAL Patent: US 6710174-A 72 23-MAR-2004;
FEATURES
source Location/Qualifiers
1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 5718 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 GCTGGTGCACGAGGAGCAACG 1663
Db 20 GCTGGGACAGAGGTCAACG 1
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RESULT 619
AX452336/c
LOCUS AX452336 20 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 22 from Patent WO0242441.
ACCESSION AX452336
VERSION AX452336.1 GI:21712247
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Leemle, B., Gerritsen, H.E., Furlan, M., Turecek, P., Schwarz, H.P., Schneiflinger, F., Antoine, G., Kerschbaumer, R., Tagliavacca, L., Zimmermann, K., and Voelkel, D.
TITLE Von willibrand factor (vwf) cleaving protease polypeptide, nucleic acid encoding the polypeptide and use of polypeptide
JOURNAL Patent: WO 0242441-A 22 30-MAY-2002;
Baxter Aktiengesellschaft (AT)
FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
primer_bind 1..20

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 182 ACGGGAGGACGAGGCTGAG 201
Db 20 ATGGGGAGGACGAGGTGAG 1
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RESULT 620
AX477161
LOCUS AX477161 20 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 252 from Patent WO0220848.
ACCESSION AX477161
VERSION AX477161.1 GI:22216414
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bodnar, J.S., Castellani, L.W., Chatterjee, A., de Jong, P., Lusis, A.J., Ohmen, J., Ross, D., Tafuri, S., and Wu, C.
TITLE Gene and sequence variation associated with cancer
JOURNAL Patent: WO 0220848-A 252 14-MAR-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
source 1..20
/organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Primer"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3651 CTTGCTTGCCTGCAGGGCCA 3670
Db 1 CTTGCATGCTGCAGGTGCA 20
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|||||

RESULT 621
AX526537
LOCUS AX526537 20 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 252 from Patent WO0220847.
ACCESSION AX526537
VERSION AX526537.1 GI:25171344
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bodnar, J.S., Castellani, L.W., Chatterjee, A., de Jong, P., Lusis, A.J., Ohmen, J., Ross, D., Tafuri, S., and Wu, C.
TITLE Gene and sequence variation associated with lipid disorder
JOURNAL Patent: WO 0220847-A 252 14-MAR-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)
FEATURES
source 1..20
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Synthetic Primer"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3651 CTTGCTTGCCTGCAGGGCCA 3670
Db 1 CTTGCATGCTGCAGGTGCA 20
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|||||

RESULT 622
AX712200/c
LOCUS AX712200 20 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 34 from Patent WO03018810.
ACCESSION AX712200
VERSION AX712200.1 GI:29823423
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Chen, E. and Stacy, C.
TITLE Modified cry3a toxins and nucleic acid sequences coding therefor
JOURNAL Patent: WO 03018810-A 34 06-MAR-2003;
Syngenta Participations AG (CH)
FEATURES
source 1..20
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/db_xref="taxon:32630"
/note="CNS16 Primer"

Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1995 CTTCAAGCAGCTGTGAGG 2014
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Db      20  CTTCTGGAGCAGGTGGAGG 1
RESULT 623
AX787161/c
LOCUS   AX787161 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 22 from Patent WO03013598.
ACCESSION AX787161
VERSION   AX787161.1 GI:32954361
KEYWORDS
SOURCE    unidentified
ORGANISM  unclassified.
REFERENCE
1 Lam,D.M., Zeng,F. and Leung,F.C.
  Novel vaccine compositions and methods of vaccine preparation for
  veterinary and human diseases
JOURNAL  Patent: WO 03013598-A 22 20-FEB-2003;
        Lam, Dominic M. K., VaxGene Corporation (CN) ; Zeng, Fanya, VaxGene
        Corporation (CN) ; Leung, Frederick C. VaxGene Corporation (CN)
FEATURES
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/notes="genus Arterivirus of Arteriviridae"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1537 CAGCTCACCTTCAAGGACCT 1556
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Db 20 CAGCTCAAGTTCGAGGACCT 1

RESULT 624
AX799916
LOCUS   AX799916 20 bp DNA linear PAT 08-OCT-2003
DEFINITION Sequence 2 from Patent WO03045995.
ACCESSION AX799916
VERSION   AX799916.1 GI:37605404
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
        artificial sequences.
REFERENCE
1 Zeng,S., Bogner,F.M., Kunert,R., Mueller,D. and Unterluggauer,F.
  Cell culture process
  Patent: WO 03045995-A 2 05-JUN-2003;
  BIOCHEMIE Gesellschaft m.b.H. (AT)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3576 AAGCTTGGAGGGAAGCCGTG 3595
||||| ||||| |||||
Db 1 AAGCTTGTGGGAAGCCGTG 20

RESULT 625
BD072884
LOCUS   BD072884 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
ACCESSION BD072884
VERSION   BD072884.1 GI:22618487
KEYWORDS
SOURCE    and method for analyzing data obtained by that method.
ORGANISM  AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
REFERENCE
1 Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
  Yokomaku,T., Koyama,O. and Furusho,K.
  Method for assaying nucleic acid, nucleic acid probe used therefor,
  and method for analyzing data obtained by that method
JOURNAL  Patent: JP 2001286300-A 33 16-OCT-2001;
        JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
        NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
        AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT   OS Artificial Sequence
        PN JP 2001286300-A/33
        PD 16-OCT-2001
        PF 20-APR-2000 JP 2000120097

KEYWORDS JP 2001286300-A/22.
SOURCE    synthetic construct
ORGANISM  artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
        and method for analyzing data obtained by that method
JOURNAL   Patent: JP 2001286300-A 22 16-OCT-2001;
        JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
        NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
        AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT   OS Artificial Sequence
        PN JP 2001286300-A/22
        PD 16-OCT-2001
        PF 20-APR-2000 JP 2000120097

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATATTTTTCGAG 3492
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Db 1 TATATATATATTTTTCGG 20

RESULT 626
BD072895/c
LOCUS   BD072895 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
ACCESSION BD072895
VERSION   BD072895.1 GI:22618498
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
        and method for analyzing data obtained by that method
JOURNAL   Patent: JP 2001286300-A 33 16-OCT-2001;
        JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
        NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
        AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT   OS Artificial Sequence
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        PD 16-OCT-2001
        PF 20-APR-2000 JP 2000120097

```

PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU, OSAMU KOYAMA, KENTA FURUSHO
PC C12Q1/68, C12M1/00, C12N15/09, G01N31/22, G01N33/53, G01N33/542, PC
G01N33/566.
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
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Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3473 TATATATATATATTTTGGAG 3492
Db 20 TATATATATATATTTTGGG 1

RESULT 627
BD106032/c
LOCUS
DEFINITION Novel LDL-receptor.
ACCESSION BD106032
VERSION BD106032.1 GI:23200850
KEYWORDS JP 2002501376-A/47.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
REFERENCE 1 (bases 1 to 20)
AUTHORS Todd J.A., Hess J.W., Caskey, C.T., Cox, R.D., Gerhold, D., Hammond, H.
and Hey, P.
TITLE Novel LDL-receptor
JOURNAL THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
INC
COMMENT
PN JP 2002501376-A/47
PD 15-JAN-2002
PF 15-APR-1998 JP 1998543635
PR 15-APR-1997 US 60/043553, 05-JUN-1997 US 60/048740 PI
JOHN ANDREW TODD, JOHN WILFRED HESS, CHARLES
THOMAS CASKEY, ROGER
PI DAVID COX,
PI DAVID GERHOLD, HOLLY HAMMOND, PATRICIA HEY
PC C12N15/12, C12N15/11, C12Q1/68, C07K14/705, C07K16/28, A61K38/17,
PC A61K39/395,
PC A61K48/00
CC Strandedness: Single;
CC Topology: Linear;
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FT source 1..20
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1..20
Location/Qualifiers
/organism="Chlamydia sp."
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Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 157 GCTCCATCCTCGGAGATGA 176
Db 20 GCTGCATCCTCTGGAGAAGA 1

RESULT 628
BD107511
LOCUS
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107511
VERSION BD107511.1 GI:23202329
KEYWORDS JP 2002000275-A/20.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurane, R., Kanekawa, T., Kamagata, Y., Kurata, S., Yamada, K. and
Yokomaku, T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 20 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT
OS Artificial Sequence
PN JP 2002000275-A/20
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE, TAKAHIRO KANEKAWA, YOICHI KAMAGATA, SHINYA PI
KURATA,
PI KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU
PC C12N15/09, C12M1/00, C12M1/34, C12Q1/68, C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..20
/organism="synthetic construct"
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QY 3473 TATATATATATTTTGGAG 3492
Db 1 TATATATATATTTTGGG 20

RESULT 629
BD107522/c
LOCUS
DEFINITION Novel quantitative polymorphism analysis method.
ACCESSION BD107522
VERSION BD107522.1 GI:23202340
KEYWORDS JP 2002000275-A/31.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kurane, R., Kanekawa, T., Kamagata, Y., Kurata, S., Yamada, K. and
Yokomaku, T.
TITLE Novel quantitative polymorphism analysis method
JOURNAL Patent: JP 2002000275-A 31 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION, KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL

Query Match 0.48; Score 15.2; DB 1; Length 20;

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INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/24
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..20
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Location/Qualifiers
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/db_xref="taxon:32630"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATATTTATTGAG 3492
DB 20 TATATATATATTTTTGGG 1
RESULT 634
BD166043
LOCUS
DEFINITION
20 bp DNA linear PAT 17-JAN-2003
BD166043
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION
BD166043
VERSION
BD166043.1 GI:27871855
KEYWORDS
JP 2002191372-A/23.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
Patent: JP 2002191372-A 23 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/23
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'
FEATURES
source
1..20
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATATTTATTGAG 3492
DB 1 TATATATATATTTTTGGG 20
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/24
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3473 TATATATATATTTATTGAG 3492
DB 1 TATATATATATTTTTGGG 20
RESULT 633
BD145054/C
LOCUS
DEFINITION
20 bp DNA linear PAT 17-JAN-2003
BD145054
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION
BD145054
VERSION
BD145054.1 GI:27850812
KEYWORDS
JP 2002119291-A/35.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL
Patent: JP 2002119291-A 35 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002119291-A/35
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
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RESULT 635
BD166054/c
LOCUS
DEFINITION
20 bp DNA linear PAT 17-JAN-2003
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
BD166054
BD166054.1 GI:27871866
VERSION
JP 2002191372-A/34.
KEYWORDS
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE
Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL
Patent: JP 2002191372-A 34 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002191372-A/34
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
CC decrease in fluorescence emission of a nucleic acid probe CC
CC labeled with CC
CC BODIBY FL/C6 upon the hybridization of the CC
CC probe with a target CC
CC nucleic CC
CC acid. Location/Qualifiers
FT key 1..20
FT source /organism='Artificial Sequence'.
FT /mol_type='genomic DNA'
FT /db_xref='taxon:32644'
FEATURES
source
1..20
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

3473 TATATATATATATTTTGGAG 3492
Db 20 TATATATATATTTTGGG 1
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Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 636
DOGH0X7B/c
LOCUS
DEFINITION
20 bp DNA linear STS 11-APR-1996
Canis familiaris Homeobox 7 (Hox7) STS DNA, 3' primer, sequence
tagged site.
L77371
L77371.1 GI:1261709
VERSION
STS; Homeobox 7; PCR identification; PCR primer; sequence tagged
site; universal mammalian STS.
KEYWORDS
Canis familiaris (dog)
SOURCE
Canis familiaris
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Vents,P.J., Brouillette,J.A., Yuzbasiyan-Gurkan,V. and Brewer,G.J.

TITLE
Gene-specific universal mammalian sequence-tagged sites:
application to the canine genome
JOURNAL
Unpublished (1996)
COMMENT
Original source text: Canis familiaris DNA.
Gene-specific universal mammalian sequence-tagged site for HOX7.
Primer for the 3' end is in exon 2. Human product is 151 bp. Canine
product is 151 bp. PCR conditions: 1 min, 94 C, 2 min, 57 C, 3 min,
72 C, 35 cycles.
FEATURES
Location/Qualifiers
source
1..20
/organism='Canis familiaris'
/mol_type='genomic DNA'
/db_xref='taxon:9615'
primer_bind
1..20
/note='PCR primer binding site'
/evidence=experimental
STS
1..20
Query Match 0.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1348 GAGATCGAGATGATGAAGAT 1367
Db 20 GAGCTGGAGAGCTGAAGAT 1
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RESULT 637
BD140705
LOCUS
DEFINITION
21 bp DNA linear PAT 18-SEP-2002
Methods for the simultaneous identification of novel biological
targets and lead structures for drug development.
ACCESSION
BD140705.1 GI:232335650
VERSION
JP 2002508507-A/7.
KEYWORDS
synthetic construct
SOURCE
artificial sequences.
REFERENCE
1 (bases 1 to 21)
AUTHORS
Heefner,D.L., Zepp,C.M., Gao,Y. and Jones,S.W.
TITLE
Methods for the simultaneous identification of novel biological
targets and lead structures for drug development
JOURNAL
Patent: JP 2002508507-A 7 19-MAR-2002;
SEPRACOR INC
COMMENT
OS Artificial Sequence
PN JP 2002508507-A/7
PD 19-MAR-2002
PF 18-DEC-1998 JP 2000539165
PR 18-DEC-1997 US 60/068035
PI DONALD L HEEFNER,CHARLES M ZEPPE,YUN GAO,STEVEN W JONES PC
G01N33/542,C12Q1/04,C12Q1/68,C12Q1/70,G01N21/00,G01N21/76, PC
G01N33/53.
PC G01N33/566//C12N15/09,C12N15/00
CC Description of Artificial Sequence: construct PH Key
FT Location/Qualifiers
FT source 1..21
FT /organism='Artificial Sequence'.
FEATURES
Location/Qualifiers
source
1..21
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2825 TATATACATATATATATATA 2844
Db 2 TATATACCTAGGTATATATA 21
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RESULT 638

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A28676/c
LOCUS A28676 21 bp RNA linear PAT 04-JUN-1995
DEFINITION dsRNA with central hinge (comp.).
ACCESSION A28676
VERSION A28676.1 GI:1248715
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS SHORT THERAPEUTIC dsRNA OF DEFINED STRUCTURE
TITLE Patent: WO 90/4090-A 4 29-NOV-1990;
JOURNAL Location/Qualifiers
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2920 GGGCGGGCGCTGGGGGGCG 2939
DB 21 GGGGGGGGGTGGGGGGGG 2
RESULT 639
AR073030/c
LOCUS AR073030 21 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 3 from patent US 5948680.
ACCESSION AR073030
VERSION AR073030.1 GI:9999793
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Baker,B.F. and Cowert,L.M.
TITLE Antisense inhibition of Elk-1 expression
JOURNAL Patent: US 5948680-A 3 07-SEP-1999;
FEATURES Location/Qualifiers
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 860 AGCTGGTGGAGCTGACGAG 879
DB 20 AGCTGGTGGATGCAGAGG 1
RESULT 640
AR084556
LOCUS AR084556 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 45 from patent US 5981185.
ACCESSION AR084556
VERSION AR084556.1 GI:10011327
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 45 09-NOV-1999;
FEATURES Location/Qualifiers
source
1. .21
/organism="unknown"

/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1351 ATGGAGATGATGAAGATGAT 1370
DB 1 ATGATGATGATGATGATGAT 20
RESULT 641
AR084560/c
LOCUS AR084560 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 49 from patent US 5981185.
ACCESSION AR084560
VERSION AR084560.1 GI:10011331
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 49 09-NOV-1999;
FEATURES Location/Qualifiers
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1351 ATGGAGATGATGAAGATGAT 1370
DB 21 ATGATGATGATGATGATGAT 2
RESULT 642
AR084593/c
LOCUS AR084593 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 82 from patent US 5981185.
ACCESSION AR084593
VERSION AR084593.1 GI:10011364
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 82 09-NOV-1999;
FEATURES Location/Qualifiers
source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1350 GATGAGATGATGAAGATGA 1369
DB 20 GATGATGATGATGATGATGA 1
RESULT 643
AR084597
LOCUS AR084597 21 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 86 from patent US 5981185.
ACCESSION AR084597
VERSION AR084597.1 GI:10011368

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KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE          Oligonucleotide repeat arrays
JOURNAL        Patent: US 5981185-A 86 09-NOV-1999;
FEATURES       Location/Qualifiers
source         1..21
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGATGATGATGA 1369
Db 2 GATGATGATGATGATGA 21

RESULT 644
BD250646/c
LOCUS          21 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation.
ACCESSION      BD250646
VERSION        BD250646.1 GI:33060416
KEYWORDS       JP 2002511276-A/200.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Cowsett,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
               Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,I.A.
TITLE          Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation
JOURNAL        Patent: JP 2002511276-A 200 16-APR-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002511276-A/200
               PD 16-APR-2002
               PR 13-APR-1999 JP 2000543647
               PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PI
               LEX M COWSETT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
               M SASNOR,
               PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
               BORCHERS,
               PI TIMOTHY A VIKKARS
               PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
               C12N15/00
               CC PCR Primer
               FH Key Location/Qualifiers
               FT source 1..21
               /organism='Artificial Sequence'.

FEATURES       source
               1..21
               Location/Qualifiers
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 860 AGCTGGTGGAGGTGACGAG 879
Db 20 AGCTGGTGGATGACAGAGGAG 1

KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE          Oligonucleotide repeat arrays
JOURNAL        Patent: US 5981185-A 86 09-NOV-1999;
FEATURES       Location/Qualifiers
source         1..21
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGATGATGATGA 1369
Db 2 GATGATGATGATGATGA 21

RESULT 644
BD250646/c
LOCUS          21 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation.
ACCESSION      BD250646
VERSION        BD250646.1 GI:33060416
KEYWORDS       JP 2002511276-A/200.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Cowsett,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasnor,H.M.,
               Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,I.A.
TITLE          Identification of genetic targets for modulation by
               oligonucleotides and generation of oligonucleotides for gene
               modulation
JOURNAL        Patent: JP 2002511276-A 200 16-APR-2002;
               ISIS PHARMACEUTICALS INC
COMMENT        OS Artificial Sequence
               PN JP 2002511276-A/200
               PD 16-APR-2002
               PR 13-APR-1999 JP 2000543647
               PR 13-APR-1998 US 60/081483, 28-APR-1998 US 09/067638 PI
               LEX M COWSETT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
               M SASNOR,
               PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
               BORCHERS,
               PI TIMOTHY A VIKKARS
               PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
               C12N15/00
               CC PCR Primer
               FH Key Location/Qualifiers
               FT source 1..21
               /organism='Artificial Sequence'.

FEATURES       source
               1..21
               Location/Qualifiers
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               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 860 AGCTGGTGGAGGTGACGAG 879
Db 20 AGCTGGTGGATGACAGAGGAG 1

KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 21)
AUTHORS        Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE          Oligonucleotide repeat arrays
JOURNAL        Patent: US 5981185-A 86 09-NOV-1999;
FEATURES       Location/Qualifiers
source         1..21
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1350 GATGGATGATGATGA 1369
Db 2 GATGATGATGATGATGA 21

RESULT 645
BD266134
LOCUS          21 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Universal arrays.
ACCESSION      BD266134
VERSION        BD266134.1 GI:33075902
KEYWORDS       JP 2002539849-A/134.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 21)
AUTHORS        Pan,J.B., Hirschhorn,J.N., Huang,X., Kaplan,P., Lander,E.S.,
               Lockhart,D.J., Ryder,T. and Sklar,P.
TITLE          Universal arrays
JOURNAL        Patent: JP 2002539849-A 134 26-NOV-2002;
               WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH,AFFYMETRIX INC
COMMENT        OS Homo sapiens (human)
               PN JP 2002539849-A/134
               PD 26-NOV-2002
               PF 27-MAR-2000 JP 2000608794
               PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
               JIAN BING PAN,JOEL N HIRSCHHORN,XIAOHUA
               HUANG,PAUL KAPLAN,ERIC
               PI S LANDER,
               PI DAVID J LOCKHART,THOMAS RYDER,PAMELA SKLAR
               PC C12Q1/68,C12M1/00,C12N15/09,C12N15/09,G01N33/53, PC
               G01N33/566,
               PC G01N37/00,C12N15/00,C12N15/00,C12N15/00
               CC Universal arrays Location/Qualifiers
               FH Key 1..21
               FT source /organism='Homo sapiens (human)'.

FEATURES       source
               1..21
               Location/Qualifiers
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 754 CACAAGCTCACCTTGAGGA 773
Db 1 CACAAGGTCARCATTGAGGA 20

RESULT 646
CQ769152
LOCUS          21 bp      DNA      linear      PAT 04-MAR-2004
DEFINITION     Sequence 13 from Patent EP1386961.
ACCESSION      CQ769152
VERSION        CQ769152.1 GI:45112910
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1
AUTHORS        Asako,H. and Shimizu,M.
TITLE          Modified reductase and its gene and use thereof
JOURNAL        Patent: EP 1386961-A 13 04-FEB-2004;
               Sumitomo Chemical Company, Limited (JP)
FEATURES       Location/Qualifiers
source         1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 860 AGCTGGTGGAGGTGACGAG 879
Db 20 AGCTGGTGGATGACAGAGGAG 1

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Thu Oct 28 12:48:19 2004

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QY 2443 TGGTGTGTCAGCACCAGGG 2462
      ||||| ||||| ||||| |||||
Db 1 TGGTACTACAGCAGCAGGG 20

RESULT 647
LOCUS CQ797933 21 bp DNA linear PAT 20-APR-2004
DEFINITION Sequence 31 from Patent WO2004029631.
ACCESSION CQ797933
VERSION CQ797933.1 GI:46426428
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Wolf,S., Jaeger,M., Bangsow,T., Bangsow,C., Jordan,D., Pelzer,B.
and Oppolzer,T.
TITLE Method for identifying bhs-specific proteins and fragments thereof
JOURNAL Patent: WO 2004029631-A 31 08-APR-2004;
Esplora GmbH, c/oTU Darmstadt Institut fuer Biochemie (DE)
FEATURES
    source
        1. .21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der k nstlichen Sequenz: Primer"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1007 TGCACAGATCTCCGCTTC 1026
      ||||| ||||| ||||| |||||
Db 2 TGCTGAAGATCTCAGCTTC 21

RESULT 648
LOCUS E08187 21 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for isolation of the promoter in rice starch-branching
enzyme.
ACCESSION E08187
VERSION E08187.1 GI:2176308
KEYWORDS JP 1994261767-A/5.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 21)
AUTHORS Baba,T. and Shinada,H.
TITLE NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE
JOURNAL Patent: JP 1994261767-A 5 20-SEP-1994;
MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1994261767-A/5
PD 20-SEP-1994
PF 22-OCT-1993 JP 92P 291719
PR 29-OCT-1992 JP 92P 291719
PI BABA TADASHI, SHIMADA HIROAKI
PC C12N15/54,A01H5/00,C12N5/10,C12P19/16//A23L1/10,C12N9/10; CC
strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1. .21
FT /organism='Artificial sequences'.
FT Location/Qualifiers
FEATURES
    source
        1. .21
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGT 2338
      ||||| ||||| ||||| |||||
Db 2 GTGTGTGTGTGTGTGTGT 21

RESULT 649
LOCUS 127608/c 21 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5565334.
ACCESSION 127608
VERSION 127608.1 GI:1818384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kufe,D. and Abe,M.
TITLE Enhancer sequence for modulating expression in epithelial cells
JOURNAL Patent: US 5565334-A 4 15-OCT-1996;
FEATURES
    source
        1. .21
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3067 TCCACACCCCACTTCC 3086
      ||||| ||||| ||||| |||||
Db 21 TCCCTCCCACTTCC 2

RESULT 650
LOCUS AR279803 21 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 49 from patent US 6518017.
ACCESSION AR279803
VERSION AR279803.1 GI:29714948
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Riley,T.A., Brown,B.D. and Arnold,L.J.
TITLE Combinatorial antisense library
JOURNAL Patent: US 6518017-A 49 11-FEB-2003;
FEATURES
    source
        1. .21
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1434 GCTGTGGAGTACGGGCCA 1453
      ||||| ||||| ||||| |||||
Db 1 GCTGTGTGAGTACTCGCCA 20

RESULT 651
LOCUS AR351501/c 21 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 82 from patent US 6586579.
ACCESSION AR351501
VERSION AR351501.1 GI:33753229
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Huang,S.
TITLE PR-domain containing nucleic acids, polypeptides, antibodies and
JOURNAL methods
PATENT: US 6586579-A 82 01-JUL-2003;
FEATURES Location/Qualifiers
source
1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1722 GAAGACAACCAAGCGCGGC 1741
Db 21 GAAGACAATCAAGCGGGC 2

RESULT 652
AR483457
LOCUS AR483457 21 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 166 from patent US 6703362.
ACCESSION AR483457
VERSION AR483457.1 GI:47246096
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Alvarez,V.L., O'Mahony,D.J., Lambkin,I.J., Patterson,C.A.,
Singleton,J., Belinka,B.A. Jr., Carter,J.M. and Cagney,G.M.
TITLE Random peptides that bind to gastro-intestinal tract (GIT)
JOURNAL transport receptors and related methods
PATENT: US 6703362-A 166 09-MAR-2004;
FEATURES Location/Qualifiers
source
1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1722 GAAGACAACCAAGCGCGGC 1741
Db 21 GAAGACAATCAAGCGGGC 2

RESULT 653
AR203590/c
LOCUS AR203590 21 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 220 from Patent WO0153520.
ACCESSION AR203590
VERSION AR203590.1 GI:15393017
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Gene chip for neonate screening
JOURNAL Patent: WO 0153520-A 220 26-JUL-2001;
Cullen, Paul (DE) ; Seedorf, Udo (DE)
FEATURES Location/Qualifiers
source
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Huang,S.
TITLE PR-domain containing nucleic acids, polypeptides, antibodies and
JOURNAL methods
PATENT: US 6586579-A 82 01-JUL-2003;
FEATURES Location/Qualifiers
source
1..21
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1722 GAAGACAACCAAGCGCGGC 1741
Db 21 GAAGACAATCAAGCGGGC 2

RESULT 654
AX226447
LOCUS AX226447 21 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 103 from Patent WO0155179.
ACCESSION AX226447
VERSION AX226447.1 GI:15555682
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Prayaga,S.K., Padigaru,M., Spytek,K.A., Li,L., Tchernev,V.T.,
Vernet,C.A., Peyman,J.A. and Macdougall,J.
TITLE Nucleic acids encoding polypeptides with homology to olfactory
JOURNAL receptors
PATENT: WO 0155179-A 103 02-AUG-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="NOV 12 Probe Primer Sequence"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1182 GCGCCGCGTGACCCCTGGGCA 1201
Db 2 GCGCCGCGTGACCCCTGCTCA 21

RESULT 655
AX250034
LOCUS AX250034 21 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 33 from Patent WO0166747.
ACCESSION AX250034
VERSION AX250034.1 GI:15864493
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Vernet,C.A., Fernandes,E., Shinkets,R.A., Herrmann,J.L.,
Majumder,K., Macdougall,J., Mishra,V., Mezes,P.S. and Rastelli,L.
TITLE Proteins named fctrx and nucleic acids encoding same
JOURNAL Patent: WO 0166747-A 33 13-SEP-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Ag427 Probe Primer"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1182 GCGCCGCGTGACCCCTGGGCA 1201
Db 2 GCGCCGCGTGACCCCTGCTCA 21

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QY 2825 TATATACATATATATATATA 2844
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Db 2 TATATACCTAGGTATATATA 21
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RESULT 658
LOCUS AR438517/c 29 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7 from patent US 6664064.
ACCESSION AR438517
VERSION AR438517.1 GI:42663388
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive PCR products
JOURNAL Patent: US 6664064-A 7 16-DEC-2003;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3308 GATTTTCTTTAGGAGATTTATTTTGG 3335
|||||
Db 28 GATTTTCTTTTATTTTATTTTGG 1
|||||

RESULT 659
LOCUS AX430216/c 29 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 7 from Patent EP1207210.
ACCESSION AX430216
VERSION AX430216.1 GI:21655581
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Dietmaier,W.
TITLE Method for melting curve analysis of repetitive pcr products
JOURNAL Patent: EP 1207210-A 7 22-MAY-2002;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES Location/Qualifiers
source 1..29
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15.2; DB 1; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3308 GATTTTCTTTAGGAGATTTATTTTGG 3335
|||||
Db 28 GATTTTCTTTTATTTTATTTTGG 1
|||||

RESULT 660
LOCUS BD165919/c 29 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for melting curve analysis of repetitive PCR products.
ACCESSION BD165919
VERSION BD165919.1 GI:27871731
KEYWORDS JP 2002191384-A/7.
SOURCE unidentified
ORGANISM unidentified

RESULT 656
LOCUS AX740291 21 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 25 from Patent EP1300419.
ACCESSION AX740291
VERSION AX740291.1 GI:30523464
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Buettner,C., Schwarz,M., Knackmuss,S., Peter,K., Roettgen,P. and Little,M.
TITLE Antibody of human origin for inhibiting thrombocyte aggregation
JOURNAL Patent: EP 1300419-A 25 09-APR-2003;
Affimed Therapeutics AG (DE)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 0.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 854 AGGAGGAGCTGGTGGAGGCT 873
|||||
Db 2 AGTGACAGCTGGTGGAGTCT 21
|||||

RESULT 657
LOCUS BD140700 22 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods for the simultaneous identification of novel biological targets and lead structures for drug development.
ACCESSION BD140700
VERSION BD140700.1 GI:23235645
KEYWORDS JP 2002508507-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS Heefner,D.L., Zepp,C.M., Gao,Y. and Jones,S.W.
TITLE Methods for the simultaneous identification of novel biological targets and lead structures for drug development
JOURNAL Patent: JP 2002508507-A 2 19-MAR-2002;
SEPRACOR INC
COMMENT OS Artificial Sequence
PN JP 2002508507-A/2
PD 19-MAR-2002
PR 18-DEC-1998 JP 2000539165
PI DONALD L. HEEFNER, CHARLES M. ZEPP, YUN GAO, STEVEN W. JONES PC
GO1N33/542, C12Q1/04, C12Q1/68, C12Q1/70, G01N21/00, G01N21/76, PC
GO1N33/53,
PC GO1N33/566//C12N15/09, C12N15/00
CC Description of Artificial Sequence: construct FH Key
Location/Qualifiers
FT source 1..22
/organism='Artificial Sequence'.
FT Location/Qualifiers
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 15.2; DB 1; Length 22;
Best Local Similarity 85.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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unclassified.
1 (bases 1 to 29)
Dietmaier, W.
TITLE
METHOD for melting curve analysis of repetitive PCR products
JOURNAL
P Hoffmann LA ROCHE AG
COMMENT
OS Homo sapiens (human)
PN JP 2002191384-A/7
PD 09-JUL-2002
PF 13-NOV-2001 JP 2001348017
PI 15-NOV-2000 EP 00124897.0
PR WOLFGANG DIETMAIER
PC C12N15/09, C12Q1/68, C12N15/00
CC Method for melting curve analysis of repetitive PCR products
FH Key Location/Qualifiers
FT source 1..29
FT Location/Qualifiers
1..29
/organism="Homo sapiens (human)"
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.2; DB 1; Length 29;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3308 GATTTTCTTAGGAGATTATTTTGT 3335
DB 28 GATTTTCTTTTCTTTTCTTTTCTTTTGT 1

RESULT 661
LOCUS I30206 30 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5580731.
ACCESSION I30206
VERSION I30206.1 GI:1820997
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
1 (bases 1 to 30)
AUTHORS Chang, C.-A., Urdea, M.S. and Horn, T.
TITLE N-4 modified pyrimidine deoxynucleotides and oligonucleotide probes synthesized therewith
JOURNAL Patent: US 5580731-A 2 03-DEC-1996;
FEATURES
source
1..30
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15.2; DB 1; Length 30;
Best Local Similarity 68.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3310 TTTTCTTAGGAGATTATTTTGT 3334
DB 1 TTTTCTTTTNNNNNTTTT 25

RESULT 662
LOCUS A79651 30 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 2 from Patent EP0780479.
ACCESSION A79651
VERSION A79651.1 GI:6092605
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
1 (bases 1 to 30)
AUTHORS Fritton, H.D. and Hinzpeter, M.D.

unclassified.
1 (bases 1 to 29)
Dietmaier, W.
TITLE
METHOD for melting curve analysis of repetitive PCR products
JOURNAL
P Hoffmann LA ROCHE AG
COMMENT
OS Homo sapiens (human)
PN JP 2002191384-A/7
PD 09-JUL-2002
PF 13-NOV-2001 JP 2001348017
PI 15-NOV-2000 EP 00124897.0
PR WOLFGANG DIETMAIER
PC C12N15/09, C12Q1/68, C12N15/00
CC Method for melting curve analysis of repetitive PCR products
FH Key Location/Qualifiers
FT source 1..29
FT Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 15.2; DB 1; Length 30;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3266 TTATTGCTTTCCTCTTTTCAGGAGAA 3293
DB 1 TTTTCTTTTCTTTTCTTTTCTTTTTCAGGCGTA 28

RESULT 663
LOCUS HSOBRI05 37 bp DNA linear PRI 19-DEC-2001
DEFINITION Human OBR gene, intron sequence immediately adjacent to the 5' end of coding exon 3.
ACCESSION U62489
VERSION U62489.1 GI:1575401
KEYWORDS
SEGMENT 5 of 35
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
AUTHORS Chung, W.K., Power-Kehoe, L., Chua, M., Lee, R. and Leibel, R.L.
TITLE Genomic structure of the human OB receptor and identification of two novel intronic microsatellites
JOURNAL Genome Res. 6 (12), 1192-1199 (1996)
MEDLINE 97129406
PUBMED 8973914
REFERENCE 2 (bases 1 to 37)
AUTHORS Chung, W.K., Power-Kehoe, L., Chua, M., Lee, R. and Leibel, R.L.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1996) Laboratory of Human Behavior and Metabolism, Rockefeller University, 1230 York Avenue, New York, NY 10021, USA
FEATURES
source
1..37
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p"
/feature="OBR"

Query Match 0.4%; Score 15.2; DB 1; Length 37;
Best Local Similarity 63.9%; Pred. No. 1.3e+03;
Matches 23; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 3307 GGATTTTCTTAGGAGATTATTTTGGACTTCA 3342
DB 1 GGGGTTTTTGTGTTTTTTTTTTTTTTTAAATTC 36

RESULT 664
LOCUS AR074710/C 15 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 7 from patent US 5955276.
ACCESSION AR074710
VERSION AR074710
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
1 (bases 1 to 15)
Morgante,M. and Vogel,J.Marie.
Compound microsatellite primers for the detection of genetic
polymorphisms
Patent: US 5955276-A 7 21-SEP-1999;
Location/Qualifiers
source
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGT 2332
Db 15 TGTGTGTGTGTGTGT 1

RESULT 665
AR074711/c
LOCUS AR074711 15 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 8 from patent US 5955276.
ACCESSION AR074711
VERSION AR074711.1 GI:10001464
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 8 21-SEP-1999;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGT 2333
Db 15 GTGTGTGTGTGTGTGT 1

RESULT 666
AR074712
LOCUS AR074712 15 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 9 from patent US 5955276.
ACCESSION AR074712
VERSION AR074712.1 GI:10001465
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 9 21-SEP-1999;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGT 2332
Db 1 TGTGTGTGTGTGTGT 15

RESULT 667
AR074713
LOCUS AR074713 15 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 10 from patent US 5955276.
ACCESSION AR074713
VERSION AR074713.1 GI:10001466
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 10 21-SEP-1999;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGT 2333
Db 1 GTGTGTGTGTGTGTGT 15

RESULT 668
AR127803/c
LOCUS AR127803 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6180777.
ACCESSION AR127803
VERSION AR127803.1 GI:14114398
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Horn,T.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 24 30-JAN-2001;
FEATURES Location/Qualifiers
source 1. .15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGT 2333
Db 15 GTGTGTGTGTGTGTGT 1

RESULT 669
AX175252
LOCUS AX175252 15 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 16 from Patent WO0144465.
ACCESSION AX175252
VERSION AX175252.1 GI:14598620
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

AUTHORS Phillips,N.C. and Filion,M.C.
TITLE Therapeutically useful synthetic oligonucleotides
JOURNAL Patent: WO 0144465-A 16 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTG 2333
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Db 1 GTGTGTGTGTGTG 15

RESULT 670
LOCUS AX721631 15 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 10 from Patent EP1298221.
ACCESSION AX721631
VERSION AX721631.1 GI:30422164
KEYWORDS synthetic construct
ORGANISM synthetic construct
SOURCE artificial sequences.

REFERENCE 1
AUTHORS van der Kuyt,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1298221-A 10 02-APR-2003;
PrimaGen Holding B.V. (NL)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Tag with increased expression in SAGE libraries KS3 and KS4"

Query Match 0.4%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3704 CATGGTGGCCAGG 3718
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Db 1 CATGGTGGCCAGG 15

RESULT 671
LOCUS AR328668 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6070 from patent US 6566127.
ACCESSION AR328668
VERSION AR328668.1 GI:33714476
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6070 20-MAY-2003;
FEATURES
source 1..16
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/mol_type="unassigned RNA"

Query Match 0.4%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;

QY 1529 CCGAGGAGCAGCTCA 1543
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Db 3 CCGAGGAGCAGCTCA 17

RESULT 674
LOCUS AX687934 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 666 from Patent EPI281758.
ACCESSION AX687934

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTG 2333
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Db 1 GTGTGTGTGTGTG 15

RESULT 672
LOCUS AR074719 17 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 16 from patent US 5955276.
ACCESSION AR074719
VERSION AR074719.1 GI:10001472
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 16 21-SEP-1999;
FEATURES
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2320 TGTGTGTGTGTGTC 2334
|||||
Db 17 TGTGTGTGTGTGTC 3

RESULT 673
LOCUS AX687933 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 665 from Patent EPI281758.
ACCESSION AX687933
VERSION AX687933.1 GI:29410631
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 665 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1529 CCGAGGAGCAGCTCA 1543
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Db 3 CCGAGGAGCAGCTCA 17

RESULT 674
LOCUS AX687934 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 666 from Patent EPI281758.
ACCESSION AX687934

VERSION AX687934.1 GI:29410632
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE
JOURNAL Patent: EP 1281758-A 666 05-FEB-2003;
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1529 CCGAGGAGCAGCTCA 1543
Db 2 CCGAGGAGCAGCTCA 16
RESULT 675
LOCUS AX687935 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 667 from Patent EP1281758.
ACCESSION AX687935
VERSION AX687935.1 GI:29410633
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE
JOURNAL Patent: EP 1281758-A 667 05-FEB-2003;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1529 CCGAGGAGCAGCTCA 1543
Db 1 CCGAGGAGCAGCTCA 15
RESULT 676
LOCUS AR076354 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 21 from patent US 5958772.
ACCESSION AR076354
VERSION AR076354.1 GI:10003100
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank., Ackermann,E.J. and Cowseert,L.M.
TITLE Antisense inhibition of cellular inhibitor of apoptosis-1 expression

JOURNAL Patent: US 5958772-A 21 28-SEP-1999;
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1606 CAGAAGTGCATCCAC 1620
Db 17 CAGAAGTGCATCCAC 3
RESULT 677
LOCUS BD234297/c 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of expression of cellular inhibitor of apoptosis-1.
ACCESSION BD234297
VERSION BD234297.1 GI:33044067
KEYWORDS JP 2002531469-A/21.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,F.C., Ackermann,E.A. and Cowseert,L.M.
TITLE Antisense modulation of expression of cellular inhibitor of
JOURNAL Patent: JP 2002531469-A 21 24-SEP-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002531469-A/21
PD 24-SEP-2002
PF 16-JUN-1999 JP 2000585447
PR 03-DEC-1998 US 09/205204
PI FRANK C BENNETT,ELIZABETH A ACKERMANN,LEX M COWSERT PC
A61K48/00,A61K31/7115,A61K31/712,A61K31/7125,A61P29/00 PC
A61P31/00,A61P35/00, C12N15/09,C12N15/00
PC A61P37/02,A61P43/00
CC Synthetic
PH Key
FT source
FT Location/Qualifiers
1. .18
/organism="Artificial Sequence".
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1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1606 CAGAAGTGCATCCAC 1620
Db 17 CAGAAGTGCATCCAC 3
RESULT 678
LOCUS AR127806/c 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 27 from patent US 6180777.
ACCESSION AR127806
VERSION AR127806.1 GI:14114401
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Horn,I.
TITLE Synthesis of branched nucleic acids
JOURNAL Patent: US 6180777-A 27 30-JAN-2001;

FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 9e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2319 GTGTGTGTGTGTGTG 2333
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Db 19 GTGTGTGTGTGTGTG 5
RESULT 679
LOCUS ARI63975 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 173 from patent US 6271030.
ACCESSION ARI63975
VERSION ARI63975.1 GI:16234857
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 173 07-AUG-2001;
FEATURES Location/Qualifiers
source
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Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2639 TCCAGCACCTTGTGC 2653
|||||
Db 2 TCCAGCACCTTGTGC 16
RESULT 680
LOCUS AR208748 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 47 from patent US 6383808.
ACCESSION AR208748
VERSION AR208748.1 GI:21509984
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Freier,S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 47 07-MAY-2002;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 382 GGCATCAAGCTGCGG 396
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Db 2 GGCATCAAGCTGCGG 16
RESULT 681
LOCUS AX482068 20 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 45 from Patent EP1225233.
ACCESSION AX482068
VERSION AX482068.1 GI:22316790
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1225233-A 45 24-JUL-2002;
FEATURES Amsterdam Support Diagnostics B.V. (NL)
Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TAG019"
modified_base 1..5
/mod_base=i
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3704 CATGTGGCCAGG 3718
|||||
Db 6 CATGTGGCCAGG 20
RESULT 682
LOCUS AX511307 20 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 45 from Patent WO2059558.
ACCESSION AX511307
VERSION AX511307.1 GI:23392184
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: WO 02059558-A 45 01-AUG-2002;
FEATURES Amsterdam Support Diagnostics B.V. (NL)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="TAG019"
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Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3704 CATGTGGCCAGG 3718
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Db 6 CATGTGGCCAGG 20
RESULT 683
LOCUS AX721667 20 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 46 from Patent EP1298221.
ACCESSION AX721667
VERSION AX721667.1 GI:30422200
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

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REFERENCE
1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1298221-A 46 02-APR-2003;
PrimaGen Holding B.V. (NL)
FEATURES
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/db_xref="taxon:32630"
/misc_feature
1..6
/note="primer used for tag confirmation"
/note="n" on positions 1 - 6 stands for 'I' = inosine"
Query Match 0.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3704 CATGTGGCCAGG 3718
DB 6 CATGTGGCCAGG 20
RESULT 684
S61964/c
LOCUS S61964 23 bp DNA linear PRI 07-MAY-1993
DEFINITION (beta c)-beta-globin (5' region) [human, Genomic Mutant, 23 nt].
ACCESSION S61964
VERSION S61964.1 GI:236198
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 23)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Nucleotide sequence evidence of the uniceutric origin of the beta c
mutation in Africa
JOURNAL Hum. Genet. 87 (5), 597-601 (1991)
MEDLINE 92009838
PUBMED 1680789
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 61964] from the original journal article.
FEATURES
source
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/db_xref="taxon:9606"
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/genes="beta-globin"
/allele="beta C"
Query Match 0.4%; Score 15; DB 1; Length 23;
Best Local Similarity 78.3%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2822 GTATATATACATATATATATA 2844
DB 23 GAAAAAAATATATATATATA 1
RESULT 685
A87890
LOCUS A87890 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 38 from Patent WO9833904.
ACCESSION A87890
VERSION A87890.1 GI:6736460
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 38 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2920 GGGCGGGCGTGGGGGG 2937
DB 1 GGGCGGGCGGGGGGGG 18
RESULT 686
A89857
LOCUS A89857 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 38 from Patent EP0856579.
ACCESSION A89857
VERSION A89857.1 GI:6738371
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 38 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2920 GGGCGGGCGTGGGGGG 2937
DB 1 GGGCGGGCGGGGGGGG 18
RESULT 687
A8187533
LOCUS A8187533 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3021 from patent US 6346398.
ACCESSION A8187533
VERSION A8187533.1 GI:20233498
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 3021 12-FEB-2002;.
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Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1391 TCAACCTGCTGGCGCCT 1408
Db 1 TTAACCTGCTGGAGCCT 18

RESULT 688
LOCUS AR190756 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6244 from patent US 6346398.
ACCESSION AR190756
VERSION AR190756.1 GI:20236721
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 6244 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred.No.9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 1 GACTTCGGCTGGCCCGG 18

RESULT 689
LOCUS AR219474 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 12 from patent US 6420346.
ACCESSION AR219474
VERSION AR219474.1 GI:23320656
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Karin,N.
TITLE Polynucleotides encoding MIP-1.alpha., MCP-1, MIP-1.beta., Rantes and TNF-.alpha., and methods for treating rheumatoid arthritis
JOURNAL Patent: US 6420346-A 12 16-JUL-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred.No.9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 550 CTGCGGGCCACACGACG 567
Db 1 CTACCGGCGACGACG 18

RESULT 690
LOCUS AR324047 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1449 from patent US 6566127.
ACCESSION AR324047
VERSION AR324047.1 GI:33709855
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1449 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred.No.9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1391 TCAACCTGCTGGCGCCT 1408
Db 1 TTAACCTGCTGGAGCCT 18

RESULT 691
LOCUS AR325602 18 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3004 from patent US 6566127.
ACCESSION AR325602
VERSION AR325602.1 GI:33711410
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3004 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred.No.9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 1 GACTTCGGCTGGCCCGG 18

RESULT 692
LOCUS AR336934 18 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 42 from patent US 6566131.
ACCESSION AR336934
VERSION AR336934.1 GI:33722788
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsert,L.M.
TITLE Antisense modulation of Smad6 expression
JOURNAL Patent: US 6566131-A 42 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred.No.9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 168 GCGAGATGACGAGACG 185
Db 1 GCGAGATGACGAGACG 185

Db 1 GCGAGTTGACGAGATGG 18

RESULT 693
AX343688
LOCUS AX343688 18 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 5 from Patent WO0200864.
ACCESSION AX343688
VERSION AX343688.1 GI:18491773
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Pankratz, M.J., Zinke, I., Luemmen, P., Benting, J. and Gunkel, N.
TITLE Histone acetyltransferase inhibitors and their use as insecticides
JOURNAL Patent: WO 0200864-A 5 03-JAN-2002;
Aventis CropScience GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
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/note="-"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2068 GCGCCTTTTCGAGCAGTAC 2085
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Db 1 GCGCTTATCGAGCAGTAC 18

RESULT 694
AX773276/c
LOCUS AX773276 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 250 from Patent WO03045426.
ACCESSION AX773276
VERSION AX773276.1 GI:32485219
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Ellendoorn, K., Baker, M., Williams, S. and Carr, F.J.
TITLE T-cell epitopes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 250 05-JUN-2003;
MERCK PATENT GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2754 TACCTTTTATGCAAAAGG 2771
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Db 18 TACCTTTTATGTAACGG 1

RESULT 695
AX773292
LOCUS AX773292 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 266 from Patent WO03045426.
ACCESSION AX773292
VERSION AX773292.1 GI:32485235
KEYWORDS synthetic construct
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ellendoorn, K., Baker, M., Williams, S. and Carr, F.J.
TITLE T-cell epitopes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 266 05-JUN-2003;
MERCK PATENT GmbH (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2754 TACCTTTTATGCAAAAGG 2771
|||||
Db 18 TACCTTTTATGTAACGG 1

RESULT 697
AX826340/c
LOCUS AX826340 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 592 from Patent WO03072821.
ACCESSION AX826340
VERSION AX826340.1 GI:39751854
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: EP 1340818-A 592 03-SEP-2003;
Epigenomics AG (DE)
FEATURES
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for APC"

Query Match 0.4%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 9.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1379 ACAAAAACATCATCAACC 1396
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Db 18 ACAAAAACATCATCCCC 1

RESULT 697
AX826340/c
LOCUS AX826340 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 592 from Patent WO03072821.
ACCESSION AX826340
VERSION AX826340.1 GI:39751854
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: WO 03072821-A 592 04-SEP-2003;
Epigenomics AG (DE)

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FEATURES
source
  Location/Qualifiers
    1..18
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"
      /note="Detection oligonucleotide for APC"
Query Match
  Best Local Similarity 0.4%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1379 ACAAAACATCATCAACC 1396
Db 18 ACAAAACATCATCCCC 1
RESULT 698
BD065403
LOCUS BD065403 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065403
VERSION BD065403.1 GI:22611006
KEYWORDS JP 2001511000-A/38.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 38 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/38
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101331.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04.A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
  FT source
  FT 1..18
    /organism='Unknown'.
FEATURES
source
  Location/Qualifiers
    1..18
      /organism="unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"
Query Match
  Best Local Similarity 0.4%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2920 GGGCGGGCGTGGGGG 2937
Db 1 GGGCGGGCGGGCGGGG 18
RESULT 699
A91634
LOCUS A91634 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 161 from Patent WO9824928.
ACCESSION A91634
VERSION A91634.1 GI:6740589
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Pallisgaard,N. and Hokland,P.
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL Patent: WO 9824928-A 161 11-JUN-1998;
FEATURES
  Location/Qualifiers
    1..19
      /organism="unidentified"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32644"
Query Match
  Best Local Similarity 0.4%; Score 14.8; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 909 CTACGGGTGGGCTTCTT 926
Db 2 CTCGGTGGTGGGCTTCTT 19
RESULT 700
AR129286
LOCUS AR129286 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6183969.
ACCESSION AR129286
VERSION AR129286.1 GI:14116948
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Gabriel,A.
TITLE Intron-based assay for detecting and characterizing chromosomal
  rearrangement
JOURNAL Patent: US 6183969-A 10 06-FEB-2001;
FEATURES
  Location/Qualifiers
    1..19
      /organism="unknown"
      /mol_type="unassigned DNA"
Query Match
  Best Local Similarity 0.4%; Score 14.8; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1050 GGAGTCCACGCGTCCAT 1067
Db 1 GGAGTTCATGCGTCCAT 18
RESULT 701
BD182533/c
LOCUS BD182533 19 bp DNA linear PAT 15-MAY-2003
DEFINITION Screening method.
ACCESSION BD182533
VERSION BD182533.1 GI:30793498
KEYWORDS WO 02093161-A/92.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Mori,M., Shimomura,Y. and Goto,M.
TITLE Screening method
JOURNAL Patent: WO 02093161-A 92 21-NOV-2002;
  TAKEDA CHEMICAL INDUSTRIES LTD,MASAOKI MORI,YUKIO SHIMOMURA, MIKA
  GOTO
COMMENT OS Artificial Sequence
  PN WO 02093161-A/92
  PD 21-NOV-2002
  PF 14-MAY-2002 WO 2002JP004635
  PR 15-MAY-2001 JP 01P 145411
  PI MASAOKI MORI,YUKIO SHIMOMURA,MIKA GOTO
  PC GOIN33/15,GOIN33/50,C07K14/705,C07K14/435
  CC Primer
  FT key
  FT source
  FT 1..19
    Location/Qualifiers
      /organism='Artificial Sequence'.
FEATURES
source
  Location/Qualifiers
    1..19
      /organism="synthetic construct"
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RESULT	705
LOCUS	AR493086/c
DEFINITION	Sequence 118 from patent US 6720137.
ACCESSION	AR493086
VERSION	AR493086.1 GI:47264497
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 19)
TITLE	Roder, M., Plaschke, J. and Ganai, M. Microsatellite markers for plants of the species Triticum aestivum and Tribe triticeae and the use of said markers Patent: US 6720137-A 118 13-APR-2004;
JOURNAL	


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FEATURES
  source      Location/Qualifiers
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Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 404 AGTGAGCCTGGTCATGG 421
||||| |||||||
Db 18 AGTGGATGCTGGTCATGG 1

RESULT 706
LOCUS      AX166727
DEFINITION Sequence 218 from Patent WO0138503.
ACCESSION AX166727
VERSION AX166727.1 GI:14547002
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 218 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
  source      Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 503 TGGACGTGCTGGAGCGCT 520
||||| |||||||
Db 1 TGGCCGTGCTGGAGCGCT 18

RESULT 707
LOCUS      AX353125/c
DEFINITION Sequence 331 from Patent EP1174518.
ACCESSION AX353125
VERSION AX353125.1 GI:18618207
KEYWORDS
SOURCE Synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Loukachov,V.V., van Gemen,B. and Goudsmit,J.
TITLE Collection of binding molecules
JOURNAL Patent: EP 1174518-A 331 23-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
  source      Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="position 108"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3609 CGTTCGTACTGTACTG 3626
||||| |||||||
Db 18 CGTCCAGTACTGTACTG 1

RESULT 710
LOCUS      BD023416
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023416
VERSION BD023416.1 GI:22564639
KEYWORDS JP 2001505428-A/161.

FEATURES
  source      Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="position 108"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3651 CTTGCTTGCTGCAGGCGC 3668
||||| |||||||
Db 18 CTTGCATGCTGCAGGTC 1

RESULT 711
LOCUS      BD023416
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023416
VERSION BD023416.1 GI:22564639
KEYWORDS JP 2001505428-A/161.

FEATURES
  source      Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="position 108"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3609 CGTTCGTACTGTACTG 3626
||||| |||||||
Db 18 CGTCCAGTACTGTACTG 1

RESULT 708
LOCUS      AX362970/c
DEFINITION Sequence 331 from Patent WO0208463.
ACCESSION AX362970
VERSION AX362970.1 GI:18695110
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Loukachov,V.V., Goudsmit,J. and van Gemen,B.
TITLE Collection of binding molecules
JOURNAL Patent: WO 0208463-A 331 31-JAN-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
  source      Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="position 108"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3609 CGTTCGTACTGTACTG 3626
||||| |||||||
Db 18 CGTCCAGTACTGTACTG 1

RESULT 709
LOCUS      AX539200/c
DEFINITION Sequence 2 from Patent WO02064774.
ACCESSION AX539200
VERSION AX539200.1 GI:25272379
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Ben-Asouli,Y. and Osman,F.
TITLE Orientation-directed construction of plasmids
JOURNAL Patent: WO 02064774-A 2 22-AUG-2002;
Gene Bio-Application Ltd. (IL)
FEATURES
  source      Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="PRIMER 2038"

Query Match      0.4%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3651 CTTGCTTGCTGCAGGCGC 3668
||||| |||||||
Db 18 CTTGCATGCTGCAGGTC 1

RESULT 710
LOCUS      BD023416
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023416
VERSION BD023416.1 GI:22564639
KEYWORDS JP 2001505428-A/161.
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SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Parisgard,N., and Hukurando,P.
 TITLE Method for detecting abnormality in chromosome
 JOURNAL Patent: JP 2001505428-A 161 24-APR-2001;
 NEILLS PARISGARD
 COMMENT PN JP 2001505428-A/161
 PD 24-APR-2001
 PF 08-DEC-1997 JP 1998525090
 PI NEILLS PARISGARD,PATER HOKURANDO
 PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers.
 FEATURES
 source 1..19
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 9.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 909 CTCACGGGTGGCTTCTT 926
 |||||
 DB 2 CTCGCTGGCTTCTT 19
 RESULT 711
 BD089758 19 bp DNA linear PAT 27-AUG-2002
 LOCUS A method of arraying genome clone.
 DEFINITION BD089758
 ACCESSION BD089758
 VERSION BD089758.1 GI:22635368
 KEYWORDS JP 2001321190-A/2002.
 SOURCE synthetic construct
 ORGANISM artificial construct
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Soeda,E.
 TITLE A method of arraying genome clone
 JOURNAL Patent: JP 2001321190-A 2002 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
 COMMENT OS Artificial Sequence
 PN JP 2001321190-A/2002
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EIICHI SOEDA
 PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
 C12N15/00,
 PC C12N15/00
 CC Description of Artificial Sequence:Synthetic DNA FH Key
 Location/Qualifiers
 FT source 1..19
 /organism="Artificial Sequence".
 FT Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 9.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1037 GACAGGTGTCCTGGAGT 1054
 |||||
 DB 1 GACAGGTGACCTGGTGT 18

RESULT 712
 AB068169 19 bp DNA linear SYN 21-MAY-2003
 LOCUS Synthetic construct DNA, reverse primer for human STS sts-cos245-T3
 DEFINITION at 1p36.
 ACCESSION AB068169
 VERSION AB068169.1 GI:15128973
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Chen,Y.Z., Hayaishi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
 Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
 Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
 and Soeda,E.
 TITLE A BAC-based STS-content map spanning a 35-Mb region of human
 chromosome 1p35-p36
 JOURNAL Genomics 74 (1), 55-70 (2001)
 MEDLINE 21269192
 PUBMED 11374902
 REFERENCE 2 (bases 1 to 19)
 AUTHORS Horii,A.
 TITLE Direct Submission
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
 Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
 Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
 Tel:81-22-717-8042, Fax:81-22-717-8047)
 FEATURES
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 misc_feature 1..19
 /note="reverse primer for human STS sts-cos245-T3 at 1p36
 sts-cos245-T3 obtained from clones B135E1, B135I1, B62M23,
 B143P11, B380E2, B154M16, B154C10, Human BAC library
 RPCI-11"
 Query Match 0.4%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 9.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1037 GACAGGTGTCCTGGAGT 1054
 |||||
 DB 1 GACAGGTGACCTGGTGT 18
 RESULT 713
 AR214196 20 bp DNA linear PAT 25-SEP-2002
 LOCUS Sequence 4 from patent US 6406890.
 DEFINITION AR214196
 ACCESSION AR214196
 VERSION AR214196.1 GI:23311726
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Mueller,M.W.
 TITLE Process for the amplification of nucleic acid
 JOURNAL Patent: US 6406890-A 4 18-JUN-2002;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2815 GTATATGGTATATATACA 2832
Db 2 GTATATGGTATATATAAA 19

RESULT 714
AR214200
LOCUS AR214200 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6406890.
ACCESSION AR214200
VERSION AR214200.1 GI:23311730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mueller,M.W.
TITLE Process for the amplification of nucleic acid
JOURNAL Patent: US 6406890-A 8 18-JUN-2002;
FEATURES
    Location/Qualifiers
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            /mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2815 GTATATGGTATATATACA 2832
Db 2 GTATATGGTATATATAAA 19

RESULT 715
AR029135/c
LOCUS AR029135 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5859221.
ACCESSION AR029135
VERSION AR029135.1 GI:5941108
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 5859221-A 11 12-JAN-1999;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2815 GTATATGGTATATATACA 2832
Db 2 GTATATGGTATATATAAA 19

RESULT 716
AR036519/c
LOCUS AR036519 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5872232.
ACCESSION AR036519
VERSION AR036519.1 GI:5953187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.

TITLE 2'-O-modified oligonucleotides
JOURNAL Patent: US 5872232-A 11 16-FEB-1999;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTGTG 2333
Db 3 TATATGTGTGTGTGTGTG 20
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QY 844 CTGCCAGCGGAGGAGGAG 861
Db 20 CTGCCAGCGGAGGAGGAG 3

RESULT 717
AR073957/c
LOCUS AR073957 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 26 from patent US 5952229.
ACCESSION AR073957
VERSION AR073957.1 GI:10000717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Boggs,R.T.
TITLE Antisense oligonucleotide modulation of raf gene expression
JOURNAL Patent: US 5952229-A 26 14-SEP-1999;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 844 CTGCCAGCGGAGGAGGAG 861
Db 20 CTGCCAGCGGAGGAGGAG 3

RESULT 718
AR074771
LOCUS AR074771 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 68 from patent US 5955276.
ACCESSION AR074771
VERSION AR074771.1 GI:10001524
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
JOURNAL Patent: US 5955276-A 68 21-SEP-1999;
FEATURES
    Location/Qualifiers
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTGTG 2333
Db 3 TATATGTGTGTGTGTGTG 20
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RESULT 719
AR074785
LOCUS
DEFINITION Sequence 82 from patent US 5955276.
ACCESSION AR074785
VERSION AR074785.1 GI:10001538
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 82 21-SEP-1999;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2316 TCTGTGTGTGTGTGTGTG 2333
Db 3 TATATGTGTGTGTGTGTG 20

RESULT 720
AR096052/c
LOCUS
DEFINITION Sequence 11 from patent US 6005087.
ACCESSION AR096052
VERSION AR096052.1 GI:10024502
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.Dan. and Kawasaki,A.Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 6005087-A 11 21-DEC-1999;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 844 CTGCCAGCCGGAGGAGGAG 861
Db 20 CTGCCAGGGGAGGAGGAG 3

RESULT 721
AR105512/c
LOCUS
DEFINITION Sequence 12 from patent US 6096720.
ACCESSION AR105512
VERSION AR105512.1 GI:12819109
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Love,W.Guy., Nicklin,P.Leslie., Hamilton,K.Ophelia. and
Phillips,J.Ann.
TITLE Liposomal oligonucleotide compositions
JOURNAL Patent: US 6096720-A 12 01-AUG-2000;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 844 CTGCCAGCCGGAGGAGGAG 861
Db 20 CTGCCAGGGGAGGAGGAG 3

RESULT 722
AR110470/c
LOCUS
DEFINITION Sequence 7 from patent US 6114517.
ACCESSION AR110470
VERSION AR110470.1 GI:12826746
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Xu,X.S.
TITLE Methods of modulating tumor necrosis factor .alpha.-induced
expression of cell adhesion molecules
JOURNAL Patent: US 6114517-A 7 05-SEP-2000;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1678 GACTTCGGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 3

RESULT 723
AR116450/c
LOCUS
DEFINITION Sequence 31 from patent US 6133246.
ACCESSION AR116450
VERSION AR116450.1 GI:14096772
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE Antisense oligonucleotide compositions and methods for the
modulation of JNK proteins
JOURNAL Patent: US 6133246-A 31 17-OCT-2000;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1678 GACTTCGGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 3

RESULT 724
AR116461
LOCUS
DEFINITION Sequence 31 from patent US 6133246.
ACCESSION AR116461
VERSION AR116461.1 GI:14096772
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE Antisense oligonucleotide compositions and methods for the
modulation of JNK proteins
JOURNAL Patent: US 6133246-A 31 17-OCT-2000;
FEATURES
LOCATION/Qualifiers
source
1..20
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1678 GACTTCGGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 3
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LOCUS       AR116461                20 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION   Sequence 42 from patent US 6133246.
ACCESSION    AR116461
VERSION      AR116461.1  GI:14096783
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE        Antisense oligonucleotide compositions and methods for the
             modulation of JNK proteins
JOURNAL      Patent: US 6133246-A 42 17-OCT-2000;
FEATURES     Location/Qualifiers
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1678  GACTTCGGCTGCGCCGG 1695
Db      1      GACTTGGCGCTGCGCCGG 18

RESULT 725
LOCUS       AR117679                20 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION   Sequence 76 from patent US 6140125.
ACCESSION    AR117679
VERSION      AR117679.1  GI:14098585
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Taylor,J.K. and Cowseert,L.M.
TITLE        Antisense inhibition of bcl-6 expression
JOURNAL      Patent: US 6140125-A 76 31-OCT-2000;
FEATURES     Location/Qualifiers
             source
               1..20
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3458  AAGTTTATATATATCTAT 3475
Db      2      AGTTTATATATATTTAT 19

RESULT 726
LOCUS       AR126603/c              20 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION   Sequence 32 from patent US 6180353.
ACCESSION    AR126603
VERSION      AR126603.1  GI:14113196
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Dean,N.M. and Cowseert,L.M.
TITLE        Antisense modulation of daxx expression
JOURNAL      Patent: US 6180353-A 32 30-JAN-2001;
FEATURES     Location/Qualifiers
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               /mol_type="unassigned DNA"

LOCUS       AR116461                20 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION   Sequence 42 from patent US 6133246.
ACCESSION    AR116461
VERSION      AR116461.1  GI:14096783
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE        Antisense oligonucleotide compositions and methods for the
             modulation of JNK proteins
JOURNAL      Patent: US 6133246-A 42 17-OCT-2000;
FEATURES     Location/Qualifiers
             source
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               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1169  GGGAGCTGCTCGGGGCC 1186
Db      18  GGGTCTGTCTCGGGGCC 1

RESULT 727
LOCUS       AR130129                20 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION   Sequence 32 from patent US 6187587.
ACCESSION    AR130129
VERSION      AR130129.1  GI:14118026
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Popoff,I., Brown-Driver,V.L. and Cowseert,L.M.
TITLE        Antisense inhibition of e2f transcription factor 1 expression
JOURNAL      Patent: US 6187587-A 32 13-FEB-2001;
FEATURES     Location/Qualifiers
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               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      620  AGCCCCACATCCAGTGGC 637
Db      18  AGAACACATCCAGTGGC 1

RESULT 728
LOCUS       AR130802/c              20 bp      DNA          linear      PAT 16-MAY-2001
DEFINITION   Sequence 53 from patent US 6190869.
ACCESSION    AR130802
VERSION      AR130802.1  GI:14119127
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Bennett,C.Frank. and Cowseert,L.M.
TITLE        Antisense inhibition of protein kinase C-theta expression
JOURNAL      Patent: US 6190869-A 53 20-FEB-2001;
FEATURES     Location/Qualifiers
             source
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               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1872  TGTGGAGGAGCTCTTCAA 1889
Db      18  TGAGGAGGAGCTCTTCCA 1

RESULT 729
LOCUS       BD177203                20 bp      DNA          linear      PAT 16-APR-2003
DEFINITION   Nucleic acid and protein of mhp3 gene of Mycoplasma hyopneumoniae
             and utilization thereof.
ACCESSION    BD177203
VERSION      BD177203.1  GI:30014463
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KEYWORDS JP 2002306169-A/16.
 SOURCE synthetic construct
 ORGANISM artificial construct
 REFERENCE 1 (bases 1 to 20)
 AUTHORS King,K.W., Madura,R.A. and Rosey,E.L.
 TITLE Nucleic acid and protein of mup3 gene of Mycoplasma hyopneumoniae
 JOURNAL and utilization thereof
 COMMENT Patent: JP 2002306169-A 16 22-OCT-2002;
 PRIZER PRODUCTS INC
 OS Artificial Sequence
 PN JP 2002306169-A/16
 PD 22-OCT-2002
 PF 30-MAR-2001 JP 2001101364
 PI KENDALL WAYNE KING,REBECCA ANN MADURA,EVERETT LEE ROSEY PC
 C12N15/09,A61K39/00,A61K39/39,A61K48/00,A61P31/04,A61P31/04, PC
 C07K14/30,
 PC C07K19/00,C12N1/21,C12P21/02,C12Q1/68,G01N33/53,G01N33/53, PC
 G01N33/566,
 PC G01N33/569/(C12P21/02,C12R1/19),C12N15/00
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 FT source 1..20
 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 3539 GCTCTCTAGGTTTATAG 3556
 Db 2 GCTCTCTAGGTTTATAG 19
 RESULT 730
 LOCUS BD183264 20 bp DNA linear PAT 17-JUN-2003
 DEFINITION Method for estimating genotype of fertility restoration gene site
 against rice BT type male sterile cytoplasm.
 ACCESSION BD183264
 VERSION BD183264.1 GI:31875464
 KEYWORDS JP 2002345485-A/3.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Komori,T., Yamamoto,T., Nitta,N. and Takemori,N.
 TITLE Method for estimating genotype of fertility restoration gene site
 against rice BT type male sterile cytoplasm
 JOURNAL Patent: JP 2002345485-A 3 03-DEC-2002;
 JAPAN TORACCO INC,SYNGENTA LTD
 OS Artificial Sequence
 PN JP 2002345485-A/3
 PD 03-DEC-2002
 PF 17-AUG-2001 JP 2001247600
 PI TOSHIYUKI KOMORI,TOSHIO YAMAMOTO,NAOTO NITTA,NAOKI TAKEMORI PC
 C12N15/09,A01H1/04,C12Q1/68,C12N15/00
 CC Oligonucleotide primer for amplification of G4003 HindIII CC
 marker sequence.
 FT Key Location/Qualifiers
 FT source 1..20
 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1678 GACTTCGGGCTGGCCGG 1695
 Db 20 GACTTCGGGCTGGCCGG 3
 RESULT 732
 LOCUS BD270713 20 bp DNA linear PAT 17-JUL-2003
 DEFINITION Selection system.
 ACCESSION BD270713
 VERSION BD270713.1 GI:33080481
 KEYWORDS JP 2002514413-A/40.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Riechmann,L., Kristensen,P., Jestin,J.L. and Winter,G.P.
 TITLE Selection system
 JOURNAL Patent: JP 2002514413-A 40 21-MAY-2002;
 DIVERSYS LTD
 OS Artificial Sequence
 PN JP 2002514413-A/40

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2044 ACCGACGAGTACCTGGAC 2061
 Db 2 ATCGACGAGTACCTGAAC 19
 RESULT 731
 LOCUS BD237317/c 20 bp DNA linear PAT 17-JUL-2003
 DEFINITION Modulation method of induction expression of tumor necrosis
 factor-alpha of cell adhesion molecules.
 ACCESSION BD237317
 VERSION BD237317.1 GI:33047087
 KEYWORDS JP 2002531574-A/7.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Monia,B.P. and Xu,X.S.
 TITLE Modulation method of induction expression of tumor necrosis
 factor-alpha of cell adhesion molecules
 JOURNAL Patent: JP 2002531574-A 7 24-SEP-2002;
 ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2002531574-A/7
 PD 24-SEP-2002
 PF 08-DEC-1999 JP 2000586746
 PI BRETT P MONIA,XIAOXING S XU
 PC A61K45/00,A61K31/712,A61K31/7125,A61K48/00,A61P1/00,A61P3/10,
 PC A61P5/14,
 PC A61P17/04,A61P17/06,A61P29/00,A61P29/00,A61P31/00,A61P35/00,
 PC A61P37/00,
 PC A61P37/06,C12N5/10,C12N15/09,C12N15/00,C12N5/00 CC antisense
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 FT source 1..20
 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1678 GACTTCGGGCTGGCCGG 1695
 Db 20 GACTTCGGGCTGGCCGG 3
 RESULT 732
 LOCUS BD270713 20 bp DNA linear PAT 17-JUL-2003
 DEFINITION Selection system.
 ACCESSION BD270713
 VERSION BD270713.1 GI:33080481
 KEYWORDS JP 2002514413-A/40.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Riechmann,L., Kristensen,P., Jestin,J.L. and Winter,G.P.
 TITLE Selection system
 JOURNAL Patent: JP 2002514413-A 40 21-MAY-2002;
 DIVERSYS LTD
 OS Artificial Sequence
 PN JP 2002514413-A/40

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PD 21-MAY-2002
PF 13-MAY-1999 JP 2000548446
PR 13-MAY-1998 GB 9810223.9,13-MAY-1998 GB 9810228.8 PI
LUTZ RIECHMANN,PETER KRISTENSEN,JEAN LUC JESTIN,GREGORY PAUL PI
WINTER
CC C12N15/00,C12N7/02,C12N15/00
CC Description of Artificial Sequence:Nucleotide sequence FH
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        /organism="synthetic construct"
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 538 CTGAGGCGGGCTGCCG 555
Db 1 CTGAGGCGGGCTGCCG 18

RESULT 733
BD272876/c
LOCUS      20 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Method of diagnosing Alzheimer's disease or its prognosis.
ACCESSION  BD272876
VERSION     BD272876.1 GI:33082644
KEYWORDS   JP 2002531063-A/2.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Nitsch,R. and Growdon,J.
TITLE     Method of diagnosing Alzheimer's disease or its prognosis
JOURNAL   Patent: JP 2002531063-A 2 24-SEP-2002;
COMMENT   ROGER NITSCH
OS       Artificial Sequence
PN       JP 2002531063-A/2
PD       24-SEP-2002
PF       22-OCT-1999 JP 2000578661
PR       23-OCT-1998 US 60/105458,06-NOV-1998 US 60/107434 PR
26-JAN-1999 EP 99101377.2
PI       ROGER NITSCH,JOHN GROWDON
PC       C12N15/09,A61K38/46,A61K38/55,A61K45/00,A61K48/00,A61P25/28,
PC       C12Q1/37,
PC       C12Q1/68,G01N33/15,G01N33/50,G01N33/50,G01N33/53, PC
G01N33/68,
PC       C12N15/00,A61K37/54,A61K37/64
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        /organism="synthetic construct"
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2940 TGGAGGAGGCCCGG 2957
Db 19 TGGTGGGAGGCCCGCATGG 2

RESULT 734
CQ763625
LOCUS      20 bp      DNA      linear      PAT 24-MAY-2004
DEFINITION Sequence 4 from Patent WO2004038416.
ACCESSION  CQ812580
VERSION     CQ812580.1 GI:47602055
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   Golz,S., Brueggemeier,U. and Summer,H.

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LOCUS      20 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 2243 from Patent WO2004003201.
ACCESSION  CQ763625
VERSION     CQ763625.1 GI:44906861
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS   Kane,C.D.
TITLE     Antisense modulation of lrlh expression
JOURNAL   Patent: WO 2004003201-A.2243 08-JAN-2004;
          Pharmacia Corporation (US)
FEATURES   Location/Qualifiers
    source
        1. .20
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        /db_xref="taxon:32630"
        /note="Human LRH1 antisense"
Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 318 CCCCACTCCCTCAATCTC 335
Db 2 CCCCACTCCCAATCTC 19

RESULT 735
CQ764398
LOCUS      20 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 3016 from Patent WO2004003201.
ACCESSION  CQ764398
VERSION     CQ764398.1 GI:44907634
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS   Kane,C.D.
TITLE     Antisense modulation of lrlh expression
JOURNAL   Patent: WO 2004003201-A.3016 08-JAN-2004;
          Pharmacia Corporation (US)
FEATURES   Location/Qualifiers
    source
        1. .20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Human LRH1 antisense"
Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 318 CCCCACTCCCTCAATCTC 335
Db 3 CCCCACTCCCAATCTC 20

RESULT 736
CQ812580/c
LOCUS      20 bp      DNA      linear      PAT 24-MAY-2004
DEFINITION Sequence 4 from Patent WO2004038416.
ACCESSION  CQ812580
VERSION     CQ812580.1 GI:47602055
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE  1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS   Golz,S., Brueggemeier,U. and Summer,H.

```

REFERENCE
 Ito, T., Fujita, T., Hara, K., Tomozuka, T. and Sakano, Y.
 TITLE
 Beta-Fructofuranosidase gene
 JOURNAL
 Patent: WO 2004038416-A 4 06-MAY-2004;
 Bayer HealthCare AG (DE)
 COMMENT
 SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES
 OS
 Arthrobacter sp.
 PN
 JP 2000342273-A/2
 PD
 12-DEC-2000
 PF
 08-JUN-1999 JP 1999160416
 PR
 TETSUYA ITO, TAKATERU FUJITA, KOZO HARA, TAKASHI TONOUZUKA, PI
 YOSHIYUKI SAKANO
 PC
 C12N15/09, C12N9/24//C12N15/09, C12R1/06, C12N15/00, (C12N15/00,
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 FH
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2015 ACCTGGACCGTGTCCCTTA 2032
 Db 19 ACTTGGACCGTGTCCCTA 2

RESULT 737
 E40652
 LOCUS
 Antihuman Fas humanized antibody-containing antirheumatic.
 DEFINITION
 E40652
 ACCESSION
 E40652.1 GI:18625145
 VERSION
 JP 2000154149-A/23.
 KEYWORDS
 synthetic construct
 SOURCE
 ORGANISM
 artificial sequences.
 1 (bases 1 to 20)
 Serizawa, N., Haruyama, H., Takahashi, W., Nakahara, K. and Yonehara, S.
 AUTHORS
 Antihuman Fas humanized antibody-containing antirheumatic
 JOURNAL
 Patent: JP 2000154149-A 23 06-JUN-2000;
 SANKYO CO LTD
 OS
 Artificial Sequence
 PN
 JP 2000154149-A/23
 PD
 06-JUN-2000
 PF
 17-SEP-1999 JP 1999263984
 PR
 NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, WATARU TAKAHASHI, PI KAORI
 NAKAHARA,
 PI SHIN YONEHARA
 PC
 A61K39/395, A61P29/00, C12N15/09, C07K16/28, C12P21/02, C12N15/00
 CC
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 FH
 Key
 FT
 source
 Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 9.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 604 GTGTACAGTGTGACGACAG 621
 Db 3 GTGTACTGTGACTACAG 20

RESULT 738
 E41257/c
 LOCUS
 Beta-Fructofuranosidase gene.
 DEFINITION
 E41257
 ACCESSION
 E41257.1 GI:18621976
 VERSION
 JP 2000342273-A/2.
 KEYWORDS
 Arthrobacter sp.
 SOURCE
 ORGANISM
 Arthrobacter sp.
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Micrococccineae; Micrococcaceae; Arthrobacter.

1 (bases 1 to 20)
 Ito, T., Fujita, T., Hara, K., Tomozuka, T. and Sakano, Y.
 TITLE
 Beta-Fructofuranosidase gene
 JOURNAL
 Patent: JP 2000342273-A 2 12-DEC-2000;
 SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE FORESTRY AND FISHERIES
 OS
 Arthrobacter sp.
 PN
 JP 2000342273-A/2
 PD
 12-DEC-2000
 PF
 08-JUN-1999 JP 1999160416
 PR
 TETSUYA ITO, TAKATERU FUJITA, KOZO HARA, TAKASHI TONOUZUKA, PI
 YOSHIYUKI SAKANO
 PC
 C12N15/09, C12N9/24//C12N15/09, C12R1/06, C12N15/00, (C12N15/00,
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 C12R1/06)
 FH
 Key
 FT
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 72.2%; Pred. No. 9.8e+02;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 528 CCGGCCCATCTCGCAGGC 545
 Db 19 CSGGSCGCTCTGAGSC 2

RESULT 739
 E49536/c
 LOCUS
 Antisense oligonucleotide regulation of raft gene expression.
 DEFINITION
 E49536
 ACCESSION
 E49536.1 GI:18628117
 VERSION
 JP 2000152797-A/26.
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 20)
 P, M.B. and T.B.R.
 Antisense oligonucleotide regulation of raft gene expression
 JOURNAL
 Patent: JP 2000152797-A 26 06-JUN-2000;
 ISIS PHARMACEUTICALS INC
 OS
 Homo sapiens (human)
 PN
 JP 2000152797-A/26
 PD
 06-JUN-2000
 PF
 18-JAN-2000 JP 2000008654
 PR
 31-MAY-1994 US 08/250856
 PI
 MONIA BURETTO P, BOGGUZZO RUSSELL T
 PC
 C12N15/09, A61K31/7088, A61K48/00, A61P17/06, A61P35/00, A61P43/00,
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 Key
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 source
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 /db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
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QY 844 CTGCCAGCCGAGGAGGAG 861
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Db 20 CTGCCAGGGGAGGAGGAG 3

RESULT 740
I27256/c
LOCUS I27256 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 26 from patent US 5563255.
ACCESSION I27256
VERSION I27256.1 GI:1818032
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P. and Boggs,R.T.
TITLE Antisense oligonucleotide modulation of raf gene expression
JOURNAL Patent: US 5563255-A 26 08-OCT-1996;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 844 CTGCCAGGGGAGGAGGAG 861
Db 20 CTGCCAGGGGAGGAGGAG 3

RESULT 741
I49606/c
LOCUS I49606 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 48 from patent US 5641497.
ACCESSION I49606
VERSION I49606.1 GI:2471826
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bevins,C.L. and Jones,D.E.
TITLE Gastrointestinal defensins, cDNA sequences and method for the production and use thereof
JOURNAL Patent: US 5641497-A 48 24-JUN-1997;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 655 AATGGCAGCAAGTGGGC 672
Db 20 AATGGCAGCAAGTGGC 3

RESULT 742
AR211552
LOCUS AR211552 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 14 from patent US 6399328.
ACCESSION AR211552
VERSION AR211552.1 GI:21514903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Vournakis,J.N., Seth,A.K. and Papas,T.S.
TITLE Methods and compositions for diagnosis and treatment of breast

cancer
JOURNAL Patent: US 6399328-A 14 04-JUN-2002;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 52 CGCTGCTGCTGCTGAAT 69
Db 1 CGCTGCTGCTGCTGATT 18

RESULT 743
AR212285/c
LOCUS AR212285 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 11 from patent US 6399754.
ACCESSION AR212285
VERSION AR212285.1 GI:21515819
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cook,P.Dan.
TITLE Sugar modified oligonucleotides
JOURNAL Patent: US 6399754-A 11 04-JUN-2002;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 844 CTGCCAGGGGAGGAGGAG 861
Db 20 CTGCCAGGGGAGGAGGAG 3

RESULT 744
AR215980/c
LOCUS AR215980 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 27 from patent US 6410518.
ACCESSION AR215980
VERSION AR215980.1 GI:23314268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P.
TITLE Antisense oligonucleotide inhibition of raf gene expression
JOURNAL Patent: US 6410518-A 27 25-JUN-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 844 CTGCCAGGGGAGGAGGAG 861
Db 20 CTGCCAGGGGAGGAGGAG 3

RESULT 745

AR231783/c
LOCUS AR231783 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6 from patent US 6455249.
ACCESSION AR231783
VERSION AR231783.1 GI:27273358
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hsu, I.-C., Highsmith, W.E. Jr. and Shih, J.
TITLE Method of amplifying DNA and RNA mismatch cleavage products
JOURNAL Patent: US 6455249-A 6 24-SEP-2002;
FEATURES
LOCATION/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2695 CCACCTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2
RESULT 746
AR281887/c
LOCUS AR281887 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 10 from patent US 6521407.
ACCESSION AR281887
VERSION AR281887.1 GI:29717815
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wardenius, H.M. and Seabra, L.A.
TITLE Methods for determining chemosensitivity of cancer cells based upon
expression of negative and positive signal transduction factors
JOURNAL Patent: US 6521407-A 10 18-FEB-2003;
FEATURES
LOCATION/Qualifiers
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2695 CCACCTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2
RESULT 747
AR296097/c
LOCUS AR296097 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7832 from patent US 6537751.
ACCESSION AR296097
VERSION AR296097.1 GI:31683381
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7832 25-MAR-2003;
FEATURES
LOCATION/Qualifiers
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/mol_type="genomic DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2974 CAGAGGACCAGGGCTTTT 2991
Db 20 CAGAGAACAGGGCTTGT 3
RESULT 748
AR315976/c
LOCUS AR315976 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6513 from patent US 6559294.
ACCESSION AR315976
VERSION AR315976.1 GI:31709402
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hojseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A.,
Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6513 06-MAY-2003;
FEATURES
LOCATION/Qualifiers
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/mol_type="genomic DNA"
Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 743 TTCTCTCCTTCACCAACG 760
Db 19 TCCTCTCTAGCAACG 2
RESULT 749
AR489974
LOCUS AR489974 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 97 from patent US 6710174.
ACCESSION AR489974
VERSION AR489974.1 GI:47257087
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of vascular endothelial growth factor
receptor-1 expression
JOURNAL Patent: US 6710174-A 97 23-MAR-2004;
FEATURES
LOCATION/Qualifiers
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1352 TCGAGATGATGAAGATGA 1369
Db 1 TCGTGATGATGACGATGA 18
RESULT 750
AX018878/c
LOCUS AX018878 20 bp DNA linear PAT 07-SEP-2000

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DEFINITION Sequence 10 from Patent WO9942839.
ACCESSION AX018878
VERSION AX018878.1 GI:10042974
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Warenius,H.
TITLE Treating cancer
JOURNAL Patent: WO 9942839-A 10 26-AUG-1999;
THERYTE LIMITED (GB); WARENIUS HILMAR (GB)
FEATURES
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/db_xref="taxon:32630"
/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2

RESULT 751
AX018893/c
LOCUS AX018893 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942834.
ACCESSION AX018893
VERSION AX018893.1 GI:10042989
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Seabra,L.A. and Warenius,H.
TITLE Treating cancer
JOURNAL Patent: WO 9942834-A 10 26-AUG-1999;
SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENIUS HILMAR
(GB)
FEATURES
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/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2

RESULT 752
AX018910/c
LOCUS AX018910 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942828.
ACCESSION AX018910
VERSION AX018910.1 GI:10043005
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942828-A 10 26-AUG-1999;
THERYTE LIMITED (GB); WARENIUS HILMAR (GB)
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/db_xref="taxon:32630"
/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2

RESULT 753
AX018925/c
LOCUS AX018925 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942821.
ACCESSION AX018925
VERSION AX018925.1 GI:10043020
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Seabra,L.A. and Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942821-A 10 26-AUG-1999;
SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENIUS HILMAR
(GB)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2

RESULT 754
AX019039/c
LOCUS AX019039 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9942090.
ACCESSION AX019039
VERSION AX019039.1 GI:10043120
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942090-A 10 26-AUG-1999;
THERYTE LIMITED (GB); WARENIUS HILMAR (GB)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
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QY 2695 CCACCTTCCACCCCTGCC 2712
Db 19 CCACCTGCCACCCCTGCAC 2
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Best Local Similarity 88.9%; Pred. No. 9.8e+02; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCTGCCC 2712
Db 19 CCACCTGCCCACCTGCAC 2

RESULT 755
AX020774/c
LOCUS AX020774 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 274 from Patent WO9334016.
ACCESSION AX020774
VERSION AX020774.1 GI:10044473
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Vider, B.Z.
TITLE A method for identifying and characterizing cells and tissues
JOURNAL Patent: WO 9334016-A 274 08-JUL-1999;
GENEVA LTD (IL); VIDER BEN ZION (IL)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1801 GACGTCGTGTCCTTGGG 1818
Db 18 GACGTCGTGTCCTTGGG 1

RESULT 756
AX084307
LOCUS AX084307 20 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 101 from Patent WO0110902.
ACCESSION AX084307
VERSION AX084307.1 GI:13185809
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Shimkets, R.A. and Fernandes, E.
TITLE Nucleic acids and secreted polypeptides encoded thereby
JOURNAL Patent: WO 0110902-A 101 15-FEB-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR PRIMER"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1495 GGCCTGGACTACTCTTC 1512
Db 3 GGCCTGGACTCTCTTC 20

RESULT 757
AX092588/c
LOCUS AX092588 20 bp DNA linear PAT 21-MAR-2001

Best Local Similarity 88.9%; Pred. No. 9.8e+02; Mismatches 2; Indels 0; Gaps 0;

QY 2695 CCACCTTCCACCTGCCC 2712
Db 19 CCACCTGCCCACCTGCAC 2

Sequence 2 from Patent WO0116364.
ACCESSION AX092588
VERSION AX092588.1 GI:13444646
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Richard, G.U. and Nitsch, R.
TITLE Methods of diagnosing or prognosticating age-related macular degeneration
JOURNAL Patent: WO 0116364-A 2 08-MAR-2001;
EVOTEC Neurosciences GmbH (DE)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2940 TGGAGGGAGGCCCCAGGG 2957
Db 19 TGGTGGGAGGCCCATGG 2

RESULT 758
AX104119/c
LOCUS AX104119 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 311 from Patent WO0122972.
ACCESSION AX104119
VERSION AX104119.1 GI:13920316
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 311 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical GmbH (DE)
FEATURES
source Location/Qualifiers
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 20 GACTTCGGCTGGCCCGG 3

RESULT 759
AX138974
LOCUS AX138974 20 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 22 from Patent EP1090995.
ACCESSION AX138974
VERSION AX138974.1 GI:14274669
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS King, K.W., Madura, R.A. and Rosey, E.L.
TITLE Mycoplasma hyopneumoniae antigen mhp3, gene encoding it and uses

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Patent: EP 1090995-A 22 11-APR-2001;
Pfizer Products Inc. (US)
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        /db_xref="taxon:32630"
        /note="Oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3539 GCTTCTAGAGTTTATAG 3556
Db 2 GCTTCTCAGTTTATAG 19

RESULT 760
AX164692/c
LOCUS AX164692 20 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2 from Patent WO0134782.
ACCESSION AX164692
VERSION AX164692.1 GI:14545586
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Itoh,N. and Kavanaugh,M.W.
AUTHORS Human fgf-23 gene and gene expression products
TITLE Patent: WO 0134792-A 2 17-MAY-2001;
JOURNAL various cancers
CHIRON CORPORATION (US) ; Kyoto University (JP)
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Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGCCCGG 1695
Db 20 GACTTGGCTGCCCGG 3

RESULT 761
AX249751/c
LOCUS AX249751 20 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 5 from Patent WO0166596.
ACCESSION AX249751
VERSION AX249751.1 GI:15864370
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Itoh,N. and Kavanaugh,M.W.
AUTHORS Human fgf-23 gene and gene expression products
TITLE Patent: WO 0166596-A 5 13-SEP-2001;
JOURNAL CHIRON CORPORATION (US) ; Kyoto University (JP)
FEATURES
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        /db_xref="taxon:32630"
        /note="Sense PCR primer"

thereof
Patent: EP 1090995-A 22 11-APR-2001;
Pfizer Products Inc. (US)
FEATURES
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        /note="Oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 825 CTCTGGTGGCTGGTGGT 842
Db 18 CTCTGAGTGGCTGGTGGT 1

RESULT 762
AX250104/c
LOCUS AX250104 20 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 5 from Patent WO0166595.
ACCESSION AX250104
VERSION AX250104.1 GI:15864512
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Itoh,N. and Kavanaugh,M.W.
AUTHORS Human fgf-23 gene and gene expression products
TITLE Patent: WO 0166595-A 5 13-SEP-2001;
JOURNAL CHIRON CORPORATION (US) ; Kyoto University (JP)
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Sense PCR primer"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 825 CTCTGGTGGCTGGTGGT 842
Db 18 CTCTGAGTGGCTGGTGGT 1

RESULT 763
AX293716/c
LOCUS AX293716 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 5478 from Patent WO0179548.
ACCESSION AX293716
VERSION AX293716.1 GI:17055399
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Barany,P., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
AUTHORS Method of designing addressable array for detection of nucleic acid
TITLE sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 5478 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 365 CGAGCACCGCATTGGAGG 383
Db 19 CGAGCACCGCATTGCACG 2

RESULT 764
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AX295588
LOCUS AX295588 20 bp DNA PAT 21-NOV-2001
DEFINITION Sequence 7350 from Patent WO0179548.
ACCESSION AX295588
VERSION AX295588.1 GI:17057277
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 7350 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
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Query Match 0.4%; Score 14.8; DB 1; Length 20;
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 120 GCGGCTACTGTGCACTT 137
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DB 2 GCGGCTACTGTGCACTT 19

RESULT 765
AX295703/c
LOCUS AX295703 20 bp DNA PAT 21-NOV-2001
DEFINITION Sequence 7465 from Patent WO0179548.
ACCESSION AX295703
VERSION AX295703.1 GI:17057392
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 7465 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
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Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 471 CAAGTTTGGCAGCATCCG 488
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DB 20 CAAGTTTGGCAGCATCCG 3

RESULT 766
AX296579
LOCUS AX296579 20 bp DNA PAT 21-NOV-2001
DEFINITION Sequence 8341 from Patent WO0179548.
ACCESSION AX296579
VERSION AX296579.1 GI:17058268
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 8341 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

Query Match 0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 100 TGGCGGCGGCGGCTCAG 117
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DB 3 TGGCGGCGGCGGCTCAG 20

RESULT 767
AX297158
LOCUS AX297158 20 bp DNA PAT 21-NOV-2001
DEFINITION Sequence 8920 from Patent WO0179548.
ACCESSION AX297158
VERSION AX297158.1 GI:17058849
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 Barany,F., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 8920 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
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/note="Hypothetical Probe Sequence"

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1692 CCGGGACGTGCACAACT 1709
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DB 2 CCGGGACGTGCACAACT 19

RESULT 768
AX355435/c
LOCUS AX355435 20 bp DNA PAT 06-FEB-2002
DEFINITION Sequence 463 from Patent WO0197843.
ACCESSION AX355435
VERSION AX355435.1 GI:18620103
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL cancer
PATENT: WO 0197843-A 463 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
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/organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
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Db 20 GACTTTGGCTGGCCCGG 3

RESULT 769
AX357565
LOCUS AX357565 20 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 36 from Patent WO0188200.
ACCESSION AX357565
VERSION AX357565.1 GI:18674589
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Wakeland,E.K., Wandstrat,A. and Morel,L.
TITLE Isolation of genes within sle-1b that mediate a break in immune
tolerance
JOURNAL Patent: WO 0188200-A 36 22-NOV-2001;
Board of Regents, The University of Texas System (US)
FEATURES
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2325 GGTGTGTGGTGTGTGTGT 2342
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Db 3 GGGTGTGTGCATGTGTGT 20

RESULT 770
AX487479/c
LOCUS AX487479 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4779 from Patent WO02053728.
ACCESSION AX487479
VERSION AX487479.1 GI:22321627
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE
1
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4779 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
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source
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/db_xref="taxon:5476"

Query Match
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QY 829 GCGTGGCTGGTGTGTGT 846
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/note="Synthetic oligonucleotide-phosphorothioate backbone"

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Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
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Db 20 GACTTTGGCTGGCCCGG 3

RESULT 771
AX547172/c
LOCUS AX547172 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 311 from Patent WO02053141.
ACCESSION AX547172
VERSION AX547172.1 GI:25812316
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 311 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Synthetic sequence"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
|||||
Db 20 GACTTTGGCTGGCCCGG 3

RESULT 772
AX552535
LOCUS AX552535 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 22 from Patent EP1245677.
ACCESSION AX552535
VERSION AX552535.1 GI:25896556
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS King,K.W., Madura,R.A. and Rosey,E.L.
TITLE Nucleic acids and proteins of the mycoplasma hyopneumoniae mhp3
JOURNAL Patent: EP 1245677-A 22 02-OCT-2002;
Pfizer Products Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 14.8; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3539 GCTTCTAGAGTTTATAG 3556
|||||
Db 2 GCTTCTCAGTTTATAG 19

RESULT 773
AX613359
LOCUS AX613359 20 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 4384 from Patent WO02072882.
ACCESSION AX613359
VERSION AX613359.1 GI:28408788
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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Cullen,P. and Seedorf,U.
TITLE         Coronary chip
JOURNAL       Patent: WO 02072882-A 4384 19-SEP-2002;
              OGHAM GmbH (DE)
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Qy 368 AGCACCGCATTTGGAGCA 385
Db 1 AGACCGCCTTGGAGCA 18

RESULT 774
AX708866
LOCUS          20 bp DNA linear PAT 04-APR-2003
DEFINITION     Sequence 48 from Patent WO02101045.
ACCESSION      AX708866
VERSION        AX708866.1 GI:29564596
KEYWORDS       synthetic construct
SOURCE         artificial sequences.
ORGANISM
REFERENCE
AUTHORS        Patapoutian,A., Song,C., Ganju,P., Peier,A., McIntyre,P. and
              Bevan,S.
TITLE          Vanilloid receptor-related nucleic acids and polypeptides
JOURNAL        Patent: WO 02101045-A 48 19-DEC-2002;
              Novartis AG (CH); IRM LLC (BM)
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  Query Match      0.4%; Score 14.8; DB 1; Length 20;
  Best Local Similarity 88.9%; Pred. No. 9.8e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 186 GGAGGACGAGGCTGAGGA 203
Db 2 GGAGGACGAGGCTGAGGA 19

RESULT 775
AX708891/c
LOCUS          20 bp DNA linear PAT 04-APR-2003
DEFINITION     Sequence 73 from Patent WO02101045.
ACCESSION      AX708891
VERSION        AX708891.1 GI:29564621
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE
AUTHORS        Patapoutian,A., Song,C., Ganju,P., Peier,A., McIntyre,P. and
              Bevan,S.
TITLE          Vanilloid receptor-related nucleic acids and polypeptides
JOURNAL        Patent: WO 02101045-A 73 19-DEC-2002;
              Novartis AG (CH); IRM LLC (BM)

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  Best Local Similarity 88.9%; Pred. No. 9.8e+02;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 186 GGAGGACGAGGCTGAGGA 203
Db 19 GGAGGACGAGGCTGAGGA 2

RESULT 776
BD014728
LOCUS          20 bp DNA linear PAT 27-AUG-2002
DEFINITION     Nucleic acid and protein of mhp3 gene of Mycoplasma hyopneumoniae
              and use thereof.
ACCESSION      BD014728
VERSION        BD014728.1 GI:22555511
KEYWORDS       JP 2001149085-A/16.
SOURCE         synthetic construct
ORGANISM       synthetic construct
              artificial sequences.
REFERENCE
AUTHORS        King,K.W., Madura,R.A. and Rosi,I.L.
TITLE          Nucleic acid and protein of mhp3 gene of Mycoplasma hyopneumoniae
              and use thereof
JOURNAL        Patent: JP 2001149085-A 16 05-JUN-2001;
              PFIZER PROD INC
COMMENT         OS Artificial Sequence
              PN JP 2001149085-A/16
              PD 05-JUN-2001
              PF 23-SEP-2000 JP 2000300778
              PR 23-SEP-1999 US 60/156602
              PI KENDALL WAIN KING,REBECCA ANNE MADURA,IBURETTO LEE ROSI PC
              C12N15/09,A61K39/02,A61P31/04,C07K14/30,C07K16/12,C07K19/00,PC
              C12N1/21,
              PC C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53//
              PC C12P21/08,
              PC
              (C12N15/09,C12R1:35),(C07K14/30,C12R1:19),(C07K19/00,C12R1:19),PC
              (C12N1/21,C12R1:19),(C12P21/02,C12R1:19),C12N15/00,(C12N15/00,PC
              C12R1:35)
              CC Description of Artificial Sequence:Oligonucleotide FH Key

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Qy 3539 GCTTCTAGAGTTTATAG 3556
Db 2 GCTTCTAGAGTTTATAG 19

RESULT 777
BD074607/c
LOCUS          20 bp DNA linear PAT 27-AUG-2002
DEFINITION     Antisense oligonucleotide composition and modulation method of JNK
              protein.
ACCESSION      BD074607
VERSION        BD074607.1 GI:23620210

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KEYWORDS      JP 2001514905-A/31.
SOURCE        synthetic construct
ORGANISM      artificial construct
REFERENCE     1 (bases 1 to 20)
AUTHORS      McKay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
TITLE        Antisense oligonucleotide composition and modulation method of JNK
JOURNAL      protein
COMMENT      Patent: JP 2001514905-A 31 18-SEP-2001;
              ISIS PHARMACEUTICALS INC
              PN JP 2001514905-A/31
              PD 18-SEP-2001
              PF 07-AUG-1998 JP 2000509875
              PR 13-AUG-1997 US 08/910629
              PI ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
              NERO, WILLIAM A GAARDE
              PC C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
              PC C12N15/00
              CC antisense sequence
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              FT source 1..20
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1678 GACTTCGGCTGGCCCGG 1695
Db 20 GACTTTGGCTGGCCCGG 3

RESULT 778
BD074618
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide composition and modulation method of JNK
            protein.
ACCESSION  BD074618.1 GI:22620221
VERSION     JP 2001514905-A/42.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     McKay,R., Dean,N., Monia,B.P., Scott,P., Nero and Gaarde,W.A.
TITLE       Antisense oligonucleotide composition and modulation method of JNK
JOURNAL     protein
COMMENT     Patent: JP 2001514905-A 42 18-SEP-2001;
              ISIS PHARMACEUTICALS INC
              OS Artificial Sequence
              PN JP 2001514905-A/42
              PD 18-SEP-2001
              PF 07-AUG-1998 JP 2000509875
              PR 13-AUG-1997 US 08/910629
              PI ROBERT MCKAY,NICHOLAS DEAN,BRETT P MONIA,PAMELA SCOTT PI
              NERO, WILLIAM A GAARDE
              PC C12Q1/68,A61K31/7088,A61K48/00,A61P35/00,C12N15/09,C12P19/34,
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Query Match      0.4%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GACTTTGGCTGGCCCGG 18

RESULT 779
BD082094
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Reagents and methods useful for detecting diseases of the
            prostate,.
ACCESSION  BD082094
VERSION     BD082094.1 GI:22627704
KEYWORDS    JP 20015233948-A/21.
SOURCE      Zea mays
ORGANISM    Zea mays
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cohen,M., Friedman,P.N., Gordon,J., Hodges,S.C., Klasse,M.R.,
            Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.
TITLE       Reagents and methods useful for detecting diseases of the prostate
JOURNAL     Patent: JP 20015233948-A 21 27-NOV-2001;
            ABBOTT LABORATORIES
COMMENT     PN JP 20015233948-A/21
            PD 27-NOV-2001 JP 1998517758
            PF 08-OCT-1997 JP 1998517758
            PR 08-OCT-1996 US 08/727688
            PI MAURICE COHEN, PAULA N FRIEDMAN, JULIAN GORDON, STEVEN C HODGES,
            PI MICHAEL R KLASS, JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C PI
            RUSSELL,
            PI STEVEN D STROUPE
            PC C12Q1/68,C07K14/47//C07K16/30,G01N33/574
            CC Strandedness: Single;
            CC Topology: Linear;
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Best Local Similarity 88.9%; Pred. No. 9.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 921 CTTCTTCCTGTTTCATCCT 938
Db 2 CTTCTTCCTGTTTCCT 19

RESULT 780
BD084635
LOCUS      20 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for diagnosis and treatment of breast
            cancer.
ACCESSION  BD084635
VERSION     BD084635.1 GI:22630245
KEYWORDS    JP 2001523096-A/13.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Vournakis,J.N., Seth,A.K. and Papas,T.S.
TITLE       Methods and compositions for diagnosis and treatment of breast
JOURNAL     Patent: JP 2001523096-A 13 20-NOV-2001;
            MUSC FOUNDATION FOR RESEARCH DEVELOPMENT
COMMENT     OS Artificial Sequence

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BD141712	
BD141712.1	GI:23236657
WO 0214506-A/3.	
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synthetic construct	
artificial sequences.	
1 (bases 1 to 20)	
Komori,T., Yamamoto,T., Nitta,N. and Takemori,N.	
Method of estimating genotype of fertility recovery locus for rice	
Bt type male sterile cytoplasm	
Patent: WO 0214506-A 3 21-FEB-2002;	
JAPAN TOBACCO INC.SYNGENTA LTD.TOSHIYUKI KOMORI,TOSHIO YAMAMOTO,	
NAOTO NITTA,NAOKI TAKEMORI	
OS Artificial Sequence	
PN WO 0214506-A/3	
PD 21-FEB-2002	
PF 16-AUG-2001 WO 2001JP007052	
PR 17-AUG-2000 JP OOP 247204	
PI TOSHIYUKI KOMORI,TOSHIO YAMAMOTO,NAOTO NITTA,NAOKI TAKEMORI PC	
C12N15/09,C12Q1/68//A01H1/00	
CC Oligonucleotide primer for amplification of G4003 HindIII CC	
marker sequence.	
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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy 2044 ACCGACGAGTACTGGAC 2061	
Db 2 ATCGACGAGTACTGAAC 19	
RESULT 783	
AB068811/c	
LOCUS	AB068811 Synthetic construct DNA, reverse primer for human STS sts-DLS170 at SYN 21-MAY-2003
DEFINITION	lp36.
ACCESSION	AB068811 GI:15129615
VERSION	AB068811
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1
AUTHORS	Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K., Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H., Morohaishi,A., Ohita,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A. and Soeda,E
TITLE	a BAC-based STS-content map spanning a 35-Mb region of human chromosome lp35-p36
JOURNAL	Genomics 74 (1), 55-70 (2001)
MEDLINE	21269192
PUBMED	11374902
REFERENCE	2 (bases 1 to 20)
AUTHORS	Horii,A.
TITLE	Direct Submission
JOURNAL	Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
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Best Local Similarity	88.9%; Pred. No. 9.8e+02;	FT	source	1. .21	/organism='Artificial Sequence'
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	FT	source	1. .21	/organism='Artificial Sequence'
QY	999 CCCACCGTGCACAGAT 1016	FT	source	1. .21	/organism='Artificial Sequence'
DB	20 CCACACATGCACAGAT 3	FT	source	1. .21	/organism='Artificial Sequence'
RESULT 784		FT	source	1. .21	/organism='Artificial Sequence'
LOCUS	AR014613	FT	source	1. .21	/organism='Artificial Sequence'
DEFINITION	Sequence 46 from patent US 5773691.	FT	source	1. .21	/organism='Artificial Sequence'
ACCESSION	AR014613	FT	source	1. .21	/organism='Artificial Sequence'
VERSION	AR014613.1 GI:3972067	FT	source	1. .21	/organism='Artificial Sequence'
KEYWORDS	Unknown.	FT	source	1. .21	/organism='Artificial Sequence'
SOURCE	Unknown.	FT	source	1. .21	/organism='Artificial Sequence'
ORGANISM	Unknown.	FT	source	1. .21	/organism='Artificial Sequence'
REFERENCE	1 (bases 1 to 21)	FT	source	1. .21	/organism='Artificial Sequence'
AUTHORS	Falco,S.Carl., Keeler,S.Jo. and Rice,J. Ann.	FT	source	1. .21	/organism='Artificial Sequence'
TITLE	Chimeric genes and methods for increasing the lysine and threonine content of the seeds of plants	FT	source	1. .21	/organism='Artificial Sequence'
JOURNAL	Patent: US 5773691-A 46 30-JUN-1998;	FT	source	1. .21	/organism='Artificial Sequence'
FEATURES	Location/Qualifiers	FT	source	1. .21	/organism='Artificial Sequence'
source	1. .21	FT	source	1. .21	/organism='Artificial Sequence'
Query Match	0.4%; Score 14.8; DB 1; Length 21;	FT	source	1. .21	/organism='Artificial Sequence'
Best Local Similarity	88.9%; Pred. No. 1e+03;	FT	source	1. .21	/organism='Artificial Sequence'
Matches	16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	FT	source	1. .21	/organism='Artificial Sequence'
QY	1353 GGAGATGATGAGATGAT 1370	FT	source	1. .21	/organism='Artificial Sequence'
DB	18 GGAGATGATGAGATGAT 1	FT	source	1. .21	/organism='Artificial Sequence'
RESULT 785		FT	source	1. .21	/organism='Artificial Sequence'
LOCUS	BD223228/c	FT	source	1. .21	/organism='Artificial Sequence'
DEFINITION	21 bp DNA linear PAT 17-JUL-2003	FT	source	1. .21	/organism='Artificial Sequence'
ACCESSION	BD223228	FT	source	1. .21	/organism='Artificial Sequence'
VERSION	BD223228.1 GI:33032998	FT	source	1. .21	/organism='Artificial Sequence'
KEYWORDS	A novel plastid-targeting nucleic acid sequence, a novel beta-amylase sequence, a stimulus-responsive promoter and uses thereof.	FT	source	1. .21	/organism='Artificial Sequence'
SOURCE	JP 2002523040-A/5.	FT	source	1. .21	/organism='Artificial Sequence'
ORGANISM	Synthetic construct	FT	source	1. .21	/organism='Artificial Sequence'
REFERENCE	1 (bases 1 to 21)	FT	source	1. .21	/organism='Artificial Sequence'
AUTHORS	Kavanagh, T.A. and Lao, N.T.	FT	source	1. .21	/organism='Artificial Sequence'
TITLE	A novel plastid-targeting nucleic acid sequence, a novel beta-amylase sequence, a stimulus-responsive promoter and uses thereof.	FT	source	1. .21	/organism='Artificial Sequence'
JOURNAL	Patent: JP 2002523040-A 5 30-JUL-2002;	FT	source	1. .21	/organism='Artificial Sequence'
COMMENT	ADVANCED TECHNOLOGIES LTD	FT	source	1. .21	/organism='Artificial Sequence'
OS	JP 2002523040-A/5	FT	source	1. .21	/organism='Artificial Sequence'
PN	JP 2002523040-A/5	FT	source	1. .21	/organism='Artificial Sequence'
PD	30-JUL-2002	FT	source	1. .21	/organism='Artificial Sequence'
PF	13-AUG-1999 JP 2000566401	FT	source	1. .21	/organism='Artificial Sequence'
PI	19-AUG-1998 GB 9817959.1, 19-AUG-1998 GB 9817963.3 PR	FT	source	1. .21	/organism='Artificial Sequence'
PT	05-JUN-1999 GB 9913014.8	FT	source	1. .21	/organism='Artificial Sequence'
PC	THOMAS ANTHONY KAVANAGH, NGA THI LAO	FT	source	1. .21	/organism='Artificial Sequence'
CC	C12N15/09, A01H5/00, C12N5/10, C12R1/91, C12N15/00, PC C12N5/00,	FT	source	1. .21	/organism='Artificial Sequence'
QY	1180 CGGCGCCGCGCTGACCCCTG 1197	FT	source	1. .21	/organism='Artificial Sequence'
DB	20 CGGCGCCGCGCTGCGCCCG 3	FT	source	1. .21	/organism='Artificial Sequence'
RESULT 787		FT	source	1. .21	/organism='Artificial Sequence'
LOCUS	BD262820	FT	source	1. .21	/organism='Artificial Sequence'
DEFINITION	Method for high-processed DNA methylation.	FT	source	1. .21	/organism='Artificial Sequence'
ACCESSION	BD262820	FT	source	1. .21	/organism='Artificial Sequence'
VERSION	BD262820.1 GI:33072588	FT	source	1. .21	/organism='Artificial Sequence'
KEYWORDS	JP 2002543852-A/6.	FT	source	1. .21	/organism='Artificial Sequence'
SOURCE	unidentified	FT	source	1. .21	/organism='Artificial Sequence'
ORGANISM	unclassified.	FT	source	1. .21	/organism='Artificial Sequence'
REFERENCE	1 (bases 1 to 21)	FT	source	1. .21	/organism='Artificial Sequence'
AUTHORS	Laird, P.W., Bads, C.A. and Danenberg, K.D.	FT	source	1. .21	/organism='Artificial Sequence'
TITLE	Method for high-processed DNA methylation	FT	source	1. .21	/organism='Artificial Sequence'
JOURNAL	Patent: JP 2002543852-A 6 24-DEC-2002;	FT	source	1. .21	/organism='Artificial Sequence'
COMMENT	unclassified.	FT	source	1. .21	/organism='Artificial Sequence'
OS	JP 2002543852-A 6 24-DEC-2002;	FT	source	1. .21	/organism='Artificial Sequence'
PN	JP 2002543852-A 6 24-DEC-2002;	FT	source	1. .21	/organism='

ORGANISM unidentified
unclassified.
1 (bases 1 to 21)
Blasczyk,R.D.
A method for determinig the histocompatibility locus antigen class
II
JOURNAL
Patent: EP 0892069-A 94 20-JAN-1999;
BIOTEST AG (DE)
FEATURES
source
Location/Qualifiers
1..21
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTG 2333
Db 18 TCTGAGTGTGTGTG 1

RESULT 797
AX020773/c
LOCUS 21 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 273 from Patent WO9934016.
ACCESSION AX020773
VERSION AX020773.1 GI:10044472
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Vider,B.Z.
TITLE A method for identifying and characterizing cells and tissues
JOURNAL Patent: WO 9934016-A 273 08-JUL-1999;
GENENA LTD (IL); VIDER BEN ZION (IL)
FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1800 TGACGTCGTCTCTTTGG 1817
Db 19 TGATGTGTCTCTTTGG 2

RESULT 798
AX092706
LOCUS 21 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 118 from Patent WO0115676.
ACCESSION AX092706
VERSION AX092706.1 GI:13444763
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Hayden,M.R., Brooks-Wilson,A.R., Pimstone,S.N. and Clee,S.M.
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels
JOURNAL Patent: WO 0115676-A 118 08-MAR-2001;
University of British Columbia (CA); Xenon Genetics Inc. (CA)
FEATURES
source
Location/Qualifiers
1..21

/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 497 ACACGCTGGACGTGCTGG 514
Db 1 ACACGCTGGGGTGTCTGG 18

RESULT 799
AX095559/c
LOCUS 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 737 from Patent WO0118250.
ACCESSION AX095559
VERSION AX095559.1 GI:13511762
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 737 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium Pharmaceuticals, Inc. (US)
FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1386 CATCATCAACCTGCTGGCG 1405
Db 20 CAACATCCAYGTGCTGGCG 1

RESULT 800
AX154199
LOCUS 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 297 from Patent WO0138576.
ACCESSION AX154199
VERSION AX154199.1 GI:14535813
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 297 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
source
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2009 TGGAGACCTGGACCGTGTG 2028

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1 TGGAGGACCTSCAGCGTGAC 20

RESULT 801
AX154392
LOCUS AX154392 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 490 from Patent WO0138576.
ACCESSION AX154392
VERSION AX154392.1 GI:14536006
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Cargill,M., Ireland,J.S. and Lander,E.S.
AUTHORS Human single nucleotide polymorphisms
TITLE Patent: WO 0138576-A 490 31-MAY-2001;
JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 899 GCATCTCAGCTACGGGGTG 918
|||||||:| |||||
2 GCATCCCCARCTCTCGGTG 21

RESULT 802
AX154452
LOCUS AX154452 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 550 from Patent WO0138576.
ACCESSION AX154452
VERSION AX154452.1 GI:14536066
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Cargill,M., Ireland,J.S. and Lander,E.S.
AUTHORS Human single nucleotide polymorphisms
TITLE Patent: WO 0138576-A 550 31-MAY-2001;
JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 905 TCAGTACGGGGTGGGCTTC 924
|||||||:| |||||
1 TCAGTACTCRGTGGGGCTC 20

RESULT 803
AX154453/c
LOCUS AX154453 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 551 from Patent WO0138576.
ACCESSION AX154453
VERSION AX154453.1 GI:14536067
KEYWORDS
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Cargill,M., Ireland,J.S. and Lander,E.S.
AUTHORS Human single nucleotide polymorphisms
TITLE Patent: WO 0138576-A 551 31-MAY-2001;
JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1242 GGAGGCCATCGGCATTGACA 1261
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21 GGAGGTCTCTCGCAATGACA 2

RESULT 804
AX342717
LOCUS AX342717 21 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 21 from Patent WO0198511.
ACCESSION AX342717
VERSION AX342717.1 GI:18152095
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Gallani,A.I., Imbert,G. and Krek,W.
AUTHORS Tumour-cell specific gene expression and its use in cancer therapy
TITLE Patent: WO 0198511-A 21 27-DEC-2001;
JOURNAL Novartis Forschungsstiftung Zweigniederlassung (CH)
FEATURES
Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2700 TCCCACCTCGCCCTCAG 2717
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3 TCCCACCGCGCACCTCAG 20

RESULT 805
AX428083/c
LOCUS AX428083 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from Patent WO0233100.
ACCESSION AX428083
VERSION AX428083.1 GI:21538110
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Liu,N. and Floeckner,J.
AUTHORS Regulation of human adenylate cyclase, type IV
TITLE Patent: WO 0233100-A 3 25-APR-2002;
JOURNAL BAYER AG (DE)
FEATURES
Location/Qualifiers
1..21
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Primer: AC4-L1"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 868 GAGGCTGACGAGCGCGGC 885
Db 21 GGGGCTGAGAGCGCGGC 4

RESULT 806
AX539458/c
LOCUS      21 bp      DNA      linear      PAT 23-NOV-2002
DEFINITION Sequence 245 from Patent WO02059142.
ACCESSION AX539458
VERSION    AX539458.1 GI:25272897
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE
AUTHORS    Brinkmann, U., Hoffmeyer, S. and Mornhinweg, E.
TITLE      Polymorphisms in the human gene for the multidrug
           resistance-associated protein 1 (mrp-1) and their use in diagnostic
           and therapeutic applications
JOURNAL     Patent: WO 02059142-A 245 01-AUG-2002;
           Epidauros Biotechnologie AG (DE)
FEATURES
source      Location/Qualifiers
            1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2791 TACATTTCTATAAATAGA 2808
Db 20 TCCATTTCTATAAATAGA 3

RESULT 807
AX539459
LOCUS      21 bp      DNA      linear      PAT 23-NOV-2002
DEFINITION Sequence 246 from Patent WO02059142.
ACCESSION AX539459
VERSION    AX539459.1 GI:25272899
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE
AUTHORS    Brinkmann, U., Hoffmeyer, S. and Mornhinweg, E.
TITLE      Polymorphisms in the human gene for the multidrug
           resistance-associated protein 1 (mrp-1) and their use in diagnostic
           and therapeutic applications
JOURNAL     Patent: WO 02059142-A 246 01-AUG-2002;
           Epidauros Biotechnologie AG (DE)
FEATURES
source      Location/Qualifiers
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               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 2791 TACATTTCTATAAATAGA 2808
Db 2 TCCATTTCTATAAATAGA 19

RESULT 808
AX553645/c
LOCUS      21 bp      DNA      linear      PAT 27-NOV-2002
DEFINITION Sequence 49 from Patent WO02074946.
ACCESSION AX553645
VERSION    AX553645.1 GI:25897643
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS    Serup, P., Heimberg, H. and Gradwohl, G.
TITLE      Method for generating insulin-secreting cells suitable for
           transplantation
JOURNAL     Patent: WO 02074946-A 49 26-SEP-2002;
           NOVO NORDISK A/S (DK)
FEATURES
source      Location/Qualifiers
            1..21
               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03; 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 472 AAGTTTGGCAGCATCCGG 489
Db 18 AAGTTTGGCGTCATCCGG 1

RESULT 809
BD010405/c
LOCUS      21 bp      DNA      linear      PAT 09-JAN-2004
DEFINITION Chimeric genes and methods for increasing the lysine content of the
           seeds of plants.
ACCESSION BD010405
VERSION    BD010405.1 GI:18638778
KEYWORDS   JP 2001502923-A/37.
SOURCE     unidentified
ORGANISM   unidentified
           unclassified.
REFERENCE    1 (bases 1 to 21)
AUTHORS      Falco, S.C., Iii, R.E.M. and Epelbaum, S.U.
TITLE        Chimeric genes and methods for increasing the lysine content of the
           seeds of plants
JOURNAL      Patent: JP 2001502923-A 37 06-MAR-2001;
           EI DU PONT DE NEMOURS AND CO
COMMENT      OS Unidentified
           PN JP 2001502923-A/37
           PD 06-MAR-2001
           PF 27-MAR-1998 JP 1998543284
           PR 27-MAR-1997 US 08/824627
           PI SAVERIO CARL FALCO, RAYMOND ERVIN MCDEVITT III, PI
           URSULA EPELBAUM
           PC C12N9/06, C12N9/12, C12N9/88, C12P13/08, C12N15/82 CC
           Strandedness: Single;
           CC Topology: Linear;
           FH Key Location/Qualifiers
           FT source 1..21
           /organism="Unidentified"
           /organism="unidentified"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32644"

FEATURES
source      Location/Qualifiers
            1..21
               /organism="unassigned DNA"
               /db_xref="taxon:32644"

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Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1353 GGAGATGATGAAGATGAT 1370
Db 18 GGAGATGATGAAGAT 1

RESULT 810
LOCUS BD088877/c 21 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088877
VERSION BD088877.1 GI:22634487
KEYWORDS JP 2001321190-A/1121.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1121 20-NOV-2001;
        THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
        GENOTECHS
COMMENT OS Artificial Sequence
        PN JP 2001321190-A/1121
        PD 20-NOV-2001
        PI EIICHI SOEDA
        PC C12N15/09.C12N15/09.C12M1/00.C12Q1/68.G01N33/53.G01N33/566, PC
        C12N15/00
        CC Description of Artificial Sequence:Synthetic DNA FH Key
        CC Location/Qualifiers
        FT source
        FT 1..21
        FT Location/Qualifiers
        source 1..21
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3268 ATTGCTTTGCTCTTTT 3285
Db 19 ATGCTTGTGCTCTTTT 2

RESULT 811
LOCUS AR264922
DEFINITION Sequence 6 from patent US 6492121.
ACCESSION AR264922
VERSION AR264922.1 GI:29693309
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 6 10-DEC-2002;
FEATURES Location/Qualifiers
        source 1..30
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTT 3284
Db 5 ATATTTTTTTTGTCTTTT 30

RESULT 812
LOCUS AR264923
DEFINITION Sequence 7 from patent US 6492121.
ACCESSION AR264923
VERSION AR264923.1 GI:29693310
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 7 10-DEC-2002;
FEATURES Location/Qualifiers
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTT 3284
Db 5 ATATTTTTTTTGTCTTTT 30

RESULT 813
LOCUS AR264928
DEFINITION Sequence 12 from patent US 6492121.
ACCESSION AR264928
VERSION AR264928.1 GI:29693315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 12 10-DEC-2002;
FEATURES Location/Qualifiers
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        /mol_type="genomic DNA"

Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTT 3284
Db 5 ATATTTTTTTTGTCTTTT 30

RESULT 814
LOCUS AR264928
DEFINITION Sequence 12 from patent US 6492121.
ACCESSION AR264928
VERSION AR264928.1 GI:29693315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 12 10-DEC-2002;
FEATURES Location/Qualifiers
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        /organism="unknown"
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTT 3284
Db 5 ATATTTTTTTTGTCTTTT 30

RESULT 814
LOCUS AR264923
DEFINITION Sequence 7 from patent US 6492121.
ACCESSION AR264923
VERSION AR264923.1 GI:29693310
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
        Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
        molecules, nucleic acid probes for the method, and method for
        analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 7 10-DEC-2002;
FEATURES Location/Qualifiers
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Yokomaku,T., Koyama,O. and Furusho,K.
Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
Patent: US 6699661-A 12 02-MAR-2004;
FEATURES             source
    Query Match      0.4%; Score 14.8; DB 1; Length 30;
    Best Local Similarity 73.1%; Pred. No. 1.3e+03;
    Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3259 AGATATTATTTGCTTTCCTTTT 3284
Db 5 ATATTTTTTTTTTCTTTTTTTTTT 30

RESULT 817
BD072867          30 bp DNA linear PAT 27-AUG-2002
LOCUS            Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION       and method for analyzing data obtained by that method.
ACCESSION        BD072867
VERSION          BD072867.1 GI:22618470
KEYWORDS         JP 2001286300-A/5.
SOURCE           synthetic construct
ORGANISM         artificial sequences.
REFERENCE         1 (bases 1 to 30)
AUTHORS          Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
                  Yokomaku,T., Koyama,O. and Furusho,K.
TITLE            Method for assaying nucleic acid, nucleic acid probe used therefor,
                  and method for analyzing data obtained by that method
JOURNAL          Patent: JP 2001286300-A 5 16-OCT-2001;
                  JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
                  NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
                  AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT          OS Artificial Sequence
                  PN JP 2001286300-A/5
                  PD 16-OCT-2001
                  PF 20-APR-2000 JP 2000120097
                  PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
                     KURATA,
                     PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
                     PC C1201/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,PC
                     GOIN33/566,
                     PC C12N15/00
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                        examining the
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                        labeled with
                        BODIPY FL/C6 upon the hybridization of the
                        probe with a target.
                     CC ,nucleic
                     CC acid.
                     FH Key
                     FT source
                     FT Location/Qualifiers
                        /organism='Artificial Sequence'.
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Query Match      0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3259 AGATATTATTTGCTTTCCTTTT 3284
Db 5 ATATTTTTTTTTTGTTCCTTTT 30

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RESULT 818
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LOCUS          30 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION     BD072873
VERSION       BD072873.1 GI:22618476
KEYWORDS      JP 2001286300-A/11.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 30)
AUTHORS       Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE         Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL       Patent: JP 2001286300-A 11 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT       OS Artificial Sequence
PN JP 2001286300-A/11
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
labeled with
decrease in fluorescence emission of a nucleic acid probe CC
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
/organism='synthetic construct'
/mol_type='genomic DNA'
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source
Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3259 AGATATTTATTGCTTGTGCTCTTTT 3284
Db 5 ATATTTTCTTTTCTTTTCTTTT 30
RESULT 820
BD107500
LOCUS          30 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION    Novel quantitative polymorphism analysis method.
ACCESSION     BD107500
VERSION       BD107500.1 GI:23202318
KEYWORDS      JP 2002000275-A/9.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 30)
AUTHORS       Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE         Novel quantitative polymorphism analysis method
JOURNAL       Patent: JP 2002000275-A 9 08-JAN-2002;
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
& TECHNOL
COMMENT       OS Artificial Sequence
PN JP 2002000275-A/9
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
CC acid.
FH Key Location/Qualifiers
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source
Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3259 AGATATTTATTGCTTGTGCTCTTTT 3284
Db 5 ATATTTTCTTTTCTTTTCTTTT 30
RESULT 819
BD107494
LOCUS          30 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION    Novel quantitative polymorphism analysis method.
ACCESSION     BD107494
VERSION       BD107494.1 GI:23202312
KEYWORDS      JP 2002000275-A/3.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 30)
AUTHORS       Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
Yokomaku,T.
TITLE         Novel quantitative polymorphism analysis method
JOURNAL       Patent: JP 2002000275-A 3 08-JAN-2002;
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/mol_type="genomic DNA"
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Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3284
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Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 821
BD145026 30 bp DNA linear PAT 17-JAN-2003
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145026
VERSION BD145026.1 GI:27850784
KEYWORDS JP 2002119291-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 7 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/7
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA.
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
hybridization of
the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..30
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/db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3284
|||||
Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 822
BD145032 30 bp DNA linear PAT 17-JAN-2003
LOCUS Method for assaying nucleic acid, nucleic acid probe used therefor,
DEFINITION and method for analyzing data obtained by that method.
ACCESSION BD145032
VERSION BD145032.1 GI:27850790
KEYWORDS JP 2002119291-A/13.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 13 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002119291-A/13
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA.
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N33/ PC
53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of
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the probe with a target nucleic acid.
FH Key Location/Qualifiers
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/db_xref="taxon:32630"

Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3259 AGATATTTTATTTGCTTTGCTCTTTT 3284
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Db 5 ATATTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 823
BD166027 30 bp DNA linear PAT 17-JAN-2003
LOCUS Novel nucleic acid probes, method for determining concentrations of
DEFINITION nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166027
VERSION BD166027.1 GI:27871839
KEYWORDS JP 2002191372-A/7.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 7 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
OS Artificial Sequence
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PN JP 2002191372-A/7
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers
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Location/Qualifiers
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/db_xref='taxon:32644'
Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3259 ACATATTTTATTTGCTTTCCTCTTTT 3284
DB 5 ATATTTTTTTTGTCTTTTTTTTTT 30

RESULT 824
BD166032
LOCUS 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method.
ACCESSION BD166032
VERSION BD166032.1 GI:27871844
KEYWORDS JP 2002191372-A/12.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of
nucleic acid by using the probes, and method for analyzing data
obtained by the method
JOURNAL Patent: JP 2002191372-A 12 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
KANKYO ENGINEERING CO LTD
OS Artificial Sequence
PN JP 2002191372-A/12
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
BODIBY FL/C6 upon the hybridization of the
probe with a target
nucleic
acid.
FH Key Location/Qualifiers

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Location/Qualifiers
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/db_xref='taxon:32644'
Query Match 0.4%; Score 14.8; DB 1; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 3259 ACATATTTTATTTGCTTTCCTCTTTT 3284
DB 5 ATATTTTTTTTGTCTTTTTTTTTT 30

RESULT 825
AR029830
LOCUS 35 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5861244.
ACCESSION AR029830
VERSION AR029830.1 GI:5943044
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 19 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..35
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.4%; Score 14.8; DB 1; Length 35;
Best Local Similarity 64.7%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 3300 TTCTATAGGATTTTCTTTTGGAGAGATTTATTTT 3333
DB 1 TTTTCTATCTTTTCTTTTCTTTTCTTTTCTTTT 34

RESULT 826
I32405
LOCUS 42 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5587443.
ACCESSION I32405
VERSION I32405.1 GI:1823196
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Heiliger,L., Schmidt,A. and Probst,J.
TITLE Polymerizable emulsifiers and reactive groups and polymers of
emulsifiers and other monomers
JOURNAL Patent: US 5587443-A 2 24-DEC-1996;
FEATURES Location/Qualifiers
source 1..42
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.4%; Score 14.8; DB 1; Length 42;
Best Local Similarity 64.7%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 3301 TCTATAGGATTTTCTTTTGGAGAGATTTATTTT 3334
DB 2 TCTACTGGCTCTTTTCTTTTCTTTTCTTTTCTTTT 35

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BD002052.1 GI:18628792
JP 2000178202-A/3.
synthetic construct

ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsutani, T. and Naito, K.
TITLE Agent for retarding the conversion of hormone-dependent cancer into hormone-independent cancer
JOURNAL Patent: JP 2000178202-A 3 27-JUN-2000;
COMMENT TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2000178202-A/3
PD 27-JUN-2000
PF 07-OCT-1999 JP 1999286856
PR
PI TOSHIYA MATSUTANI, KENICHIRO NAITO
PC A61K38/04, A61K38/22, A61K45/00, A61P13/08, A61P35/00//C07K7/23 CC

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FT /organism='Artificial Sequence'.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14.6; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 9.1e+02;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1618 CACAGGACCTGGCTGC 1534
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DB 1 CAYMGRGACVTKGWC 17

RESULT 832
LOCUS I29931/c
DEFINITION Sequence 44 from patent US 5578468.
ACCESSION I29931
VERSION I29931.1 GI:1820722
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Pickup, D.J., Patel, D. and Antczak, J.B.
TITLE Site-specific RNA cleavage
JOURNAL Patent: US 5578468-A 44 26-NOV-1996;
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source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.6; DB 1; Length 37;
Best Local Similarity 62.2%; Pred. No. 1.5e+03;
Matches 23; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 3299 TTCTCTAGGATTTTCTTTAGGAGATTTATTTTGG 3335
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RESULT 833
LOCUS AR222446/c
DEFINITION Sequence 4 from patent US 6429300.
ACCESSION AR222446
VERSION AR222446.1 GI:23329977
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 39)

AUTHORS Kurz, M., Lohse, P. and Wagner, R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 4 06-AUG-2002;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
Query Match 0.4%; Score 14.6; DB 1; Length 39;
Best Local Similarity 69.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3262 TATTTTATTTGCTTTCTCTTTTTCAGGA 3290
|||||::|||::|||::|||
DB 35 TTTTNTTTTTTTTTTTTTTTTTTTTTTTAGAA 7

RESULT 834
LOCUS AR029978/c
DEFINITION Sequence 167 from patent US 5861244.
ACCESSION AR029978
VERSION AR029978.1 GI:5943192
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Wang, C.-G. and Hepburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 167 19-JAN-1999;
FEATURES
source Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 923 TCTTCCTGTTTCATCCT 938
|||||::|||::|||
DB 16 TCTTCCTCTTCATCCT 1

RESULT 835
LOCUS AR050989
DEFINITION Sequence 58 from patent US 5830644.
ACCESSION AR050989
VERSION AR050989.1 GI:5974353
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS West, M.D., Shay, J. and Wright, W.E.
TITLE Method for screening for agents which increase telomerase activity in a cell
JOURNAL Patent: US 5830644-A 58 03-NOV-1998;
FEATURES
source Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
|||||::|||::|||
DB 1 TGGGTGTGTGTGTGTG 16

```

RESULT 836
E32226/c
LOCUS          E32226          16 bp      DNA          linear          PAT 18-JUN-2001
DEFINITION     Method for isolating satellite sequence.
ACCESSION      E32226
VERSION        E32226.1 GI:13021862
KEYWORDS       JP 2000060559-A/28.
SOURCE         Haliotis discus discus
ORGANISM       Haliotis discus discus
REFERENCE      1 (bases 1 to 16)
AUTHORS        Hideaki T. and Masashi S.
TITLE          Method for isolating satellite sequence
JOURNAL        Patent: JP 2000060559-A 28 29-FEB-2000;
               NATL INST OF AGRICULTURAL RESOURCES
COMMENT        OS Haliotis discus discus
               PN JP 2000060559-A/28
               PD 29-FEB-2000
               PF 18-AUG-1998 JP 1998232153
               PR HIDEAKI TAKAHASHI,MASASHI SEKINO
               PC C12N15/09,C12O1/68,C12N15/00
               CC
               FH Key
               FT source
               FT Location/Qualifiers
FEATURES       source
               1..16
               /organism="Haliotis discus discus"
               /mol_type="genomic DNA"
               /db_xref="taxon:91233"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2316 TCTGTGTGTGTGTGTG 2331
      ||| ||||| ||||| |||||
Db 16 TCTGTGTGTGTGTGTG 1

RESULT 837
I33563
LOCUS          I33563          16 bp      DNA          linear          PAT 06-FEB-1997
DEFINITION     Sequence 2 from patent US 5593834.
ACCESSION      I33563
VERSION        I33563.1 GI:1824354
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Lane,M.J., Benight,A.S. and Faldasz,B.D.
TITLE          Method of preparing DNA sequences with known ligand binding
JOURNAL        Patent: US 5593834-A 2 14-JAN-1997;
               Location/Qualifiers
FEATURES       source
               1..16
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3464 ATATATATCTATATAT 3479
      ||||| ||||| ||||| |||||
Db 1 ATATATAGCTATATAT 16

RESULT 838
I33563/c
LOCUS          I33563          16 bp      DNA          linear          PAT 06-FEB-1997
DEFINITION     Sequence 2 from patent US 5593834.
ACCESSION      I33563
VERSION        I33563.1 GI:1824354
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Lane,M.J., Benight,A.S. and Faldasz,B.D.
TITLE          Method of preparing DNA sequences with known ligand binding
JOURNAL        Patent: US 5593834-A 2 14-JAN-1997;
               Location/Qualifiers
FEATURES       source
               1..16
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3464 ATATATATCTATATAT 3479
      ||||| ||||| ||||| |||||
Db 16 ATATATAGCTATATAT 1

RESULT 839
I38642
LOCUS          I38642          16 bp      DNA          linear          PAT 13-MAY-1997
DEFINITION     Sequence 2 from patent US 5614617.
ACCESSION      I38642
VERSION        I38642.1 GI:2084696
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Cook,P.D. and Sanghvi,Y.S.
TITLE          Nuclease resistant, pyrimidine modified oligonucleotides that
               detect and modulate gene expression
JOURNAL        Patent: US 5614617-A 2 25-MAR-1997;
               Location/Qualifiers
FEATURES       source
               1..16
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2824 ATATATACATATATAT 2839
      ||||| ||||| ||||| |||||
Db 1 ATATATATATATATAT 16

RESULT 840
I38642/c
LOCUS          I38642          16 bp      DNA          linear          PAT 13-MAY-1997
DEFINITION     Sequence 2 from patent US 5614617.
ACCESSION      I38642
VERSION        I38642.1 GI:2084696
KEYWORDS       .
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 16)
AUTHORS        Cook,P.D. and Sanghvi,Y.S.
TITLE          Nuclease resistant, pyrimidine modified oligonucleotides that
               detect and modulate gene expression
JOURNAL        Patent: US 5614617-A 2 25-MAR-1997;
               Location/Qualifiers
FEATURES       source
               1..16
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3464 ATATATATCTATATAT 3479
      ||||| ||||| ||||| |||||
Db 1 ATATATAGCTATATAT 16

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FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATAT 2839
Db 16 ATATATATATATAT 1

RESULT 841
LOCUS I51790 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 58 from patent US 5645986.
ACCESSION I51790
VERSION I51790.1 GI:2472991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
Wright,W.E., Blackburn,E.H. and Vaziri,H.
TITLE Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
JOURNAL Patent: US 5645986-A 58 08-JUL-1997;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 842
LOCUS I84399 16 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 57 from patent US 5695932.
ACCESSION I84399
VERSION I84399.1 GI:3021919
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.
TITLE Telomerase activity assays for diagnosing pathogenic infections
JOURNAL Patent: US 5695932-A 57 09-DEC-1997;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 843
LOCUS I51790 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 58 from patent US 5645986.
ACCESSION I51790
VERSION I51790.1 GI:2472991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
Wright,W.E., Blackburn,E.H. and Vaziri,H.
TITLE Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
JOURNAL Patent: US 5645986-A 58 08-JUL-1997;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 844
LOCUS AR307317 16 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 80 from patent US 6551774.
ACCESSION AR307317
VERSION AR307317.1 GI:31697844
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 80 22-APR-2003;
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTG 2333
Db 1 TGGGTGTGTGTGTGTG 16

RESULT 845
LOCUS AR328417 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 5819 from patent US 6566127.
ACCESSION AR328417
VERSION AR328417.1 GI:33714225
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5819 20-MAY-2003;
FEATURES
  Location/Qualifiers

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source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1295 TGAAGATGCTGAAGA 1310
|||||
Db 1 TGAAGATGCTGAAGA 16

RESULT 846
AR328446
LOCUS
DEFINITION Sequence 5848 from patent US 6566127.
ACCESSION AR328446
VERSION AR328446.1 GI:33714254
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES
Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1658 ACAACGTGTGAAGAT 1673
|||||
Db 1 ACAACGTGTGAAGAT 16

RESULT 847
AR328669
LOCUS
DEFINITION Sequence 6071 from patent US 6566127.
ACCESSION AR328669
VERSION AR328669.1 GI:33714477
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL related to levels of vascular endothelial growth factor receptor
FEATURES
Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2321 GTGTGTGTGTGGT 2336
|||||
Db 1 GTGTGTGTGTGGT 16

RESULT 848
AX067878/c
LOCUS
DEFINITION Sequence 19 from Patent WO0077205.
ACCESSION AX067878
VERSION AX067878.1 GI:12329735
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
1 Homo sapiens
AUTHORS Barber,G.N., Saunders,L. and Perkins,D.
TITLE Human nuclear factors associated with dsrna (nfmr)
JOURNAL Patent: WO 0077205-A 19 21-DEC-2000;
FEATURES
Location/Qualifiers
source
1..16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2673 GCCTCCCTACCTCCAG 2688
|||||
Db 16 GCCTCCCTACCTCCAG 1

RESULT 849
AX135452
LOCUS
DEFINITION Sequence 9 from Patent EP1113080.
ACCESSION AX135452
VERSION AX135452.1 GI:14271800
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Wang,X.B.
AUTHORS Personal gene library
TITLE Patent: EP 1113080-A 9 04-JUL-2001;
JOURNAL Wang, Xiao Bing (US); Morisawa, Shinkatsu (JP)
FEATURES
Location/Qualifiers
source
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1642 GTGCTGTGACCGAG 1657
|||||
Db 1 GTGCTGTGACCGAG 16

RESULT 850
BD002055/c
LOCUS
DEFINITION Agent for retarding the conversion of hormone-dependent cancer into
hormone-independent cancer.
ACCESSION BD002055
VERSION BD002055.1 GI:18628795
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 16)
AUTHORS Matsutani,T. and Naito,K.

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TITLE Agent for retarding the conversion of hormone-dependent cancer into hormone-independent cancer
JOURNAL Patent: JP 2000178202-A 6 27-JUN-2000;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Artificial Sequence
PN JP 2000178202-A/6
PD 27-JUN-2000
PF 07-OCT-1999 JP 1999286956
PR
PI TOSHIYA MATSUTANI,KENICHIRO NAITO
PC A61K38/04,A61K38/22,A61K45/00,A61P13/08,A61P35/00//C07K7/23 CC
FH Key Location/Qualifiers
FT source 1..16
FT /organism='Artificial Sequence'.
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 9.2e+02;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1798 AGTGCGTCTGGTCCT 1813
||:|:|:|:|:|:|:
Db 16 AGVGAGTGTGGTCYT 1
RESULT 851
BD016424
LOCUS Personal gene library. 16 bp DNA linear PAT 27-AUG-2002
DEFINITION BD016424
ACCESSION BD016424
VERSION BD016424.1 GI:22557562
KEYWORDS JP 2001186882-A/9.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Wang,X.
TITLE Personal gene library
JOURNAL Patent: JP 2001186882-A 9 10-JUL-2001;
XIAOBING WANG,SHINKATSU MORISAWA
COMMENT OS Unidentified
PN JP 2001186882-A/9
PD 10-JUL-2001
PF 17-NOV-2000 JP 2000350702
PR 01-DEC-1999 US 60/168297,09-NOV-2000 US 09/708493 PI
PC C12N15/09,C12N15/00,C12M1/00,C12Q1/68,C12N15/00,C12N15/00 CC
XIAOBING WANG
Strandedness: Single;
CC Topology: Linear;
CC Personal gene library
FH Key Location/Qualifiers
FT source 1..16
FT /organism='Unidentified'.
FEATURES
source
1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1642 GTGCTGTGACCGAGG 1657
|||||:|:|:|:|:|:|:
Db 1 GTGCTGTGACCGAGG 16

RESULT 852
AR046263
LOCUS Sequence 1056 from patent US 5817796. 17 bp DNA linear PAT 29-SEP-1999
DEFINITION AR046263
ACCESSION AR046263
VERSION AR046263.1 GI:5967728
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myd ribozymes having 2'-5'-linked adenylyate residues
JOURNAL Patent: US 5817796-A 1056 06-OCT-1998;
FEATURES Location/Qualifiers
1..17
source /organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2833 TATATATATATACAT 2848
|||||:|:|:|:|:|:|:
Db 17 TATATATATATAAAT 2
RESULT 853
AR057459
LOCUS Sequence 1663 from patent US 5837542. 17 bp DNA linear PAT 29-SEP-1999
DEFINITION AR057459
ACCESSION AR057459
VERSION AR057459.1 GI:5983036
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1663 17-NOV-1998;
FEATURES Location/Qualifiers
1..17
source /organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1878 GGAGCTCTTCAGCTG 1893
|||||:|:|:|:|:|:|:
Db 1 GAAGCTCTTCAAGCTG 16
RESULT 854
AR057807
LOCUS Sequence 2011 from patent US 5837542. 17 bp DNA linear PAT 29-SEP-1999
DEFINITION AR057807
ACCESSION AR057807
VERSION AR057807.1 GI:5983384
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 2011 17-NOV-1998;
FEATURES Location/Qualifiers

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source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16

RESULT 855
LOCUS AR115217 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1663 from patent US 6132967.
ACCESSION AR115217
VERSION AR115217.1 GI:14095539
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1663 17-OCT-2000;
FEATURES
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16

RESULT 856
LOCUS AR115565 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2011 from patent US 6132967.
ACCESSION AR115565
VERSION AR115565.1 GI:14095887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 2011 17-OCT-2000;
FEATURES
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16

RESULT 857
LOCUS CO617262/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2002 from Patent WO0192524.
ACCESSION CO617262
VERSION CO617262.1 GI:41667480
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2002 06-DEC-2001;
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3194 CCCCGGAGCTGGAGGA 3209
Db 17 CCCCGGGGCTGGAGGA 2

RESULT 858
LOCUS CO617263/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2003 from Patent WO0192524.
ACCESSION CO617263
VERSION CO617263.1 GI:41667481
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2003 06-DEC-2001;
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3194 CCCCGGAGCTGGAGGA 3209
Db 16 CCCCGGGGCTGGAGGA 1

RESULT 859
LOCUS CO617265/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2005 from Patent WO0192524.
ACCESSION CO617265
VERSION CO617265.1 GI:41667483
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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<p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.</p> <p>Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.</p> <p>Myosin-like gene expressed in human heart and muscle</p> <p>Patent: WO 0192524-A 2005 06-DEC-2001;</p> <p>Aeomica, Inc. (US)</p> <p>Location/Qualifiers</p> <p>1. .17</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>	<p>1. .17</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>
<p>Query Match</p> <p>Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;</p> <p>Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>Query Match</p> <p>Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;</p> <p>Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>
<p>1487 GGCCCCCGGCTGGA 1502</p> <p>17 GGCCCCCGGCTGGA 2</p>	<p>1992 CACCTTCAAGCAGCTG 2007</p> <p>2 CACCATCAAGCAGCTG 17</p>
<p>RESULT 860</p> <p>LOCUS CQ617266/c</p> <p>DEFINITION Sequence 2006 from Patent WO0192524.</p> <p>ACCESSION CQ617266</p> <p>VERSION CQ617266.1 GI:41667484</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.</p>	<p>RESULT 862</p> <p>LOCUS CQ623257</p> <p>DEFINITION Sequence 7997 from Patent WO0192524.</p> <p>ACCESSION CQ623257</p> <p>VERSION CQ623257.1 GI:41673475</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.</p>
<p>1487 GGCCCCCGGCTGGA 1502</p> <p>17 GGCCCCCGGCTGGA 2</p>	<p>1992 CACCTTCAAGCAGCTG 2007</p> <p>2 CACCATCAAGCAGCTG 17</p>
<p>Query Match</p> <p>Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;</p> <p>Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>Query Match</p> <p>Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;</p> <p>Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>
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<p>RESULT 861</p> <p>LOCUS CQ623255</p> <p>DEFINITION Sequence 7995 from Patent WO0192524.</p> <p>ACCESSION CQ623255</p> <p>VERSION CQ623255.1 GI:41673473</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.</p>	<p>RESULT 863</p> <p>LOCUS I53315/c</p> <p>DEFINITION Sequence 1056 from patent US 5646042.</p> <p>ACCESSION I53315</p> <p>VERSION I53315.1 GI:2474518</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 17)</p> <p>AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.</p> <p>TITLE C-myb targeted ribozymes</p> <p>JOURNAL Patent: US 5646042-A 1056 08-JUL-1997;</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1. .17</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>
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<p>Query Match</p> <p>Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;</p> <p>Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>Query Match</p> <p>Best Local Similarity 0.4%; Score 14.4; DB 1; Length 17;</p> <p>Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>
<p>1487 GGCCCCCGGCTGGA 1502</p> <p>17 GGCCCCCGGCTGGA 1</p>	<p>1993 ACCTTCAAGCAGCTGG 2008</p> <p>1 ACCATCAAGCAGCTGG 16</p>
<p>RESULT 861</p> <p>LOCUS CQ623255</p> <p>DEFINITION Sequence 7995 from Patent WO0192524.</p> <p>ACCESSION CQ623255</p> <p>VERSION CQ623255.1 GI:41673473</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.</p>	<p>RESULT 863</p> <p>LOCUS I53315/c</p> <p>DEFINITION Sequence 1056 from patent US 5646042.</p> <p>ACCESSION I53315</p> <p>VERSION I53315.1 GI:2474518</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 17)</p> <p>AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.</p> <p>TITLE C-myb targeted ribozymes</p> <p>JOURNAL Patent: US 5646042-A 1056 08-JUL-1997;</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1. .17</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>
<p>1487 GGCCCCCGGCTGGA 1502</p> <p>17 GGCCCCCGGCTGGA 1</p>	<p>1993 ACCTTCAAGCAGCTGG 2008</p> <p>1 ACCATCAAGCAGCTGG 16</p>
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<p>1487 GGCCCCCGGCTGGA 1502</p> <p>17 GGCCCCCGGCTGGA 1</p>	<p>1993 ACCTTCAAGCAGCTGG 2008</p> <p>1 ACCATCAAGCAGCTGG 16</p>
<p>RESULT 861</p> <p>LOCUS CQ623255</p> <p>DEFINITION Sequence 7995 from Patent WO0192524.</p> <p>ACCESSION CQ623255</p> <p>VERSION CQ623255.1 GI:41673473</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.</p>	<p>RESULT 863</p> <p>LOCUS I53315/c</p> <p>DEFINITION Sequence 1056 from patent US 5646042.</p> <p>ACCESSION I53315</p> <p>VERSION I53315.1 GI:2474518</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGANISM Unclassified.</p> <p>REFERENCE 1 (bases 1 to 17)</p> <p>AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.</p> <p>TITLE C-myb targeted ribozymes</p> <p>JOURNAL Patent: US 5646042-A 1056 08-JUL-1997;</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1. .17</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>
<p>1487 GGCCCCCGGCTGGA 1502</p> <p>17 GGCCCCCGGCTGGA 1</p>	<p>1993 ACCTTCAAGCAGCTGG 2008</p> <p>1 ACCATCAAGCAGCTGG 16</p>
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<p>1487 GGCCCCCGGCTGGA 1502</p> <p>17 GGCCCCCGGCTGGA 1</p>	<p>1993 ACCTTCAAGCAGCTGG 2008</p> <p>1 ACCATCAAGCAGCTGG 16</p>
<p>RESULT 861</p> <p>LOCUS CQ623255</p> <p>DEFINITION Sequence 7995 from Patent WO0192524.</p> <p>ACCESSION CQ623255</p> <p>VERSION CQ623255.1 GI:41673473</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.</p>	<p>RESULT 863</p> <p>LOCUS I53315/c</p> <p>DEFINITION Sequence 1056 from patent US 5646042.</p> <p>ACCESSION I53315</p> <p>VERSION I53315.1 GI:2474518</p> <p>KEYWORDS</p> <p>SOURCE Unknown.</p> <p>ORGAN</p>

RESULT 864
LOCUS AR190295 17 bp DNA PAT 20-APR-2002
DEFINITION Sequence 5783 from patent US 6346398.
ACCESSION AR190295
VERSION AR190295.1 GI:20236260
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5783 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1608 GAAGTGCATCCACAGG 1623
Db 2 GAAGTGTATCCACAGG 17
RESULT 865
LOCUS AR325248 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 2650 from patent US 6566127.
ACCESSION AR325248
VERSION AR325248.1 GI:33711056
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2650 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
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/mol_type="unassigned RNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1608 GAAGTGCATCCACAGG 1623
Db 2 GAAGTGTATCCACAGG 17
RESULT 866
LOCUS AR327351 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 4753 from patent US 6566127.
ACCESSION AR327351
VERSION AR327351.1 GI:33713159
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6566127-A 4753 20-MAY-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1393 AACCTGCTGGCGCCT 1408
Db 2 AACCTGCTGGAGCCT 17
RESULT 867
LOCUS AR329330 17 bp RNA PAT 17-AUG-2003
DEFINITION Sequence 6732 from patent US 6566127.
ACCESSION AR329330
VERSION AR329330.1 GI:33715138
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6732 20-MAY-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1619 ACAGGGACCTGGCTGC 1634
Db 1 ACAGGGACCTGGCGGC 16
RESULT 868
LOCUS AR458325 17 bp DNA PAT 20-FEB-2004
DEFINITION Sequence 2002 from patent US 6686188.
ACCESSION AR458325
VERSION AR458325.1 GI:42693382
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2002 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
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Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3194 CCCCAGCTGGAGGA 3209
Db 17 CCCCAGCTGGAGGA 2

RESULT 869
AR458326/c
LOCUS AR458326 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2003 from patent US 6686188.
ACCESSION AR458326
VERSION AR458326.1 GI:42693383
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2003 03-FEB-2004;
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source Location/Qualifiers
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/organism="unknown"
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Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3194 CCCCGGAGCTGGAGGA 3209
Db 16 CCCCGGGGCTGGAGGA 1

RESULT 870
AR458328/c
LOCUS AR458328 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2005 from patent US 6686188.
ACCESSION AR458328
VERSION AR458328.1 GI:42693385
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2005 03-FEB-2004;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCCTGGA 1502
Db 17 GGCCCCCGGGGCTGGA 2

RESULT 871
AR458329/c
LOCUS AR458329 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2006 from patent US 6686188.
ACCESSION AR458329
VERSION AR458329.1 GI:42693386
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

Shannon, M.E.
Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
Patent: US 6686188-A 2006 03-FEB-2004;
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source Location/Qualifiers
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Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCCTGGA 1502
Db 16 GGCCCCCGGGGCTGGA 1

RESULT 872
AR464318
LOCUS AR464318 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7995 from patent US 6686188.
ACCESSION AR464318
VERSION AR464318.1 GI:42699375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7995 03-FEB-2004;
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source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1992 CACCTTCAAGCAGCTG 2007
Db 2 CACCATCAAGCAGCTG 17

RESULT 873
AR464320
LOCUS AR464320 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7997 from patent US 6686188.
ACCESSION AR464320
VERSION AR464320.1 GI:42699377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7997 03-FEB-2004;
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source Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1487 GGCCCCCGGGCCTGGA 1502
Db 17 GGCCCCCGGGGCTGGA 2

RESULT 874
AR464329/c
LOCUS AR464329 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2007 from patent US 6686188.
ACCESSION AR464329
VERSION AR464329.1 GI:42699387
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

[illegible]


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REFERENCE
AUTHORS      Jarvis,T., von Carlowitz,I., Meswigen,J.A., Hamblin,P.A. and
              Ellis,J.H.
TITLE        Method and reagent for the inhibition of grid
JOURNAL      Patent: WO 012911-A 880 30-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
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RESULT 879
LOCUS      AX530932              17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 441 from Patent EP1239051.
ACCESSION  AX530932
VERSION     AX530932.1 GI:25253654
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 441 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source      1. .17
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      546 GGGCTGCGCGCCCAAC 561
Db      2 GCGCTGCTCGCGCCCAAC 17
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      546 GGGCTGCGCGCCCAAC 561
Db      2 GCGCTGCTCGCGCCCAAC 17
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              /db_xref="taxon:9606"

RESULT 880
LOCUS      AX530934              17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 443 from Patent EP1239051.
ACCESSION  AX530934
VERSION     AX530934.1 GI:25253658
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 443 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source      1. .17
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      547 GGGCTGCGCGCCCAACC 562
Db      1 GCGCTGCGCGCCCAACC 16
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

RESULT 881
LOCUS      AX530935              17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 444 from Patent EP1239051.
ACCESSION  AX530935
VERSION     AX530935.1 GI:25253660
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 444 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source      1. .17
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Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      549 GCTGCGCGCCCAACCAG 564
Db      2 GCTGCGCGCCCAACCTG 17
              ||| ||||| ||||| |||||
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

RESULT 882
LOCUS      AX530936              17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 445 from Patent EP1239051.
ACCESSION  AX530936
VERSION     AX530936.1 GI:25253662
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 445 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source      1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      549 GCTGCGCGCCCAACCAG 564
Db      1 GCTGCGCGCCCAACCTG 16
              ||| ||||| ||||| |||||
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

RESULT 883
LOCUS      AX530937              17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 446 from Patent EP1239051.
ACCESSION  AX530937
VERSION     AX530937.1 GI:25253664
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 446 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source      1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
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Thu Oct 28 12:48:19 2004

AX634548
LOCUS AX634548 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1687 from Patent EP1260586.
ACCESSION AX634548
VERSION AX634548.1 GI:28470162
KEYWORDS
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
AUTHORS Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL Patent: EP 1260586-A 1687 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1. 17
/organism="unclassified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16
RESULT 884
AX634866
LOCUS AX634866 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 2005 from Patent EPI260586.
ACCESSION AX634866
VERSION AX634866.1 GI:28470480
KEYWORDS
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
AUTHORS Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL Patent: EP 1260586-A 2005 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1. 17
/organism="unclassified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1878 GGAGCTCTTCAAGCTG 1893
Db 1 GAAGCTCTTCAAGCTG 16
RESULT 885
AX687397
LOCUS AX687397 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 129 from Patent EPI281758.

AX687397
ACCESSION AX687397.1 GI:29410091
VERSION
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 129 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1295 TGAAGATGCTGAAGA 1310
Db 2 TGAAGATGCTTAAGA 17
RESULT 886
AX687398
LOCUS AX687398 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 130 from Patent EPI281758.
ACCESSION AX687398
VERSION AX687398.1 GI:29410092
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Shannon,M., Gu,Y. and Nguyen,C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12
JOURNAL Patent: EP 1281758-A 130 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 9.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1295 TGAAGATGCTGAAGA 1310
Db 1 TGAAGATGCTTAAGA 16
RESULT 887
AX734671/c
LOCUS AX734671 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 261 from Patent WO03025177.
ACCESSION AX734671
VERSION AX734671.1 GI:30513948
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Telerman,A., Amson,R. and Tuijnder,M.

Db 3 GTCCTCCGAGTGC 18

RESULT 892
A87891/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 39 from Patent WO9833904.
ACCESSION A87891
VERSION A87891.1 GI:6736461
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch, W. and Schlingsiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 39 06-AUG-1998;
BIOGHOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2160 CCCGGCCCCCAGC 2175
Db 18 CCCGGCCCCCAGC 3

RESULT 893
A89858/c
LOCUS 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 39 from Patent EP0856579.
ACCESSION A89858
VERSION A89858.1 GI:6738372
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Brysch, W.D. and Schlingsiepen, K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 39 05-AUG-1998;
BIOGHOSTIK GES (DE)
FEATURES
source 1..18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2160 CCCGGCCCCCAGC 2175
Db 18 CCCGGCCCCCAGC 3

RESULT 894
AR035673
LOCUS 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5871922.
ACCESSION AR035673
VERSION AR035673.1 GI:5952341
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stinchcomb, D.T., Jarvis, T. and McSwiggen, J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 5871922-A 12 16-FEB-1999;
FEATURES
source 1..18
/organism="unassigned DNA"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 18)
AUTHORS Salmond, G. Peacock, Copeland., McGowan, S. James., Sebahia, M., Cox, A. Richard, John., Holden, M. Thomas, Geoffrey., Porter, L. Elizabeth., Bycroft, B. Walsham., Williams, P. and Stewart, G. Sidney, Anderson, Birnie.
TITLE Genes involved in the biosynthetic pathway of carbapenem
JOURNAL Patent: US 5871922-A 12 16-FEB-1999;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1599 GGCCTCCGAGTGC 1614
Db 3 GTCCTCCGAGTGC 18

RESULT 895
AR104208
LOCUS 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 24 from patent US 6093545.
ACCESSION AR104208
VERSION AR104208.1 GI:12816916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Goodheart, A.D.J. and Glucksmann, M. Alexandra.
TITLE Methods for detecting nucleic acid molecules encoding a member of the muscarinic family of receptors
JOURNAL Patent: US 6093545-A 24 25-JUL-2000;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3658 GCCTCCGAGTGC 3673
Db 1 GCCTCCGAGTGC 16

RESULT 896
AR134314/c
LOCUS 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2739 from patent US 6194150.
ACCESSION AR134314
VERSION AR134314.1 GI:14123219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Stinchcomb, D.T., Jarvis, T. and McSwiggen, J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 2739 27-FEB-2001;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2899 ACAGGAGGCGAGGCATG 2914
Db      16 ACAGGAGGCGAGGCATG 1

RESULT 897
AR165360
LOCUS      AR165360      18 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 6 from patent US 6274790.
ACCESSION AR165360
VERSION    AR165360.1 GI:16238940
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Kunst L. and Millar A.A.
TITLE      Nucleic acids encoding a plant enzyme involved in very long chain
            fatty acid synthesis
JOURNAL    Patent: US 6274790-A 6 14-AUG-2001;
FEATURES   Location/Qualifiers
            source          1..18
                        /organism="unknown"
                        /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3106 GCGGAGAGTTTAAAT 3121
Db      2 GTCGGAGAGTTTAAAT 17

RESULT 898
BD175407
LOCUS      BD175407      18 bp      DNA      linear      PAT 18-MAR-2003
DEFINITION Secretary and transmembrane polypeptide and nucleic acid encoding
            the same.
ACCESSION  BD175407.1 GI:29121103
VERSION     BD175407.1 GI:29121103
KEYWORDS    JP 2002253280-A/189.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE  1 (bases 1 to 18)
AUTHORS     Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
            Yuan, J.
TITLE      Secretary and transmembrane polypeptide and nucleic acid encoding
            the same
JOURNAL     Patent: JP 2002253280-A 189 10-SEP-2002;
COMMENT     GENENTECH INC
OS          Artificial Sequence
PN          JP 2002253280-A/189
PD          10-SEP-2002
PF          18-DEC-2001 JP 2001385319
PR          17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR
21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR
24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR
24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR
24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR
27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR
28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR
28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR
28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR
29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR
29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR
29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

QY      1101 GCTGTCTCCTCAGGGGAG 1116
Db      3 GCTGTCTCCTCAGGGGAG 18

RESULT 900
AR410785
LOCUS      AR410785      18 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 229 from patent US 6635468.
ACCESSION  AR410785
VERSION     AR410785.1 GI:40162285
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS     Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N.,
            Filvaroff, E., Fong, S., Gao, W.-O., Gerber, H., Gerritsen, M.E.,
            Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J.,
            Kijavini, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A.,
            Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
JOURNAL     Patent: US 6635468-A 229 21-OCT-2003;
COMMENT     Location/Qualifiers
            source          1..18
                        /organism="unknown"
                        /mol_type="genomic DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1101 GCTGTCTCCTCAGGGGAG 1116
Db      3 GCTGTCTCCTCAGGGGAG 18

RESULT 900

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AR439149
 LOCUS AR439149 18 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 229 from patent US 6664376.
 ACCESSION AR439149
 VERSION AR439149.1 GI:42664998
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: US 6664376-A 229 16-DEC-2003;
 FEATURES
 source Location/Qualifiers
 1..18
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1101 GCTGTCTCTCAGGGGAG 1116
 Db 3 GCTGTCTCAGGGGAG 18
 RESULT 901
 AR473169
 LOCUS AR473169 18 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 229 from patent US 6686451.
 ACCESSION AR473169
 VERSION AR473169.1 GI:42708544
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Mather, J.P., Williams, P.M. and Wood, W.I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: US 6686451-A 229 03-FEB-2004;
 FEATURES
 source Location/Qualifiers
 1..18
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1101 GCTGTCTCTCAGGGGAG 1116
 Db 3 GCTGTCTCAGGGGAG 18
 RESULT 902
 AX352818
 LOCUS AX352818 18 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 24 from Patent EP1174518.
 ACCESSION AX352818
 VERSION AX352818.1 GI:18617900
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1

Loukachov, V.V., van Gemen, B. and Goudsmit, J.
 Collection of binding molecules
 Patent: EP 1174518-A 24 23-JAN-2002;
 Amsterdam Support Diagnostics B.V. (NL)
 FEATURES
 source Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="position 41"
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2845 ACATATATGGAAGAGG 2860
 Db 3 ACATTTATGGAAGAGG 18
 RESULT 903
 AX362663
 LOCUS AX362663 18 bp DNA linear PAT 15-FEB-2002
 DEFINITION Sequence 24 from Patent WO0208463.
 ACCESSION AX362663
 VERSION AX362663.1 GI:18694803
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Loukachov, V.V., Goudsmit, J. and van Gemen, B.
 TITLE Collection of binding molecules
 JOURNAL Patent: WO 0208463-A 24 31-JAN-2002;
 Amsterdam Support Diagnostics B.V. (NL)
 FEATURES
 source Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="position 41"
 Query Match 0.4%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 1e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2845 ACATATATGGAAGAGG 2860
 Db 3 ACATTTATGGAAGAGG 18
 RESULT 904
 AX683709/c
 LOCUS AX683709 18 bp DNA linear PAT 29-MAR-2003
 DEFINITION Sequence 26 from Patent WO03006504.
 ACCESSION AX683709
 VERSION AX683709.1 GI:29370739
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Thomson, A.M. and Dunbar, D.R.
 TITLE Allelic variants of gpr50
 JOURNAL Patent: WO 03006504-A 26 23-JAN-2003;
 Akzo Nobel N.V. (NL)
 FEATURES
 source Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

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Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1356 GATGATGAGATGATC 1371
Db 16 GATGTTGAGATGATC 1

RESULT 905
AX697638
LOCUS AX697638 18 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 229 from Patent WO0104311.
ACCESSION AX697638
VERSION AX697638.1 GI:29498731
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L., Ferrara,N.,
Filveroff,E., Fong,S., Gao,W.O., Gerber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Hillan,K.J.,
KlJavin,I.J., Mather,J.P., Pan,J., Paoni,N.F., Roy,M.A.,
Stewart,T.A., Tumas,D., Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0104311-A 229 18-JAN-2001;
Genentech Inc. (US)
FEATURES
source
1. .18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Probe"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1101 GCTGTCCTCAGGGGAG 1116
Db 3 GCTGTCACAGGGGAG 18

RESULT 906
AX773279
LOCUS AX773279 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 253 from Patent WO03045426.
ACCESSION AX773279
VERSION AX773279.1 GI:32485222
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ellendoorn,K., Baker,M., Williams,S. and Carr,F.J.
TITLE T-cell epitodes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 253 05-JUN-2003;
MERCK PATENT GmbH (DE)
FEATURES
source
1. .18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"

Query Match      0.4%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1295 TGAAGATGCTGAAGA 1310
Db 17 TGAAGATGCTGAAGA 2

RESULT 907
AX773295/c
LOCUS AX773295 18 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 269 from Patent WO03045426.
ACCESSION AX773295
VERSION AX773295.1 GI:32485238
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ellendoorn,K., Baker,M., Williams,S. and Carr,F.J.
TITLE T-cell epitodes in carboxypeptidase g2
JOURNAL Patent: WO 03045426-A 269 05-JUN-2003;
MERCK PATENT GmbH (DE)
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QY 1295 TGAAGATGCTGAAGA 1310
Db 17 TGAAGATGCTGAAGA 2

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DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065404
VERSION BD065404.1 GI:22611007
KEYWORDS JP 2001511000-A/39.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingsiefen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 39 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/39
PD 07-AUG-2001
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DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding
ACCESSION  BD075556
VERSION     BD075556.1 GI:22621159
KEYWORDS    JP 2001516580-A/189.
SOURCE      synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.
TITLE        Secretory and transmembrane polypeptide and nucleic acid encoding
JOURNAL
COMMENT      Patent: JP 2001516580-A 189 02-OCT-2001;
              GENENTECH INC
              OS Artificial Sequence
              PN JP 2001516580-A/189
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              JEAN CHEN,
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Db 3 GCTGTCCACACGGGGAG 18

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DEFINITION G protein-coupled receptor and utilization thereof.
ACCESSION  BD086292
VERSION     BD086292.1 GI:22631902
KEYWORDS    JP 2001525174-A/8.
SOURCE      unidentified
ORGANISM     unidentified
              unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Goodearl,A.D.J., Glucksmann,A.M., Xie,M. and Distefano,P.
TITLE        G protein-coupled receptor and utilization thereof
JOURNAL      Patent: JP 2001525174-A 8 11-DEC-2001;
              MILLENNIUM PHARMACEUTICALS INC
              OS Unidentified
              PN JP 2001525174-A/8
              PD 11-DEC-2001
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              ANDREW D J GOODEARL,ALEXANDRA M GLUCKSMANN,MICHAEL XIE,PETER PI
              DISTEFANO
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              CC Topology: Linear;
              CC G protein-coupled receptor and utilization thereof FH Key
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ACCESSION  BD172416
VERSION     BD172416.1 GI:28413716
KEYWORDS    JP 200223786-A/189.
SOURCE      synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
              Yuan,J.
TITLE        Secreted and transmembrane polypeptides and nucleic acids encoding
              the same
JOURNAL      Patent: JP 200223786-A 189 13-AUG-2002;
              GENENTECH INC
              OS Artificial Sequence
              PN JP 200223786-A/189
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24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066511 PR
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC
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Db 3 GCTGTCCACAGGGGAG 18

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DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
BD172735
ACCESSION BD172735.1 GI:28414039
VERSION JP 2002238586-A/189.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238586-A 189 27-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002238586-A/189
PD 27-AUG-2002
PR 18-DEC-2001 JP 2001385205
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QY 1101 GCTGTCTCAGGGGAG 1116
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Db 3 GCTGTCCACAGGGGAG 18

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BD173054
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DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
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BD173054
ACCESSION BD173054.1 GI:28414360
VERSION JP 2002238587-A/189.
KEYWORDS JP 2002238587-A/189.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: JP 2002238587-A 189 27-AUG-2002;
GENENTECH INC
OS Artificial Sequence
PN JP 2002238587-A/189
PD 27-AUG-2002
PR 18-DEC-2001 JP 2001385248

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PI JEAN YUAN
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Qy 1101 GCTGTCTCTCAGGGGAG 1116
Db 3 GCTGTCCACAGGGGAG 18

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DEFINITION Secreted and transmembrane polypeptides and nucleic acids encoding
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ACCESSION BD173373
VERSION BD173373.1 GI:28414684
KEYWORDS JP 2002238588-A/189.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: JP 2002238588-A 189 27-AUG-2002;
GENENTECH INC
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PN JP 2002238588-A/189
PD 27-AUG-2002

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PI JEAN YUAN
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Best Local Similarity 93.8%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
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Qy 1101 GCTGTCTCTCAGGGGAG 1116
Db 3 GCTGTCCACAGGGGAG 18

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DEFINITION Sequence 18 from patent US 6194142.
ACCESSION AR131366
VERSION AR131366.1 GI:14120269
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Montcany,M. and Montagnier,L.
TITLE Nucleotide sequences derived from the genome of retroviruses of the
HIV-1, HIV-2, and SIV type, and their uses in particular for the
amplification of the genomes of these retroviruses and for the in
vitro diagnosis of the diseases due to these viruses
Patent: US 6194142-A 18 27-FEB-2001;
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RESULT 916
CQ785575      19 bp DNA linear PAT 24-MAR-2004
LOCUS
DEFINITION Sequence 17 from Patent EP1398632.
ACCESSION CQ785575
VERSION CQ785575.1 GI:45720505
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kauschat,D. and Froehlen,B.
TITLE P2y11 receptor agonists and the use in the field of erythropoiesis
JOURNAL Patent: EP 1398632-A 17 17-MAR-2004;
Bayer HealthCare AG (DE)
FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3706 TGGTGCCGACGAGTGT 3721
Db 3 TGGTGCCGACGAGTGT 18
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RESULT 917
E09395/c
LOCUS
DEFINITION Oligonucleotide primer for biotin carboxyl carrier
protein(BCCP1-BCCP4).
ACCESSION E09395
VERSION E09395.1 GI:22026022
KEYWORDS JP 1995143887-A/16.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Yanai,Y., Shimada,H. and Ichikawa,N.
TITLE ACETYL COA CARBOXYLASE GENE OF PLANT
JOURNAL Patent: JP 1995143887-A 16 06-JUN-1995;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995143887-A/16
PD 06-JUN-1995
PF 28-JUN-1994 JP 1994146827
PR 17-AUG-1993 JP 93P 203477
PI YANAI YUKIHIRO, SHIMADA HIROAKI, ICHIKAWA NORIO PC
CL2N15/09,A01H5/00/C12N5/10,C12N9/00;
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FH Key
FT source 1..19
FT /organism='Artificial sequences'.
FEATURES
source Location/Qualifiers
1..19

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2632 CCACATGTCACGACC 2647
Db 1 CCACATTCACGACC 16
|||||
|

RESULT 916
CQ785575      19 bp DNA linear PAT 24-MAR-2004
LOCUS
DEFINITION Sequence 17 from Patent EP1398632.
ACCESSION CQ785575
VERSION CQ785575.1 GI:45720505
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kauschat,D. and Froehlen,B.
TITLE P2y11 receptor agonists and the use in the field of erythropoiesis
JOURNAL Patent: EP 1398632-A 17 17-MAR-2004;
Bayer HealthCare AG (DE)
FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3706 TGGTGCCGACGAGTGT 3721
Db 3 TGGTGCCGACGAGTGT 18
|||||
|

RESULT 917
E09395/c
LOCUS
DEFINITION Oligonucleotide primer for biotin carboxyl carrier
protein(BCCP1-BCCP4).
ACCESSION E09395
VERSION E09395.1 GI:22026022
KEYWORDS JP 1995143887-A/16.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Yanai,Y., Shimada,H. and Ichikawa,N.
TITLE ACETYL COA CARBOXYLASE GENE OF PLANT
JOURNAL Patent: JP 1995143887-A 16 06-JUN-1995;
MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
COMMENT OS None
OC Artificial sequences.
PN JP 1995143887-A/16
PD 06-JUN-1995
PF 28-JUN-1994 JP 1994146827
PR 17-AUG-1993 JP 93P 203477
PI YANAI YUKIHIRO, SHIMADA HIROAKI, ICHIKAWA NORIO PC
CL2N15/09,A01H5/00/C12N5/10,C12N9/00;
CC strandedness: Double;
CC topology: Linear;
FH key Location/Qualifiers
FH Key
FT source 1..19
FT /organism='Artificial sequences'.
FEATURES
source Location/Qualifiers
1..19

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1e+03;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAGATGATC 1371 -
Db 19 GAGTTATGAGATGATC 2
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RESULT 918
AR482127      19 bp DNA linear PAT 14-MAY-2004
LOCUS
DEFINITION Sequence 6 from patent US 6699985.
ACCESSION AR482127
VERSION AR482127.1 GI:47244096
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Burcoglu,A.
TITLE Method of treating HIV infection and related secondary infections
JOURNAL Patent: US 6699985-A 6 02-MAR-2004;
thereof
FEATURES
source Location/Qualifiers
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2814 TGTATATGATATATAT 2829
Db 19 TGTATATGATATATTT 4
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|

RESULT 919
AX117795/c
LOCUS
DEFINITION Sequence 2918 from Patent WO0129262.
ACCESSION AX117795
VERSION AX117795.1 GI:14034746
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2918 26-APR-2001;
Orchid BioSciences, Inc. (US)
FEATURES
source Location/Qualifiers
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match      0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2736 CCTGAAGATGGGAGCC 2751
Db 19 CTTGAAGATGGGAGCC 4
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RESULT 920
AX131096/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Robbins,J.M. and Triz,R.
TITLE
Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL
Patent: WO 0130362-A 2314 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/notes="Cyclin E ribozyme binding site"
Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2868 TGGTACACGAGGCC 2883
DB 16 TGGTACACGAGGCC 1

RESULT 921
BD001771
LOCUS
DEFINITION
Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
types.
ACCESSION
BD001771.1 GI:18626330
VERSION
JP 2000093187-A/18.
KEYWORDS
synthetic construct
SOURCE
artificial sequences.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Moncany,M. and Montagnier,L.
TITLE
Immunogenic compounds containing a translation product of
nucleotide sequence from retrovirus genome of HIV-1, HIV-2 and SIV
types
JOURNAL
Patent: JP 2000093187-A 18 04-APR-2000;
INST PASTEUR, INST NATL DE LA SANTE & DE LA RECHERCHE MEDICAL
COMMENT
OS Artificial Sequence
PN JP 2000093187-A/18
PD 04-APR-2000
PF 24-SEP-1999 JP 1999270165
PR 02-JUN-1989 FR 89/07354,20-SEP-1989 FR 89/12371 PI
MAURICE MONCANY, LUC MONTAGNIER
PC C12N15/09,A61K39/21,A61K48/00,A61P31/18,C07H21/04,C07K14/155,
C07K14/16,
PC C12Q1/68,C12Q1/70,G01N33/569,C12N15/00
CC CC
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Artificial Sequence'.
FEATURES
source
1..19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1e+03;

MATCHES 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2632 CCACATGCTCCAGCAC 2647
DB 1 CCACATGCTCCAGCAC 16

RESULT 922
AR020466
LOCUS
DEFINITION
Sequence 3 from patent US 5789165.
ACCESSION
AR020466
VERSION
AR020466.1 GI:3975081
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS
Oku,Y. and Toyoda,N.
TITLE
Method and reagent for simultaneously assaying one or more ligands
in a group of preselected ligands
JOURNAL
Patent: US 5789165-A 3 04-AUG-1998;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3651 CTTGCTGCTGCAGG 3666
DB 4 CTTGCTGCTGCAGG 19

RESULT 923
AR026501
LOCUS
DEFINITION
Sequence 8 from patent US 5856099.
ACCESSION
AR026501
VERSION
AR026501.1 GI:5937341
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS
Miraglia,L., Bennett,C.,Frank., Dean,N. and Geiger,T.
TITLE
Antisense compositions and methods for modulating type I
interleukin-1 receptor expression
JOURNAL
Patent: US 5856099-A 8 05-JAN-1999;
FEATURES
Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2587 GCGCTCGGCCCTCC 2602
DB 2 GCGCTCGGCCCTCC 17

RESULT 924
AR063688/c
LOCUS
DEFINITION
Sequence 12 from patent US 5846718.
ACCESSION
AR063688
VERSION
AR063688.1 GI:5992996
KEYWORDS
Unknown.
SOURCE
Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zhang,Y. and Scorpio,A.
TITLE Identification of pyrazinamide-resistant mycobacteria and methods
JOURNAL for treating mycobacterial infections
FEATURES Patent: US 5846718-A 12 08-DEC-1998;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TGGAGCGCTCCGCCGA 527
Db 20 TGGAGCGCTCCGCCGA 5

RESULT 925
AR116436
LOCUS AR116436 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6133246.
ACCESSION AR116436
VERSION AR116436.1 GI:14096758
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE Antisense oligonucleotide compositions and methods for the
JOURNAL modulation of JNK proteins
FEATURES Patent: US 6133246-A 17 17-OCT-2000;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1060 GCGTCATGAGCTCCA 1075
Db 5 GCATCATGAGCTCCA 20

RESULT 926
AR130803/c
LOCUS AR130803 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 54 from patent US 6190869.
ACCESSION AR130803
VERSION AR130803.1 GI:14119128
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Cowser,L.M.
TITLE Antisense inhibition of protein kinase C-theta expression
JOURNAL Patent: US 6190869-A 54 20-FEB-2001;
FEATURES Patent: US 6190869-A 54 20-FEB-2001;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zhang,Y. and Scorpio,A.
TITLE Identification of pyrazinamide-resistant mycobacteria and methods
JOURNAL for treating mycobacterial infections
FEATURES Patent: US 5846718-A 12 08-DEC-1998;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 512 TGGAGCGCTCCGCCGA 527
Db 20 TGGAGCGCTCCGCCGA 5

RESULT 925
AR116436
LOCUS AR116436 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6133246.
ACCESSION AR116436
VERSION AR116436.1 GI:14096758
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.
TITLE Antisense oligonucleotide compositions and methods for the
JOURNAL modulation of JNK proteins
FEATURES Patent: US 6133246-A 17 17-OCT-2000;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1060 GCGTCATGAGCTCCA 1075
Db 5 GCATCATGAGCTCCA 20

RESULT 926
AR130803/c
LOCUS AR130803 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 54 from patent US 6190869.
ACCESSION AR130803
VERSION AR130803.1 GI:14119128
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Cowser,L.M.
TITLE Antisense inhibition of protein kinase C-theta expression
JOURNAL Patent: US 6190869-A 54 20-FEB-2001;
FEATURES Patent: US 6190869-A 54 20-FEB-2001;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1908 CCGCATGGACACAGCCC 1923
Db 18 CCGCATGGACACATCCC 3

RESULT 927
BD233551/c
LOCUS BD233551 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Targeted integration into chromosome by using retrovirus vector.
ACCESSION BD233551
VERSION BD233551.1 GI:33043321
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Guenzburg W., Salmmons,B., Goller,S. and Klein,D.
TITLE Targeted integration into chromosome by using retrovirus vector
JOURNAL Patent: JP 2002519069-A 20 02-JUL-2002;
COMMENT AUSTRIAN NORDIC BIOTHERAPEUTICS AG
PN JP 2002519069-A/20
PD 02-JUL-2002
PF 30-JUN-1999 JP 2000558225
PR 01-JUL-1998 DK PA 199801016
PI WALTER GUENZBURG,BRIAN SALMONS,SABINE GOLLER,DIETER KLEIN PC
C12N15/09,A61K48/00,A61P31/12,A61P43/00,C12N5/00,C12N7/00, PC
C12N15/00,
PC C12N5/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
1..20
FT source /organism='Artificial Sequence'.

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3781 ACACCTGGTTGCTAAC 3796
Db 16 ACACCTGGTTGCTGAC 1

RESULT 928
I25851
LOCUS I25851 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 11 from patent US 5552526.
ACCESSION I25851
VERSION I25851.1 GI:1605721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakamura,Y. and Emi,M.
TITLE MDC proteins and DNAs encoding the same
JOURNAL Patent: US 5552526-A 11 03-SEP-1996;
FEATURES Patent: US 5552526-A 11 03-SEP-1996;
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 CCAGGACACCCCGCAGC 2112
Db 18 CCAGGACACCCCGCAGC 3

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Db 1 CCAGGACAGCCCCAGC 16

RESULT 929
I43488
LOCUS I43488
DEFINITION Sequence 11 from patent US 5631351.
ACCESSION I43488
VERSION I43488.1 GI:2468732
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nakamura, Y. and Emi, M.
TITLE Antibodies to MDC proteins
JOURNAL Patent: US 5631351-A 11 20-MAY-1997;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 CCAGGACAGCCCCAGC 2112
|||||
Db 1 CCAGGACAGCCCCAGC 16

RESULT 930
AR208766/c
LOCUS AR208766
DEFINITION Sequence 65 from patent US 6383808.
ACCESSION AR208766
VERSION AR208766.1 GI:21510006
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P. and Freier, S.M.
TITLE Antisense inhibition of clusterin expression
JOURNAL Patent: US 6383808-A 65 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2097 CCAGGACAGCCCCAGC 2112
|||||
Db 1 CCAGGACAGCCCCAGC 16

RESULT 931
AR435720/c
LOCUS AR435720
DEFINITION Sequence 20 from patent US 6656727.
ACCESSION AR435720
VERSION AR435720.1 GI:40198796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gunzburg, W.H., Salmons, B., Goller, S. and Klein, D.
TITLE Targeted integration into chromosomes using retroviral vectors
JOURNAL Patent: US 6656727-A 20 02-DEC-2003;

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2407 CTGGGTGTCCCGCTG 2422
|||||
Db 20 CTGGGTGTCCCGCTG 5

RESULT 932
AR475721/c
LOCUS AR475721
DEFINITION Sequence 88 from patent US 6692960.
ACCESSION AR475721
VERSION AR475721.1 GI:42715204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Freier, S.M.
TITLE Antisense modulation of sphingosine-1-phosphate lyase expression
JOURNAL Patent: US 6692960-A 88 17-FEB-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3781 ACACCTGGTTGCTAAC 3796
|||||
Db 16 ACACCTGGTTGCTGAC 1

RESULT 933
AX006846/c
LOCUS AX006846
DEFINITION Sequence 20 from Patent WO0001835.
ACCESSION AX006846
VERSION AX006846.1 GI:9994862
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Goller, S., Klein, D., Guenzburg, W. and Salmons, B.
TITLE Targeted integration into chromosomes using retroviral vectors
JOURNAL Patent: WO 0001835-A 20 13-JAN-2000;
GOLLER SABINE (AT); KLEIN DIETER (AT); GUENZBURG WALTER (AT);
SALMONS BRIAN (DE); BAVARIAN NORDIC RES INST AS (DK)

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3781 ACACCTGGTTGCTAAC 3796
|||||
Db 16 ACACCTGGTTGCTGAC 1

RESULT 934
AX006846/c
LOCUS AX006846
DEFINITION Sequence 20 from Patent WO0001835.
ACCESSION AX006846
VERSION AX006846.1 GI:9994862
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Goller, S., Klein, D., Guenzburg, W. and Salmons, B.
TITLE Targeted integration into chromosomes using retroviral vectors
JOURNAL Patent: WO 0001835-A 20 13-JAN-2000;
GOLLER SABINE (AT); KLEIN DIETER (AT); GUENZBURG WALTER (AT);
SALMONS BRIAN (DE); BAVARIAN NORDIC RES INST AS (DK)

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3007 TTGTTTAAACTGGA 3022
|||||
Db 20 TTGTTTAAAGACTGGA 5

RESULT 935
AX006846/c
LOCUS AX006846
DEFINITION Sequence 20 from Patent WO0001835.
ACCESSION AX006846
VERSION AX006846.1 GI:9994862
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Goller, S., Klein, D., Guenzburg, W. and Salmons, B.
TITLE Targeted integration into chromosomes using retroviral vectors
JOURNAL Patent: WO 0001835-A 20 13-JAN-2000;
GOLLER SABINE (AT); KLEIN DIETER (AT); GUENZBURG WALTER (AT);
SALMONS BRIAN (DE); BAVARIAN NORDIC RES INST AS (DK)

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3007 TTGTTTAAACTGGA 3022
|||||
Db 20 TTGTTTAAAGACTGGA 5

RESULT 936
AX006846/c
LOCUS AX006846
DEFINITION Sequence 20 from Patent WO0001835.
ACCESSION AX006846
VERSION AX006846.1 GI:9994862
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Goller, S., Klein, D., Guenzburg, W. and Salmons, B.
TITLE Targeted integration into chromosomes using retroviral vectors
JOURNAL Patent: WO 0001835-A 20 13-JAN-2000;
GOLLER SABINE (AT); KLEIN DIETER (AT); GUENZBURG WALTER (AT);
SALMONS BRIAN (DE); BAVARIAN NORDIC RES INST AS (DK)

Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3781 ACACCTGGTTGCTAAC 3796
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Db 16 ACACCTGGTTGCTGAC 1

RESULT 934
AX078019
LOCUS AX078019 20 bp DNA linear PAT 23-FEB-2001
DEFINITION Sequence 33 from Patent WO0105435.
ACCESSION AX078019
VERSION AX078019.1 GI:13157774
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gleave, M.
TITLE Antisense therapy for hormone-regulated tumors
JOURNAL Patent: WO 0105435-A 33 25-JAN-2001;
THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
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1. .20
/organism="Homo sapiens"
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Query Match 0.4%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2618 CCTGCAGGGAAGCCCC 2633
Db 1 CCTGCAGGGAAGCCTC 16
RESULT 935
AX304783
LOCUS AX304783 20 bp DNA linear PAT 11-DEC-2001
DEFINITION Sequence 18 from Patent EP1158045.
ACCESSION AX304783
VERSION AX304783.1 GI:17644464
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Schneider, Y.J. and Burteau, N.
TITLE Culture conditions allowing to modulate the expression of cyp3a4 in
JOURNAL caco2 cells
Patent: EP 1158045-A 18 28-NOV-2001;
UNIVERSITE CATHOLIQUE DE LOUVAIN (BE)
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/notes="oligonucleotide"
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Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1188 GCTGACCTGGGCAAG 1203
Db 2 GCTGACCTGGGAAG 17
RESULT 936
AX404665/c
LOCUS AX404665/c 20 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 39 from Patent WO224745.
ACCESSION AX404665
VERSION AX404665.1 GI:21437946
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Abken, H. and Schinkoethe, T.
TITLE Method for detecting tumor cells
JOURNAL Patent: WO 0224745-A 39 28-MAR-2002;
Abken, Hinrich (DE)
FEATURES
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1. .20
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/db_xref="taxon:9606"
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Best Local Similarity 93.8%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3651 CTTGCTTGCTGCAGG 3666
Db 17 CTTGCTGCCTGCAGG 2
RESULT 937
AX494234/c
LOCUS AX494234 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from Patent WO02059379.
ACCESSION AX494234
VERSION AX494234.1 GI:23339844
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Shuber, A.P.
TITLE Methods for detecting, grading or monitoring an H. pylori infection
JOURNAL Patent: WO 02059379-A 10 01-AUG-2002;
EXACT SCIENCES CORP (US)
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source
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/db_xref="taxon:32630"
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QY 856 GAGGAGCTGCTGCAGG 871
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RESULT 938
AX553634/c
LOCUS AX553634 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 38 from Patent WO02074946.
ACCESSION AX553634
VERSION AX553634.1 GI:25897632
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Serup, P., Heimborg, H. and Gradwohl, G.
TITLE Method for generating insulin-secreting cells suitable for
JOURNAL transplantation
Patent: WO 02074946-A 38 26-SEP-2002;
NOVO NORDISK A/S (DK)
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/db_xref="taxon:9606"

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Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 17 TGTACCGTGGCGGTG 2

RESULT 939
LOCUS AX740160/c
DEFINITION Sequence 2 from Patent WO03000927.
ACCESSION AX740160
VERSION AX740160.1 GI:30519337
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baird,D.M.
TITLE Method for the determination of telomere length
JOURNAL Patent: WO 03000927-A 2 03-JAN-2003;
UNIVERSITY University of Wales College of Medicine (GB)
FEATURES
source
Location/Qualifiers
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/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3782 CACTGGTTGCTAACC 3797
DB 16 CACTGGTTGATAACC 1

RESULT 940
LOCUS AX785898
DEFINITION Sequence 407 from Patent WO03050299.
ACCESSION AX785898
VERSION AX785898.1 GI:32953518
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Cullen,P. and Seedorf,U.
TITLE Method for analysing hereditary masculine infertility
JOURNAL Patent: WO 03050299-A 407 19-JUN-2003;
UNIVERSITY OGHAM GmbH (DE)
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/db_xref="taxon:9606"

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QY 2051 AGTACTGGACCTGTC 2066
DB 1 ACTACTGGACCTGTC 16

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Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1281 TGTACCGTAGCGGTG 1296
DB 17 TGTACCGTGGCGGTG 2

RESULT 941
LOCUS AX926289/c
DEFINITION Sequence 31 from Patent WO03085112.
ACCESSION AX926289
VERSION AX926289.1 GI:40245622
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Meyer,U.A., Fraser,D.J., Kaufmann,M.R., Podvinec,M. and Zumsteg,A.
TITLE Enhancer sequence of the 5-aminolevulinic synthase gene
JOURNAL Patent: WO 03085112-A 31 16-OCT-2003;
UNIVERSITAET Basel (CH)
FEATURES
source
Location/Qualifiers
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/note="Forward PCR primer"

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Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2145 CCACGACCTGCTGCC 2160
DB 17 CCTCGACCTGCTGCC 2

RESULT 942
LOCUS AX926579
DEFINITION Sequence 31 from Patent WO03085113.
ACCESSION AX926579
VERSION AX926579.1 GI:40246517
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Meyer,U.A., Fraser,D.J., Kaufmann,M.R., Podvinec,M. and Zumsteg,A.
TITLE Enhancer sequence of the 5-aminolevulinic acid synthase gene
JOURNAL Patent: WO 03085113-A 31 16-OCT-2003;
UNIVERSITAET Basel (CH)
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match
Best Local Similarity 0.4%; Score 14.4; DB 1; Length 20;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2145 CCACGACCTGCTGCC 2160
DB 17 CCTCGACCTGCTGCC 2

RESULT 943
LOCUS BD074593
DEFINITION Antisense oligonucleotide composition and modulation method of JNK
ACCESSION BD074593
VERSION BD074593.1 GI:22620196
KEYWORDS JP 2001514905-A/17.
SOURCE synthetic construct
ORGANISM synthetic construct

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Qy	Db	3264	TTTATTGCTTGTGCTTTTCA	3287
25	TTTTTTTCTTTTGTTTTTTA	2		
<p>RESULT 945</p> <p>AX043454/c</p> <p>LOCUS AX043454 25 bp DNA linear PAT 23-NOV-2000</p> <p>DEFINITION Sequence 1020 from Patent WO0065088.</p> <p>ACCESSION AX043454</p> <p>VERSION AX043454.1 GI:11342062</p> <p>KEYWORDS synthetic construct</p> <p>SOURCE synthetic construct</p> <p>ORGANISM artificial construct</p> <p>REFERENCE 1</p> <p>AUTHORS Ulfendahl, P.J. and Wong, K.C.</p> <p>TITLE Primers for identifying typing or classifying nucleic acids</p> <p>JOURNAL Patent: WO 0065088-A, 1020 02-NOV-2000;</p> <p>Amersham Pharmacia Biotech AB (SE)</p> <p>FEATURES</p> <p>source</p> <p>1. .25</p> <p>Location/Qualifiers</p> <p>/organism="synthetic construct"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32630"</p> <p>/note="DRB345 Heterozygote Primer Sequence"</p> <p>Query Match 0.4%; Score 14.4; DB 1; Length 25;</p> <p>Best Local Similarity 75.0%; Pred. No. 1.3e+03;</p> <p>Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>				
Qy	Db	1362	GAAGATGATCGGGAACACAAAA	1385
24	GAACCTGATCAGAAAAA	1		
<p>RESULT 946</p> <p>A63569</p> <p>LOCUS A63569 26 bp DNA linear PAT 12-MAR-1998</p> <p>DEFINITION Sequence 10 from Patent WO9720924.</p> <p>ACCESSION A63569</p> <p>VERSION A63569.1 GI:3717224</p> <p>KEYWORDS unidentified</p> <p>SOURCE unidentified</p> <p>ORGANISM unclassified.</p> <p>REFERENCE 1</p> <p>AUTHORS Scaggiante, B. and Quadrioglio, F.</p> <p>TITLE A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMORAL AGENTS</p> <p>JOURNAL Patent: WO 9720924-A 10 12-JUN-1997;</p> <p>SAICOM S R L (IT)</p> <p>COMMENT Other publication IT MI952539 19970604</p> <p>Other publication AU 1175497 19970627.</p> <p>FEATURES</p> <p>source</p> <p>1. .26</p> <p>Location/Qualifiers</p> <p>/organism="unidentified"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:32644"</p> <p>Query Match 0.4%; Score 14.4; DB 1; Length 26;</p> <p>Best Local Similarity 75.0%; Pred. No. 1.3e+03;</p> <p>Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;</p>				
Qy	Db	3262	TATTTATTGCTTGTCTTTT	3285
3	TTTTTTGTTTTTTTGTTTTTT	26		
<p>RESULT 947</p> <p>E33560</p> <p>LOCUS E33560 26 bp DNA linear PAT 31-JAN-2002</p> <p>DEFINITION Stress-responsive gene promoter.</p>				

Thu Oct 28 12:48:19 2004

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ACCESSION E33560
VERSION E33560.1 GI:18624133
KEYWORDS JP 2000078977-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Tsujimoto,Y., Izawa,S., Inoue,Y., Kimura,H. and Sato,N.
TITLE Stress-responsive gene promoter
JOURNAL Patent: JP 2000078977-A 5 21-MAR-2000;
MARUHA CORP
OS Artificial Sequence
PN JP 2000078977-A/5
PD 21-MAR-2000
PR 04-SEP-1998 JP 1998251390
PI YOSHIYUKI TSUJIMOTO,SHINGO IZAWA,YOSHIHARU INOUE,HIKARU
KIMURA,
PC C12N15/09,C12N1/19,C12P21/02///(C12N15/09,C12R1:865), (C12N1/19,
C12R1:865),
PC (C12P21/02,C12R1:865),C12N15/00,(C12N15/00,C12R1:865) CC
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FT source 1..36
FT Location/Qualifiers
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/db_xref="taxon:32630"
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Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3113 AGTTTAAATTAACTTATTCAG 3136
Db 2 ATTTTATTTTATTTTTCAG 25
RESULT 948
AR264927
LOCUS AR264927 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 11 from patent US:6492121.
ACCESSION AR264927
VERSION AR264927.1 GI:29693314
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 11 10-DEC-2002;
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Best Local Similarity 75.0%; Pred. No. 1.4e+03;
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Db 1 ATATATATAATTATTTCCTTTTTT 24
RESULT 949
AR478208
LOCUS AR478208 30 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 11 from patent US 6699661.
ACCESSION AR478208
VERSION AR478208.1 GI:47236856
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 11 02-MAR-2004;
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Query Match 0.4%; Score 14.4; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 3474 ATATATATAATTATTGAGTTTTT 3497
Db 1 ATATATATAATTATTTCCTTTTTT 24
RESULT 950
BD072872
LOCUS BD072872 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072872
VERSION BD072872.1 GI:22618475
KEYWORDS JP 2001286300-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokomaku,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 10 16-OCT-2001.
JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT OS Artificial Sequence
PN JP 2001286300-A/10
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINVA PI
KURATA,
PC KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
decrease in fluorescence emission of a nucleic acid probe CC
labeled with
probe with a target nucleic CC
acid. CC
PH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.
FT Location/Qualifiers
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Query Match
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Best Local Similarity 75.0%; Pred. No. 1.4e+03;
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Db 1 ATATATATATTTTCTTTT 24

RESULT 951
BD107499
LOCUS
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DEFINITION
  Novel quantitative polymorphism analysis method.
ACCESSION
  BD107499
VERSION
  BD107499.1 GI:23202317
KEYWORDS
  JP 2002000275-A/8.
SOURCE
  synthetic construct
ORGANISM
  artificial sequences.
REFERENCE
  1 (bases 1 to 30)
AUTHORS
  Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
  Yokomaku,T.
TITLE
  Novel quantitative polymorphism analysis method
JOURNAL
  Patent: JP 2002000275-A 8 08-JAN-2002;
  JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
  & TECHNOL
COMMENT
  OS Artificial Sequence
  PN JP 2002000275-A/8
  PD 08-JAN-2002
  PF 27-JUN-2000 JP 2000193133
  PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA
    PI KURATA,
    PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
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Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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  ||||| ||||| ||||| |||||
Db 1 ATATATATATTTTCTTTT 24

RESULT 952
BD145031
LOCUS
  30 bp DNA linear PAT 17-JAN-2003
DEFINITION
  Method for assaying nucleic acid, nucleic acid probe used therefor,
  and method for analyzing data obtained by that method.
ACCESSION
  BD145031
VERSION
  BD145031.1 GI:27850789
KEYWORDS
  JP 2002119291-A/12.
SOURCE
  synthetic construct
ORGANISM
  synthetic construct

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artificial sequences.
  1 (bases 1 to 30)
AUTHORS
  Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
  Yamada,K. and Yokomaku,T.
TITLE
  Method for assaying nucleic acid, nucleic acid probe used therefor,
  and method for analyzing data obtained by that method
JOURNAL
  Patent: JP 2002119291-A 12 23-APR-2002;
  JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
  INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
  OS Artificial Sequence
  PN JP 2002119291-A/12
  PD 23-APR-2002
  PF 27-APR-2001 JP 2001133529
  PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI
    TORIMURA,
    PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
    C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/
    53, G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
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    CC decrease in fluorescence emission of
    CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
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    CC the probe with a target nucleic acid.
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Query Match
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Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3474 ATATATATAATTATTAGCTTTT 3497
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Db 1 ATATATATATTTTCTTTT 24

RESULT 953
BD166031
LOCUS
  30 bp DNA linear PAT 17-JAN-2003
DEFINITION
  Novel nucleic acid probes, method for determining concentrations of
  nucleic acid by using the probes, and method for analyzing data
  obtained by the method.
ACCESSION
  BD166031
VERSION
  BD166031.1 GI:27871843
KEYWORDS
  JP 2002191372-A/11.
SOURCE
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  ORGANISM
  unclassified.
REFERENCE
  1 (bases 1 to 30)
AUTHORS
  Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
  Yamada,K. and Yokomaku,T.
TITLE
  Novel nucleic acid probes, method for determining concentrations of
  nucleic acid by using the probes, and method for analyzing data
  obtained by the method
JOURNAL
  Patent: JP 2002191372-A 11 09-JUL-2002;
  NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
  KANKYO ENGINEERING CO LTD
COMMENT
  OS Artificial Sequence
  PN JP 2002191372-A/11
  PD 09-JUL-2002
  PF 26-SEP-2001 JP 2001295145
  PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,VOICHI KAMAGATA,MASAKI
    TORIMURA,
    PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC

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C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examine the decrease in fluorescence emission of a nucleic acid probe CC
labeled with BODIBY FI/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH key Location/Qualifiers
FT source 1..30
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/db_xref="taxon:32644"
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source
Query Match 0.4%; Score 14.4; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3474 ATATATATAATTATTAGTATTTT 3497
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Db 1 ATATATATTTTATTTTCTTTT 24
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RESULT 954
AR051291
LOCUS AR051291 32 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5830662.
ACCESSION AR051291
VERSION AR051291.1 GI:5974655
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Soares,M.B. and Efstratiadis,A.
TITLE Method for construction of normalized cDNA libraries
JOURNAL Patent: US 5830662-A 8 03-NOV-1998;
FEATURES
Location/Qualifiers
source 1..32
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Query Match 0.4%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3311 TTTTCTTTAGGAGATTTATTTT 3334
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Db 1 TTTTCTTTAATAATTTT 24
/mol_type="unassigned DNA"
RESULT 955
I16939
LOCUS I16939 32 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 8 from patent US 5482845.
ACCESSION I16939
VERSION I16939.1 GI:1251847
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Soares,M.B. and Efstratiadis,A.
TITLE Method for construction of normalized cDNA libraries
JOURNAL Patent: US 5482845-A 8 09-JAN-1996;
FEATURES
Location/Qualifiers
source 1..32
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Query Match 0.4%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3311 TTTTCTTTAGGAGATTTATTTT 3334
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Db 1 TTTTCTTTAATAATTTT 24
/mol_type="unassigned DNA"
RESULT 956
I45733
LOCUS I45733 32 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5637685.
ACCESSION I45733
VERSION I45733.1 GI:2469835
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 32)
AUTHORS Soares,M.B. and Efstratiadis,A.
TITLE Normalized cDNA libraries
JOURNAL Patent: US 5637685-A 8 10-JUN-1997;
FEATURES
Location/Qualifiers
source 1..32
/mol_type="unassigned DNA"
Query Match 0.4%; Score 14.4; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3311 TTTTCTTTAGGAGATTTATTTT 3334
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Db 1 TTTTCTTTAATAATTTT 24
/mol_type="unassigned DNA"
RESULT 957
BD170449/c
LOCUS BD170449/c 40 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of detecting DNA polymorphism using mass spectrometry.
ACCESSION BD170449
VERSION BD170449.1 GI:27876261
KEYWORDS synthetic construct
SOURCE artificial sequences.
ORGANISM 1 (bases 1 to 40)
REFERENCE Inoko,H., Tamiya,G., Nakajima,K., Kimura,N., Nagashima,R.,
AUTHORS Morikawa,M. and Okamoto,K.
TITLE Method of detecting DNA polymorphism using mass spectrometry
JOURNAL Patent: WO 0250307-A 4 27-JUN-2002;
CHUGAI PHARMACEUTICAL CO LTD,HIDETOSHI INOKO,GEN TAMIYA,KENJI
NAKAJIMA, NAOKI KIMURA,RENPEI NAGASHIMA,MINORU MORIKAWA,KOICHI
OKAMOTO
COMMENT OS Artificial Sequence
PN WO 0250307-A/4
PD 27-JUN-2002
PP 12-DEC-2001 WO 2001JP010892
PR 12-DEC-2000 JP 00P 378091
PI HIDETOSHI INOKO,GEN TAMIYA,KENJI NAKAJIMA,NAOKI KIMURA,RENPEI
NAGASHIMA,
PI MINORU MORIKAWA,KOICHI OKAMOTO
PC C1201/68,C12N15/09,G01N33/53,G01N27/62,G01N33/566,C12M1/00 CC
Description of Artificial Sequence:an artificially synthesized CC
DNA sequence
FH key Location/Qualifiers
FT source 1..40
/mol_type="Artificial Sequence".
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Location/Qualifiers
source 1..40
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RESULT 962

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A44390
LOCUS       A44390               19 bp      DNA          linear      PAT 07-MAR-1997
DEFINITION   Sequence 20 from Patent EP0653439.
ACCESSION   A44390
VERSION     A44390.1  GI:2299219
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 19)
AUTHORS    Peyman,A.D., Uhlmann,E.D., Mag,M., Kretschmar,G.D., Helsberg,M.D.
TITLE      Stabilized oligonucleotides and the use thereof
JOURNAL    HOECHST AG (DE)
COMMENT    Patent: EP 0653439-A 20 17-MAY-1995;
Other publication JP 7194385 950801
Other publication CA 2135591 950513
Other publication AU 779994- 950518
Other publication DE 438704 950518.
Other publication Location/Qualifiers
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source     1..19
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            /db_xref="taxon:9606"
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Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
      ||| |||| |||| |||| ||||
Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 963
A47177
LOCUS       A47177               19 bp      DNA          linear      PAT 07-MAR-1997
DEFINITION   Sequence 20 from Patent EP0680969.
ACCESSION   A47177
VERSION     A47177.1  GI:2301219
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 19)
AUTHORS    Seela,F.P. and Lampe,S.D.
TITLE      Modified oligonucleotides, their preparation and their use
JOURNAL    HOECHST AG (DE)
COMMENT    Patent: EP 0680969-A 20 08-NOV-1995;
Other publication JP 8003186 960109
Other publication AU 1778295 951109
Other publication DE 4415370 951109.
Other publication Location/Qualifiers
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source     1..19
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Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
      ||| |||| |||| |||| ||||
Db 1 GGGAGGAGGAGGATGAGG 19

A44390
LOCUS       A44390               19 bp      DNA          linear      PAT 07-MAR-1997
DEFINITION   Sequence 20 from Patent EP0653439.
ACCESSION   A44390
VERSION     A44390.1  GI:2299219
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 19)
AUTHORS    Peyman,A.D., Uhlmann,E.D., Mag,M., Kretschmar,G.D., Helsberg,M.D.
TITLE      Stabilized oligonucleotides and the use thereof
JOURNAL    HOECHST AG (DE)
COMMENT    Patent: EP 0653439-A 20 17-MAY-1995;
Other publication JP 7194385 950801
Other publication CA 2135591 950513
Other publication AU 779994- 950518
Other publication DE 438704 950518.
Other publication Location/Qualifiers
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Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. NO. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
      ||| |||| |||| |||| ||||
Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 963
A47177
LOCUS       A47177               19 bp      DNA          linear      PAT 07-MAR-1997
DEFINITION   Sequence 20 from Patent EP0680969.
ACCESSION   A47177
VERSION     A47177.1  GI:2301219
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 19)
AUTHORS    Seela,F.P. and Lampe,S.D.
TITLE      Modified oligonucleotides, their preparation and their use
JOURNAL    HOECHST AG (DE)
COMMENT    Patent: EP 0680969-A 20 08-NOV-1995;
Other publication JP 8003186 960109
Other publication AU 1778295 951109
Other publication DE 4415370 951109.
Other publication Location/Qualifiers
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exon       1..19
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Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. NO. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
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Db 1 GGGAGGAGGAGGATGAGG 19

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RESULT 964
A56651
LOCUS       A56651               19 bp      DNA          linear      PAT 03-MAR-1998
DEFINITION   Sequence 18 from Patent EP0739898.
ACCESSION   A56651
VERSION     A56651.1  GI:3712696
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1
AUTHORS    Peyman,A.D., Uhlmann,E.D., Breipohl,G.D. and Wallmeier,H.D.
TITLE      Phosphonomonoester nucleic acids, methods for their preparation and
            their use
JOURNAL    Patent: EP 0739898-A 18 30-OCT-1996;
            HOECHST AG (DE)
COMMENT    Other publication CZ 9600743 961016
            Other publication CN 1138588 961225
            Other publication PL 313207 960916
            Other publication JP 8259579 961008
            Other publication NO 961006 960916
            Other publication CA 2171589 960914
            Other publication AU 4802896 960926
            Other publication DE 19508923 960919.
            Other publication Location/Qualifiers
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source     1..19
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Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. NO. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
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Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 965
A80372
LOCUS       A80372               19 bp      DNA          linear      PAT 20-OCT-1999
DEFINITION   Sequence 18 from Patent EP0726274.
ACCESSION   A80372
VERSION     A80372.1  GI:6093099
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 19)
AUTHORS    Peyman,A.D. and Uhlmann,E.D.
TITLE      G-CAP STABILIZED OLIGONUCLEOTIDES
JOURNAL    Patent: EP 0726274-A 18 14-AUG-1996;
            HOECHST AG (DE)
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source     1..19
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
exon       1..19
Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. NO. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGACGAGCTGAGG 202
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Db 1 GGGAGGAGGAGGATGAGG 19

RESULT 966
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LOCUS       AR111775              19 bp      DNA          linear      PAT 14-FEB-2001

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PR	26-MAR-1999	US	60/126473,23-JUN-1999	US	60/140359	PI
JIAN BING FAN, JOEL N HIRSCHORN, XIAOHUA HUANG, PAUL KAPLAN, ERIC S LANDER, DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR						
GOIN33/566, GOIN37/00, C12N15/00, C12N15/09, C12N15/09, C12N15/09, GOIN33/53, PC						
CC Primer						
FH Key						
FT source						
FT						
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/db_xref="taxon:32630"						
Query Match						
Best Local Similarity						
Matches						
0.4%; Score 14.2; DB 1; Length 19;						
84.2%; Pred. No. 1.1e+03;						
Conservative 0; Mismatches 3; Indels 0; Gaps 0;						
QY						
2191						
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2209						
DB						
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RESULT 969						
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LOCUS						
DEFINITION						
Sequence 25 from Patent WO2004031411.						
ACCESSION						
CQ800200						
VERSION						
CQ800200.1						
GI:46849118						
KEYWORDS						
synthetic construct						
synthetic construct						
artificial sequences.						
SOURCE						
ORGANISM						
REFERENCE						
1						
AUTHORS						
Nakamura, Y. and Katagiri, T.						
TITLE						
Genes and polypeptides relating to human pancreatic cancers						
JOURNAL						
Patent: WO 2004031411-A 25 15-APR-2004;						
Oncotherapy Science, Inc. (JP); Japan as represented by The						
President of the University of Tokyo (JP)						
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84.2%; Pred. No. 1.1e+03;						
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2046						
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2064						
DB						
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CGACGAGTACCTGGACCTG						
19						
RESULT 970						
I46926						
LOCUS						
DEFINITION						
Sequence 19 from patent US 5639655.						
ACCESSION						
I46926						
VERSION						
I46926.1						
GI:2470891						
KEYWORDS						
Unknown.						
SOURCE						
ORGANISM						
Unknown.						
REFERENCE						
1						
(bases 1 to 19)						
AUTHORS						
Thompson, J.D. and Draper, K.G.						
TITLE						
PML-RARA targeted ribozymes						

JOURNAL Patent: US 5639655-A 19 17-JUN-1997;
 FEATURES Location/Qualifiers
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Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 860 AGCTGCTGGAGGCTGTGGA 878
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 Db 1 AGCTGCTGGAGGCTGTGGA 19

RESULT 971
 184730 184730 19 bp DNA linear PAT 04-APR-1998
 DEFINITION Sequence 18 from patent US 5696248.
 ACCESSION 184730
 VERSION 184730.1 GI:3022250
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Feynman,A., Uhlmann,E. and Carolus,C.
 TITLE 3'-modified oligonucleotide derivatives
 JOURNAL Patent: US 5696248-A 18 09-DEC-1997;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
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 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 972
 AR193516 184730 19 bp DNA linear PAT 20-APR-2002
 LOCUS AR193516
 DEFINITION Sequence 20 from patent US 6348312.
 ACCESSION AR193516
 VERSION AR193516.1 GI:20240108
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Peyman,A., Uhlmann,E., Mag,M., Kretzschmar,G., Helsberg,M. and Winkler,I.
 TITLE Stabilized oligonucleotides and their use
 JOURNAL Patent: US 6348312-A 20 19-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
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 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 973
 AR193516 184730 19 bp DNA linear PAT 20-APR-2002
 LOCUS AR193516
 DEFINITION Sequence 20 from patent US 6348312.
 ACCESSION AR193516
 VERSION AR193516.1 GI:20240108
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Peyman,A., Uhlmann,E., Mag,M., Kretzschmar,G., Helsberg,M. and Winkler,I.
 TITLE Stabilized oligonucleotides and their use
 JOURNAL Patent: US 6348312-A 20 19-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
 ||||| ||||| ||||| ||||| |||||
 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 974
 AR292967 184730 19 bp DNA linear PAT 12-JUN-2003
 LOCUS AR292967
 DEFINITION Sequence 4702 from patent US 6537751.
 ACCESSION AR292967
 VERSION AR292967.1 GI:31680251
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 4702 25-MAR-2003;
 FEATURES Location/Qualifiers
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Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGGAGGACGAGGCTGAGG 202
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 Db 1 GGGGAGGAGGAGGATGAGG 19

RESULT 975
 AR294648 184730 19 bp DNA linear PAT 12-JUN-2003
 LOCUS AR294648
 DEFINITION Sequence 6383 from patent US 6537751.
 ACCESSION AR294648
 VERSION AR294648.1 GI:31681932
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 6383 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 19 GGTATTTCGGAAGACTAG 1

Db	19	AATGGCAGAAAGCTAGGCC	1						19 bp	DNA	linear	PAT 15-MAY-2001
Query Match		0.4%;	Score 14.2;	DB 1;	Length 19;							
Best Local Similarity		84.2%;	Pred. No. 1.1e+03;									
Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;			
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Db	19	GTTGTGTTTGTGAGTCT	1									
RESULT 976												
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LOCUS												
DEFINITION												
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ACCESSION												
VERSION												
AX081351.1												
GI:11170193												
KEYWORDS												
synthetic construct												
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artificial sequences.												
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ORGANISM												
REFERENCE												
1												
Uhlmann,E., Greiner,B., Unger,E., Gothe,G. and Schwerdel,M.												
Conjugates and methods for the production thereof, and their use												
for transporting molecules via biological membranes												
PATENT: WO 0108707-A 30 08-FEB-2001;												
Aventis Pharma Deutschland GmbH (DE)												
LOCATION/Qualifiers												
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source												
Query Match		0.4%;	Score 14.2;	DB 1;	Length 19;							
Best Local Similarity		84.2%;	Pred. No. 1.1e+03;									
Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;			
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Db	1	GCGGAGGAGGAGTAGG	19									
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AX128989												
ACCESSION												
AX128989.1												
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KEYWORDS												
Homo sapiens (human)												
SOURCE												
ORGANISM												
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;												
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.												
REFERENCE												
1												
Robbins,J.M. and Tritz,R.												
Ribozyme therapy for the treatment of proliferative skin and eye												
diseases												
PATENT: WO 0130362-A 207 03-MAY-2001;												
IMMUSOL, INC. (US)												
LOCATION/Qualifiers												
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source												
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DEFINITION Sequence 584 from Patent WO0130362.
ACCESSION AX129366
VERSION AX129366.1 GI:14135671
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Robbins,J.M. and Tritz,R.
AUTHORS Ribozyme therapy for the treatment of proliferative skin and eye
TITLE diseases
JOURNAL Patent: WO 0130362-A 584 03-MAY-2001;
IMMUSOL, INC. (US)
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/organism="Homo sapiens"
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Query Match 0.4%; Score 14.2; DB 1; Length 19;
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1673 TCGCAGACTTCGGCTGGC 1691
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Db 1 TCGTGACTTCGGCCTTGC 19

RESULT 981
AX129367
LOCUS AX129367 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 585 from Patent WO0130362.
ACCESSION AX129367
VERSION AX129367.1 GI:14135672
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Robbins,J.M. and Tritz,R.
AUTHORS Ribozyme therapy for the treatment of proliferative skin and eye
TITLE diseases
JOURNAL Patent: WO 0130362-A 585 03-MAY-2001;
IMMUSOL, INC. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk6 ribozyme binding site"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1674 CGCAGACTTCGGCTGGCC 1692
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Db 1 CGCTGACTTCGGCCTTGC 19

RESULT 982
AX129652
LOCUS AX129652 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 870 from Patent WO0130362.
ACCESSION AX129652
VERSION AX129652.1 GI:14135957
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Robbins,J.M. and Tritz,R.
AUTHORS Ribozyme therapy for the treatment of proliferative skin and eye
TITLE diseases
JOURNAL Patent: WO 0130362-A 870 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
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1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk8 ribozyme binding site"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2001 GCAGCTGGTGGAGGACCTG 2019
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Db 1 GGAGCGGGTCGAGGACCTG 19

RESULT 983
AX130617
LOCUS AX130617 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1835 from Patent WO0130362.
ACCESSION AX130617
VERSION AX130617.1 GI:14136922
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Robbins,J.M. and Tritz,R.
AUTHORS Ribozyme therapy for the treatment of proliferative skin and eye
TITLE diseases
JOURNAL Patent: WO 0130362-A 1835 03-MAY-2001;
IMMUSOL, INC. (US)
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1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cyclin D1 ribozyme binding site"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1875 GGAGGAGCTCTTCAAGCTG 1893
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Db 1 GGAGGAGGTCTTCCGCTG 19

RESULT 984
AX131319
LOCUS AX131319 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 2537 from Patent WO0130362.
ACCESSION AX131319
VERSION AX131319.1 GI:14137624
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Robbins,J.M. and Tritz,R.
AUTHORS Ribozyme therapy for the treatment of proliferative skin and eye
TITLE diseases
JOURNAL Patent: WO 0130362-A 2537 03-MAY-2001;
IMMUSOL, INC. (US)
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
        /note="Cyclin F ribozyme binding site"

Query Match
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  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2120 CCTCAGGAGGACGACTCCGT 2138
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Db 1 CCTCAGGAGTCTCTCCGT 19

RESULT 985
AX132490
LOCUS AX132490 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 3708 from Patent WO0130362.
ACCESSION AX132490
VERSION AX132490.1 GI:14138795
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Robbins,J.M. and Tritz,R.
FEATURES Ribozyme therapy for the treatment of proliferative skin and eye
  source
    Patent: WO 0130362-A 3708 03-MAY-2001;
    IMMUSOL, INC. (US)
    Location/Qualifiers
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        /organism="Homo sapiens"
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        /db_xref="taxon:9606"
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Query Match
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QY 2745 GGGAGCCTTTACCTTTAT 2763
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Db 1 GGGAGCCTTAACTTATAT 19

RESULT 986
AX204959/c
LOCUS AX204959 19 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 6 from Patent WO0155362.
ACCESSION AX204959
VERSION AX204959.1 GI:15394242
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE 1
AUTHORS Zheng,C., O'Connell,B. and Baum,B.J.
TITLE Hybrid adeno-retroviral vector for the transfection of cells
JOURNAL Patent: WO 0155362-A 6 02-AUG-2001;
  THE SECRETARY, DEPARTMENT OF HEALTH AND SOCIAL SERVICES (US)
FEATURES
  source
    Location/Qualifiers
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        /db_xref="taxon:32630"
        /note="PCR primer"

Query Match
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Query Match
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QY 184 GGGAGGAGGAGGAGTGAGG 202
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Db 1 GGGAGGAGGAGGAGTGAGG 19

RESULT 987
AX283181
LOCUS AX283181 19 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 19 from Patent WO0179216.
ACCESSION AX283181
VERSION AX283181.1 GI:17044062
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
  producing them
JOURNAL Patent: WO 0179216-A 19 25-OCT-2001;
  Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
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Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGAGGAGGCTGAGG 202
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Db 1 GGGAGGAGGAGGAGTGAGG 19

RESULT 988
AX283247
LOCUS AX283247 19 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 11 from Patent WO0179249.
ACCESSION AX283247
VERSION AX283247.1 GI:17044128
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
  artificial sequences.
REFERENCE 1
AUTHORS Uhlmann,E., Breipohl,G. and Will,D.W.
TITLE Polyamide nucleic acid derivatives, agents and methods for
  producing the same
JOURNAL Patent: WO 0179249-A 11 25-OCT-2001;
  Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
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    /note="Beschreibung der kuenstlichen Sequenz:
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Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 19;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 GGGAGGAGGAGGCTGAGG 202
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Db 1 GGGAGGAGGAGGAGTGAGG 19
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Thu Oct 28 12:48:19 2004

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RESULT 989
AX384647
LOCUS AX384647 19 bp DNA linear PAT 19-MAR-2002
DEFINITION Sequence 19 from Patent EP1182206.
ACCESSION AX384647
VERSION AX384647.1 GI:19577842
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Feymann,A., Uhlmann,E., Mag,M., Kretschmar,G., Helsenberg,M. and
Winkler,I.
TITLE Stabilized oligonucleotides and the use thereof
JOURNAL Patent: EP 1182206-A 19 27-FEB-2002;
HOECHST AKTIENGESELLSCHAFT (DE)
FEATURES
source
1 ..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Antisense Oligonukleotid"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 184 GGGGAGGACGAGCTGAGG 202
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Db 1 GGGGAGGACGAGCTGAGG 19

RESULT 990
AX474023/c
LOCUS AX474023 19 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 177 from Patent WO0246458.
ACCESSION AX474023
VERSION AX474023.1 GI:22208178
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Deneffe,P., Rosier-Montus,M.F., Prades,C., Arnould-Reguigne,I.,
Duverger,N., Allikmets,R. and Dean,M.
TITLE Nucleic acids of the human abca5, abca6, abca9, and abca10 genes,
vectors containing such nucleic acids and uses thereof
JOURNAL Patent: WO 0246458-A 177 13-JUN-2002;
Aventis Pharma S.A. (FR) ; The Secretary, Department of Health and
Human Services (US)
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Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2485 GTGCAGAAATGTAAGTGGGC 2503
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Db 19 GTGCAGAAATGTAAGTGGGC 1

RESULT 991
AX513754/c
LOCUS AX513754 19 bp DNA linear PAT 05-OCT-2002
DEFINITION Sequence 19 from Patent WO0234947.
ACCESSION AX513754
VERSION AX513754.1 GI:23559900
KEYWORDS

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SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Khripin,Y.
TITLE Detecting specific nucleotide sequences
JOURNAL Patent: WO 0234947-A 19 02-MAY-2002;
Khripin, Yuri (US)
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source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1160 ACCCAATGGAGCTGTC 1178
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Db 19 ACTTCAATGGAGCTGTC 1

RESULT 992
AX644866/c
LOCUS AX644866 19 bp DNA linear PAT 27-FEB-2003
DEFINITION Sequence 14 from Patent WO02061104.
ACCESSION AX644866
VERSION AX644866.1 GI:28610842
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Zheng,C., Baum,B.J. and O'Connell,B.C.
TITLE Hybrid adenoviral vector
JOURNAL Patent: WO 02061104-A 14 08-AUG-2002;
The Secretary Department of Health and Human Services (US)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide primer"
Query Match 0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3061 TCTTGTTCACACCCCA 3079
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Db 19 TATTGTTACACACCCCA 1

RESULT 993
AX928387
LOCUS AX928387 19 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 22 from Patent WO03072822.
ACCESSION AX928387
VERSION AX928387.1 GI:40251950
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Hamelin,R. and Suraweera,N.
TITLE Mononucleotide repeats microsatellite markers for detecting
microsatellite instability
JOURNAL Patent: WO 03072822-A 22 04-SEP-2003;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE; (INSERM)
(FR)
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/notes="Primer"

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/db_xref="taxon:32630"
/note="PCR primer"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1570 TACCAGGTGCGCGGCGCA 1588
Db 1 TACCAGGTGCGCAAGGCGCA 19

RESULT 994
AX956746
LOCUS          19 bp      DNA      linear      PAT 08-JAN-2004
DEFINITION    Sequence 296 from Patent WO03097869.
ACCESSION    AX956746
VERSION      AX956746.1 GI:40785255
KEYWORDS
SOURCE       Rosa sp.
ORGANISM     Rosa sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.

REFERENCE 1
AUTHORS      Suess,K.H.
TITLES       Microsatellite markers for genetic analyses and the differentiation
of roses
JOURNAL      Con/Cipio GmbH (DE)
FEATURES     Location/Qualifiers
source       1..19
/organism="Rosa sp."
/mol_type="unassigned DNA"
/db_xref="taxon:36598"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2104 ACCCCAGCTCCAGCTCCT 2122
Db 1 ACCTCAGCACCACTCCT 19

RESULT 995
BD002098/c
LOCUS          19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION    Method and kit for detection of specific nucleotide sequence.
ACCESSION    BD002098
VERSION      BD002098.1 GI:18628838
KEYWORDS     JP 2000189198-A/19.
SOURCE       synthetic construct
ORGANISM     artificial sequences.

REFERENCE 1 (bases 1 to 19)
AUTHORS      Ehrlich,H.A.; Horne,G.T.; Saiki,R.K. and Maris,C.B.
TITLES       Method and kit for detection of specific nucleotide sequence
JOURNAL      F HOFFMANN LA ROCHE AG
COMMENT      OS Artificial Sequence
PN JP 2000189198-A/19
PD 11-JUL-2000
PF 24-FEB-2000 JP 2000052306
PR 13-MAR-1986 US 839331,22-AUG-1986 US 899344 PI
HENRY ANTHONY EHRLICH,GLENN THOMAS HORNE,RANDALL KEICHI SAIKI, PI
CURRY BANKS MARIS
PC C12Q1/68//C12N15/09,C12N15/00
CC
FH Key       Location/Qualifiers

source          1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 835 CTGCTGGGCTGCTGCCGCG 853
Db 19 CTGCTGGGCTGCTGCCGCG 1

RESULT 997
BD008057/c
LOCUS          19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION    Method of detecting peritoneal thickening.
ACCESSION    BD008057
VERSION      BD008057.1 GI:18636430
KEYWORDS     JP 2001066306-A/16.
SOURCE       synthetic construct
ORGANISM     artificial sequences.

REFERENCE 1 (bases 1 to 19)
AUTHORS      Hirahara,I. and Uneyama,K.
TITLES       Method of detecting peritoneal thickening
JOURNAL      Patent: JP 2001066306-A 16 16-MAR-2001;

source          1..19
/organism="Artificial Sequence".
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 835 CTGCTGGGCTGCTGCCGCG 853
Db 19 CTGCTGGGCTGCTGCCGCG 1

RESULT 997
BD008057/c
LOCUS          19 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION    Method of detecting peritoneal thickening.
ACCESSION    BD008057
VERSION      BD008057.1 GI:18636430
KEYWORDS     JP 2001066306-A/16.
SOURCE       synthetic construct
ORGANISM     artificial sequences.

REFERENCE 1 (bases 1 to 19)
AUTHORS      Hirahara,I. and Uneyama,K.
TITLES       Method of detecting peritoneal thickening
JOURNAL      Patent: JP 2001066306-A 16 16-MAR-2001;

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Db	19	TTGCTGCTGCAGGTCGA	1
RESULT 999	A32748/c	20 bp	DNA linear PAT 09-JUL-1996
LOCUS	A32748		
DEFINITION	Synthetic capture probe for E.coli beta-glucuronidase gene.		
ACCESSION	A32748		
VERSION	A32748.1	GI:1567596	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 20)		
AUTHORS			
TITLE	METHOD FOR DETECTING A NUCLEOTIDE SEQUENCE BY SANDWICH		
JOURNAL	HYBRIDIZATION		
FEATURES	Patent: WO 9119812-A 48 26-DEC-1991;		
source	Location/Qualifiers		
	1..20		
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	/mol_type="unassigned DNA"		
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Query Match	0.4%;	Score 14.2;	DB 1; Length 20;
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;	
Matches	16;	Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
QY	1659	CAACGTGATGAGATGCGA	1677
Db	20	CAGCGTGATATAGATCGCA	2
RESULT 1000	A47852/c	20 bp	DNA linear PAT 07-MAR-1997
LOCUS	A47852		
DEFINITION	Sequence 66 from Patent WO9533851.		
ACCESSION	A47852		
VERSION	A47852.1	GI:2301738	
KEYWORDS			
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 20)		
AUTHORS	De.B.H., Portaeis, F., Machtelinckx, L., Jannes, G. and Roseau, R.		
TITLE	METHOD FOR THE DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF		
JOURNAL	MYCOBACTERIUM SPECIES		
COMMENT	Patent: WO 9533851-A 66 14-DEC-1995;		
FEATURES	INNOGENETICS NV (BE)		
source	Other publication AU 2789695 960104.		
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	/organism="unidentified"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32644"		
Query Match	0.4%;	Score 14.2;	DB 1; Length 20;
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;	
Matches	16;	Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
QY	355	GAGTTCGGCGGAGCACC	373
Db	20	GAGTTCGGCGGAGCACC	2
RESULT 1001	A63042	20 bp	DNA linear PAT 12-MAR-1998
LOCUS	A63042		
DEFINITION	Sequence 13 from Patent WO9718308.		
ACCESSION	A63042		
VERSION	A63042.1	GI:3716906	
KEYWORDS			
SOURCE	unidentified		
TERUMO CORP			
OS	Artificial Sequence		
PN	JP 2001066306-A/16		
PD	16-MAR-2001		
PF	30-AUG-1999	JP 1999244079	
PR	ICHIRO HIRAHARA, KAZUO UMEYAMA		
PI	G01N33/53, A61M1/28, C12N15/09, C12Q1/68, G01N33/50, G01N33/68, PC		
CC	C12N15/00		
Key	Location/Qualifiers		
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FT	/organism="Artificial Sequence".		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:32630"		
Query Match	0.4%;	Score 14.2;	DB 1; Length 19;
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;	
Matches	16;	Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
QY	2608	CAAAGCTGAGCTGCAGGG	2626
Db	19	CAGAGCTGCGCTGCAGAG	1
RESULT 998	AB067988/c	19 bp	DNA linear SYN 21-MAY-2003
LOCUS	AB067988		
DEFINITION	Synthetic construct DNA, forward primer for human STS sts-190018T7		
ACCESSION	AB067988		
VERSION	AB067988.1	GI:15128792	
KEYWORDS			
SOURCE	synthetic construct		
ORGANISM	synthetic construct		
REFERENCE	1		
AUTHORS	Chen, Y.Z., Hayashi, Y., Wu, J.G., Takaoka, E., Maekawa, K.,		
	Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,		
	Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.		
	and Soeda, E.		
TITLE	A BAC-based STS-content map spanning a 35-Mb region of human		
JOURNAL	chromosome 1p35-p36		
MEDLINE	Genomics 74 (1), 55-70 (2001)		
PUBMED	21269192		
REFERENCE	2 (bases 1 to 19)		
AUTHORS	Horii, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-AUG-2001) Akira Horii, Tohoku University School of		
	Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,		
	Miyagi 980-8575, Japan [E-mail: horii@mail.cc.tohoku.ac.jp,		
	Tel: 81-22-717-8042, Fax: 81-22-717-8047]		
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	/db_xref="taxon:32630"		
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	/note="forward primer for human STS sts-190018T7 at 1p36		
	sts-190018T7 obtained from clones B151P10, 170B16, B31617,		

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ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Ashcroft,F., Sakura,H., Ashfield,R. and Ashcroft,S.J.
TITLE K-ATP CHANNEL PROTEIN AND METHODS RELATING TO IT
JOURNAL Patent: WO 9718308-A 13 22-MAY-1997;
COMMENT WELLCOME TRUST LIMITED AS TRUS (GB)
FEATURES Other publication AU 7583296 19970605.
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                /mol_type="unassigned DNA"
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Query Match
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1351 ATGGAGATGATGAAGATGA 1369
Db 1 AAGGACATGGTGAAGATGA 19

RESULT 1002
A97518
LOCUS A97518 20 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 18 from Patent WO9915696.
ACCESSION A97518
VERSION A97518.1 GI:6780864
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Qin,Y.
TITLE METHOD AND KIT FOR EARLY DIAGNOSIS OF AUTOIMMUNITY AND LYMPHOMA IN
JOURNAL CENTRAL NERVOUS SYSTEM
PATENT: WO 9915696-A 18 01-APR-1999;
QIN YUPEN (CA)
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Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 986 AAGGCTGGGGCTCCCCAC 1004
Db 1 ATGGCTGGGGCTCCCTAC 19

RESULT 1003
AR012029
LOCUS AR012029 20 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 6 from patent US 5763186.
ACCESSION AR012029
VERSION AR012029.1 GI:3970019
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ludtke,D.N., Monahan,J.E. and Unger,J.T.
TITLE Use of antisense oligomers in a process for controlling
JOURNAL contamination in nucleic acid amplification reactions
PATENT: US 5763186-A 6 09-JUN-1998;
FEATURES Location/Qualifiers
          source
            1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Ashcroft,F., Sakura,H., Ashfield,R. and Ashcroft,S.J.
TITLE K-ATP CHANNEL PROTEIN AND METHODS RELATING TO IT
JOURNAL Patent: WO 9718308-A 13 22-MAY-1997;
COMMENT WELLCOME TRUST LIMITED AS TRUS (GB)
FEATURES Other publication AU 7583296 19970605.
          Location/Qualifiers
            source
              1..20
                /organism="unidentified"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 812 GGTTCCTCATCTCTGC 830
Db 1 GGTTCCTCATCTCTCTAC 19

RESULT 1004
AR062662
LOCUS AR062662 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 62 from patent US 5843738.
ACCESSION AR062662
VERSION AR062662.1 GI:5990353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5843738-A 62 01-DEC-1998;
FEATURES Location/Qualifiers
          source
            1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTCTCCAGCAGGG 3398
Db 2 CTGTGTCTCTGGAGGG 20

RESULT 1005
AR062829/c
LOCUS AR062829 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5843757.
ACCESSION AR062829
VERSION AR062829.1 GI:5990520
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Vogelstein,B., Kinzler,K.W. and Nicolaides,N.C.
TITLE Human JTV1 gene overlaps PMS2 gene
JOURNAL Patent: US 5843757-A 16 01-DEC-1998;
FEATURES Location/Qualifiers
          source
            1..20
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795
Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1006
AR076718/c
LOCUS AR076718 20 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 83 from patent US 5959096.
ACCESSION AR076718
VERSION AR076718.1 GI:10003464
KEYWORDS
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., and Dean,N.
TITLE Antisense oligonucleotides against human protein kinase C
JOURNAL Patent: US 593096-A 83 28-SEP-1999;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1812 CTTTGGGTCCTGCTCTGG 1830
Db 19 CTGTGGGTCCTGCTCTGG 1

RESULT 1007
AR079558/c AR079558 20 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 2 from patent US 5965712.
DEFINITION AR079558
ACCESSION AR079558
VERSION AR079558.1 GI:10006302
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Conrad,D.H. and Kelly,A.E.
TITLE L2-CD23 chimera for inhibition of IgE-mediated allergic disease
JOURNAL Patent: US 5965712-A 2 12-OCT-1999;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1294 GTGAAGATGCTGAAGACG 1312
Db 19 GTGAAGATGCTGAAGAG 1

RESULT 1008
AR104765 AR104765 20 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 62 from patent US 6093811.
DEFINITION AR104765
ACCESSION AR104765
VERSION AR104765.1 GI:12817473
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 6093811-A 62 25-JUL-2000;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGCCAGGACGG 3398

Db 2 CTGTGTGCTCGGAGG 20

RESULT 1009
AR105587 AR105587 20 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 62 from patent US 6096722.
DEFINITION AR105587
ACCESSION AR105587
VERSION AR105587.1 GI:12819184
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Mirabelli,C.K. and Baker,B.
TITLE Antisense modulation of cell adhesion molecule expression and
treatment of cell adhesion molecule-associated diseases
JOURNAL Patent: US 6096722-A 62 01-AUG-2000;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGCCAGGACGG 3398
Db 2 CTGTGTGCTCGGAGG 20

RESULT 1010
AR108646 AR108646 20 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 10 from patent US 6111075.
DEFINITION AR108646
ACCESSION AR108646
VERSION AR108646.1 GI:12824133
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Xu,W.-F., Presnell,S.R., Yee,D.P. and Foster,D.C.
TITLE Protease-activated receptor PAR4 (ZCHEMR2)
JOURNAL Patent: US 6111075-A 10 29-AUG-2000;
FEATURES Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2415 CCCCCTGCTGTGCAACGG 2433
Db 20 CCATGCTGCTGTGCTACGG 2

RESULT 1011
AR116480 AR116480 20 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 61 from patent US 6133246.
DEFINITION AR116480
ACCESSION AR116480
VERSION AR116480.1 GI:14096802
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay,R., Dean,N., Monia,B.P., Nero,P.S. and Gaarde,W.A.


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TITLE      Antisense oligonucleotide compositions and methods for the
JOURNAL    modulation of JNK proteins
FEATURES   Patent: US 6133246-A 61 17-OCT-2000;
           Location/Qualifiers
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3379 GCTGTGTGTCCTCCAGGAGG 3397
      ||||| ||||| ||||| |||||
Db 2 GCTGGCTTTCGAGGCGG 20

RESULT 1012
ARI22482/c
LOCUS      ARI22482      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 36 from patent US 6165728.
ACCESSION  ARI22482
VERSION    ARI22482.1 GI:14106799
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ward,D.T. and Cowseert,L.M.
TITLE     Antisense modulation of NCK-2 expression
JOURNAL   Patent: US 6165728-A 36 26-DEC-2000;
FEATURES   Location/Qualifiers
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1293 CGTGAAGATGCTGAAGAC 1311
      ||||| ||||| ||||| |||||
Db 19 CGTGAAGACCTGAAGAC 1

RESULT 1013
ARI22500/c
LOCUS      ARI22500      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 54 from patent US 6165728.
ACCESSION  ARI22500
VERSION    ARI22500.1 GI:14106817
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ward,D.T. and Cowseert,L.M.
TITLE     Antisense modulation of NCK-2 expression
JOURNAL   Patent: US 6165728-A 54 26-DEC-2000;
FEATURES   Location/Qualifiers
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 865 GTGAGGCTGACGAGCGG 883
      ||||| ||||| ||||| |||||
Db 20 GAGGAGGTGACGAGGCGG 2

TITLE      Antisense oligonucleotide compositions and methods for the
JOURNAL    modulation of JNK proteins
FEATURES   Patent: US 6133246-A 61 17-OCT-2000;
           Location/Qualifiers
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTGTCCCGAGGAGG 3398
      ||||| ||||| ||||| |||||
Db 2 CTGTGTGTCCCTGGGAGG 20

RESULT 1016
ARI27702
LOCUS      ARI27702      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 120 from patent US 6180774.
ACCESSION  ARI27702
VERSION    ARI27702.1 GI:14114297
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Brown,S.Marie., Dean,D.Allen., Fromm,M.Ernest. and
           Sanders,P.Rigden.
TITLE     Synthetic DNA sequences having enhanced expression in
           monocotyledonous plants and method for preparation thereof
JOURNAL   Patent: US 6180774-A 120 30-JAN-2001;
FEATURES   Location/Qualifiers
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source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2617 GCTGCGAGGAGCCAC 2635
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GCTGCGAGGAGCCAC 20

RESULT 1017
AR129756/c 20 bp DNA PAT 16-MAY-2001
LOCUS AR129756 Sequence 160 from patent US 6187545.
DEFINITION AR129756
ACCESSION AR129756
VERSION AR129756.1 GI:14117653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Butler, M.M., Wyatt, J. and Cowsert, L.M.
TITLE Antisense modulation of peptidocytosolic expression
JOURNAL Patent: US 6187545-A 160 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 42 GGGCCCCAGCGCTGCAG 60
| | | | | | | | | | | | | | | | | | | | | |
Db 20 GAGGCCACAGCTGCTGCAG 2

RESULT 1018
AR142705/c 20 bp DNA PAT 08-AUG-2001
LOCUS AR142705 Sequence 3 from patent US 6203998.
DEFINITION AR142705
ACCESSION AR142705
VERSION AR142705.1 GI:15103991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Civelli, O. and Van Tol, H. Henri.-Marie.
TITLE Human dopamine receptor and its uses
JOURNAL Patent: US 6203998-A 3 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 98 GCTGCCGCGAGCGGCTCAC 116
| | | | | | | | | | | | | | | | | | | | | |
Db 19 GCGGCCGAGCGGCTCAC 1

RESULT 1019
AR162412/c 20 bp DNA PAT 17-OCT-2001
LOCUS AR162412 Sequence 92 from patent US 6258600.
DEFINITION

ACCESSION AR162412
VERSION AR162412.1 GI:16229590
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zhang, H. and Cowsert, L.M.
TITLE Antisense modulation of caspase 8 expression
JOURNAL Patent: US 6258600-A 92 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3260 GATATTTTATTTGCTTGT 3278
| | | | | | | | | | | | | | | | | | | | | |
Db 19 GCTATTTTGTGTTTGT 1

RESULT 1020
AR163862/c 20 bp DNA PAT 17-OCT-2001
LOCUS AR163862 Sequence 60 from patent US 6271030.
DEFINITION AR163862
ACCESSION AR163862
VERSION AR163862.1 GI:16234657
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P., Butler, M.M. and Wyatt, J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 60 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 243 CGAGCGGATGGACAGAGAG 261
| | | | | | | | | | | | | | | | | | | | | |
Db 20 CGAGCGGCTGCAGAGAG 2

RESULT 1021
AR163924 20 bp DNA PAT 17-OCT-2001
LOCUS AR163924 Sequence 122 from patent US 6271030.
DEFINITION AR163924
ACCESSION AR163924
VERSION AR163924.1 GI:16234757
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Monia, B.P., Butler, M.M. and Wyatt, J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 122 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 44 GGCCCGGCGGCTGCAGGT 62
|||||
Db 1 GGCGCGAGCGGCTCCAGGT 19
|||||

RESULT 1022
ARI64041/c
LOCUS ARI64041 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 241 from patent US 6271030.
ACCESSION ARI64041
VERSION ARI64041.1 GI:16234953
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 241 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3250 TTCACGTGAAGATATTTTA 3268
|||
Db 20 TTAAGTGAAGACATTTTA 2
|||||

RESULT 1023
ARI74372/c
LOCUS ARI74372 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 32 from patent US 6306655.
ACCESSION ARI74372
VERSION ARI74372.1 GI:17914692
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Monia,B.P., Butler,M.M. and Wyatt,J.
TITLE Antisense inhibition of C/EBP alpha expression
JOURNAL Patent: US 6306655-A 32 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2041 TCACCGCAGGACTCTGG 2059
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Db 19 TTCACGCGAGGTTCTCTGG 1
|||||

RESULT 1024
ARI77628/c
LOCUS ARI77628 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 11 from patent US 6312939.
ACCESSION ARI77628
VERSION ARI77628.1 GI:17919983
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Roberts,J., MacAllister,T.W., Sethuraman,N. and Freeman,A.G.
TITLE Genetically engineered glutaminase and its use in antiviral and anticancer therapy
JOURNAL Patent: US 6312939-A 11 06-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 845 TGCCAGCCGAGGAGGAGCT 863
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Db 19 TGCCAGCCCTGCAGGAGCT 1
|||||

RESULT 1025
BD181148/c
LOCUS BD181148 20 bp DNA linear PAT 15-MAY-2003
DEFINITION Human DNA mismatch repair proteins.
ACCESSION BD181148
VERSION BD181148.1 GI:30792066
KEYWORDS JP 2002325588-A/52.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 20)
AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and Rosen,C.A.
TITLE Human DNA mismatch repair proteins
JOURNAL Patent: JP 2002325588-A 52 12-NOV-2002;
COMMENT HUMAN GENOME SCIENCES INC
OS Artificial Sequence
PN JP 2002325588-A/52
PD 12-NOV-2002
PF 25-JAN-2002 JP 2002016830
PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
23-AUG-1994 US 08/294312
PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EWEN F
PI KIRKNESS,
PI CRAIG A ROSEN
PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68// (C12P21/02,C12R1:19),
PC C12N15/00
CC hMLH3 primer
FH Key Location/Qualifiers
FT source 1..20
/organism='Artificial Sequence'

FEATURES
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795
|||||
Db 20 GACGAGTCTTCACTAACCC 2
|||||

RESULT 1026
BD181159/c
LOCUS BD181159 20 bp DNA linear PAT 15-MAY-2003
DEFINITION Human DNA mismatch repair proteins.
ACCESSION BD181159
VERSION BD181159.1 GI:30792077
KEYWORDS JP 2002325588-A/63.

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SOURCE          synthetic construct
ORGANISM        /organism="synthetic construct"
REFERENCE       1 (bases 1 to 20)
AUTHORS         Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
                Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and Rosen,C.A.
TITLE           Human DNA mismatch repair proteins
JOURNAL         Patent: JP 2002325588-A 63 12-NOV-2002;
                HUMAN GENOME SCIENCES INC
COMMENT         OS Artificial Sequence
                PN JP 2002325588-A/63
                PD 12-NOV-2002
                PR 25-JAN-2002 JP 2002016830
                PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
                23-AUG-1994 US 08/294312
                PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
                PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EVEN F
                PI KIRKNESS,
                PI CRAIG A ROSEN
                PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68//(C12P21/02,C12R1:19),
                PC C12N15/00
                CC primer useful for amplifying codons 1 to 863 hMLH3 FH Key
                Location/Qualifiers
                FT source 1..20
                FT /organism='Artificial Sequence'.

FEATURES
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    Query Match 0.4%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 1.1e+03;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

    QY 1777 GACCGAGCTCTACACTCACC 1795
    Db 20 GACAGAGCTCTCACTAACC 2

  RESULT 1027
  LOCUS      BD181162 20 bp DNA linear PAT 15-MAY-2003
  DEFINITION Human DNA mismatch repair proteins.
  ACCESSION  BD181162
  VERSION    BD181162.1 GI:30792080
  KEYWORDS  JP 2002325588-A/66.
  SOURCE     synthetic construct
  ORGANISM   artificial sequences.
  1 (bases 1 to 20)
  AUTHORS    Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
  TITLE     Human DNA mismatch repair proteins
  JOURNAL   Patent: JP 2002325588-A 66 12-NOV-2002;
  COMMENT   OS Artificial Sequence
  PN JP 2002325588-A/66
  PD 12-NOV-2002
  PR 25-JAN-2002 JP 2002016830
  PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
  23-AUG-1994 US 08/294312
  PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
  PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EVEN F
  PI KIRKNESS,
  PI CRAIG A ROSEN
  PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68//(C12P21/02,C12R1:19),
  PC C12N15/00
  CC primer useful for amplifying codons 415 to 863 of hMLH3 FH
  Key      Location/Qualifiers
  FT source 1..20
  FT /organism='Artificial Sequence'.

  Location/Qualifiers

  Query Match 0.4%; Score 14.2; DB 1; Length 20;
  Best Local Similarity 84.2%; Pred. No. 1.1e+03;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 1777 GACCGAGCTCTACACTCACC 1795
  Db 20 GACAGAGCTCTCACTAACC 2

  RESULT 1027
  LOCUS      BD181162 20 bp DNA linear PAT 15-MAY-2003
  DEFINITION Human DNA mismatch repair proteins.
  ACCESSION  BD181162
  VERSION    BD181162.1 GI:30792080
  KEYWORDS  JP 2002325588-A/66.
  SOURCE     synthetic construct
  ORGANISM   artificial sequences.
  1 (bases 1 to 20)
  AUTHORS    Haseltine,W.A., Ruben,S.M., Wei,Y.F., Adams,M.D., Fleischmann,R.D.,
  TITLE     Human DNA mismatch repair proteins
  JOURNAL   Patent: JP 2002325588-A 66 12-NOV-2002;
  COMMENT   OS Artificial Sequence
  PN JP 2002325588-A/66
  PD 12-NOV-2002
  PR 25-JAN-2002 JP 2002016830
  PR 27-JAN-1994 US 08/187757,16-MAR-1994 US 08/210143 PR
  23-AUG-1994 US 08/294312
  PI WILLIAM A HASELTINE,STEVEN M RUBEN,YING FEI WEI,MARK D ADAMS,
  PI ROBERT D FLEISCHMANN,CLAIRE M FRASER,REBECCA A FULDNER,EVEN F
  PI KIRKNESS,
  PI CRAIG A ROSEN
  PC C12N15/09,C07K14/47,C12P21/02,C12Q1/68//(C12P21/02,C12R1:19),
  PC C12N15/00
  CC primer useful for amplifying codons 415 to 863 of hMLH3 FH
  Key      Location/Qualifiers
  FT source 1..20
  FT /organism='Artificial Sequence'.

  Location/Qualifiers

  Query Match 0.4%; Score 14.2; DB 1; Length 20;
  Best Local Similarity 84.2%; Pred. No. 1.1e+03;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 2004 GCTGGTGGAGGACCTGGAC 2022
  Db 19 GCTGGTGGAGGACGAGTGGAC 1

  RESULT 1029
  LOCUS      BD225060 20 bp DNA linear PAT 17-JUL-2003
  DEFINITION Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF).
  ACCESSION  BD225060
  VERSION    BD225060.1 GI:33034830
  KEYWORDS  JP 2002526095-A/195.
  SOURCE     synthetic construct
  ORGANISM   artificial sequences.
  1 (bases 1 to 20)
  AUTHORS    Baker,B.F., Cowsett,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF)

  Location/Qualifiers

  Query Match 0.4%; Score 14.2; DB 1; Length 20;
  Best Local Similarity 84.2%; Pred. No. 1.1e+03;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

  QY 2004 GCTGGTGGAGGACCTGGAC 2022
  Db 19 GCTGGTGGAGGACGAGTGGAC 1

  RESULT 1029
  LOCUS      BD225060 20 bp DNA linear PAT 17-JUL-2003
  DEFINITION Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF).
  ACCESSION  BD225060
  VERSION    BD225060.1 GI:33034830
  KEYWORDS  JP 2002526095-A/195.
  SOURCE     synthetic construct
  ORGANISM   artificial sequences.
  1 (bases 1 to 20)
  AUTHORS    Baker,B.F., Cowsett,L.M., Monia,B.P. and Xu,X.S.
  TITLE     Antisense modulation of expression of tumor necrosis factor
                receptor-associated factor (TRAF)

  Location/Qualifiers

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JOURNAL Patent: JP 2002526095-A 195 20-AUG-2002;
COMMENT  ISIS PHARMACEUTICALS INC
        OS Artificial Sequence
        PN JP 2002526095-A/195
        PD 20-AUG-2002
        PP 05-OCT-1999 JP 2000574546
        PR 06-OCT-1998 US 09/167109
        PI BRENDIA F BAKER, LEX M COMSERT, BRETT P MONIA, XIAOXING S XU PC
        C12N15/09, A61K31/7105, A61K48/00, A61P29/00, A61P35/00, C12N15/00 CC
        antisense sequence
        FH Key Location/Qualifiers
        FT source 1..20 /organism='Artificial Sequence'.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1998 CAGGCGCTGGTAGGAC 20
Db 2 CAGGCGCTGGTAGGAC 20

RESULT 1030
BD230252/c
LOCUS 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Total genome radiation hybrid map of canine genome and its use for
ACCESSION identification of interesting genes.
VERSION BD230252.1 GI:33040022
KEYWORDS JP 2002530091-A/121.
SOURCE Canis familiaris
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE Galibert, F. and Andre, C.
JOURNAL Total genome radiation hybrid map of canine genome and its use for
COMMENT identification of interesting genes
Patent: JP 2002530091-A 121 17-SEP-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/121
PD 17-SEP-2002
PP 15-NOV-1999 JP 2000582596
PR 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT, CATHERINE ANDRE
PC C12N15/09, C12Q1/68, C12N15/00
CC A0076
FH Key Location/Qualifiers
FT source 1..25 /organism='Canis familiaris (dog)'.
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/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 749 CCTGCACACGTCACCTT 767
Db 20 CCTGCACACGACCCCTT 2

RESULT 1031
JOURNAL Patent: JP 2002526095-A 195 20-AUG-2002;
COMMENT  ISIS PHARMACEUTICALS INC
        OS Artificial Sequence
        PN JP 2002526095-A/195
        PD 20-AUG-2002
        PP 05-OCT-1999 JP 2000574546
        PR 06-OCT-1998 US 09/167109
        PI BRENDIA F BAKER, LEX M COMSERT, BRETT P MONIA, XIAOXING S XU PC
        C12N15/09, A61K31/7105, A61K48/00, A61P29/00, A61P35/00, C12N15/00 CC
        antisense sequence
        FH Key Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1006 GTGCACAGATCTCCGCT 1024
Db 1 GTGCTCAAGATGCCCGCT 19

RESULT 1032
CQ762181
LOCUS 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 799 from Patent WO2004003201.
ACCESSION CQ762181
VERSION CQ762181.1 GI:44905417
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane, C.D.
TITLE Antisense modulation of lrlh expression
JOURNAL Patent: WO 2004003201-A 799 08-JAN-2004;
Pharmacia Corporation (US)
FH Key Location/Qualifiers
FT source 1..20 /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Human LRLH antisense"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3558 CTGGACTGCTACCTTTCAA 3576
Db 2 CTGCACAGCTACCTTTAA 20

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<p>AUTHORS Kane, C.D. TITLE Antisense modulation of lrlh1 expression JOURNAL Patent: WO 2004003201-A 1498 08-JAN-2004; Pharmacia Corporation (US) FEATURES Location/Qualifiers source 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Human LRH1 antisense"</p>		<p>0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 1.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>	
<p>QY 2306 AGAGCTTTGTCTGTGTGT 2324 Db 19 AGAGCTTTGTCCCGTGTGT 1</p>	<p>20 bp DNA Sequence 2129 from Patent WO2004003201. CO763511 CO763511 CO763511.1 GI:44906747 synthetic construct synthetic construct artificial sequences.</p>	<p>linear PAT 03-MAR-2004</p>	
<p>RESULT 1036 LOCUS CO763511 DEFINITION Sequence 2129 from Patent WO2004003201. ACCESSION CO763511 VERSION CO763511.1 GI:44906747 KEYWORDS . ORGANISM synthetic construct synthetic construct artificial sequences.</p>			
<p>REFERENCE 1 AUTHORS Kane, C.D. TITLE Antisense modulation of lrlh1 expression JOURNAL Patent: WO 2004003201-A 2129 08-JAN-2004; Pharmacia Corporation (US) FEATURES Location/Qualifiers source 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Human LRH1 antisense"</p>	<p>0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 1.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>		
<p>QY 319 CCCACTCCCTCCATCTCT 337 Db 1 CCCACTCCCCCAATCTCTT 19</p>		<p>20 bp DNA Sequence 3082 from Patent WO2004003201. CO764464 CO764464 CO764464.1 GI:44907700 synthetic construct synthetic construct artificial sequences.</p>	<p>linear PAT 03-MAR-2004</p>
<p>RESULT 1037 LOCUS CO764464/c DEFINITION Sequence 3082 from Patent WO2004003201. ACCESSION CO764464 VERSION CO764464.1 GI:44907700 KEYWORDS . ORGANISM synthetic construct synthetic construct artificial sequences.</p>			
<p>REFERENCE 1 AUTHORS Kane, C.D. TITLE Antisense modulation of lrlh1 expression JOURNAL Patent: WO 2004003201-A 3082 08-JAN-2004; Pharmacia Corporation (US) FEATURES Location/Qualifiers source 1..20 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Human LRH1 antisense"</p>	<p>0.4%; Score 14.2; DB 1; Best Local Similarity 84.2%; Pred. No. 1.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;</p>		

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Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3561 GACTGCTACTTTCAAAGC 3579
      ||||| | ||||| |||||
Db 20 GACTACAACACTTCAAAGC 2

RESULT 1038
LOCUS CQ764591/c 20 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 3209 from Patent WO2004003201.
ACCESSION CQ764591
VERSION CQ764591.1 GI:44907827
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Kane, C.D.
TITLE Antisense modulation of lrlh expression
JOURNAL Patent: WO 2004003201-A 3209 08-JAN-2004;
Pharmacia Corporation (US)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Human LRLH antisense"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3561 GACTGCTACTTTCAAAGC 3579
      ||||| | ||||| |||||
Db 19 GACTACAACACTTCAAAGC 1

RESULT 1039
LOCUS CQ779747/c 20 bp DNA linear PAT 17-MAR-2004
DEFINITION Sequence 27 from Patent WO2004016812.
ACCESSION CQ779747
VERSION CQ779747.1 GI:45535915
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Clinton, M.
TITLE Avian sex determination method
JOURNAL Patent: WO 2004016812-A 27 26-FEB-2004;
ROSLIN INSTITUTE (EDINBURGH) (GB)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2455 ACCGAGGGCGCTTTGTCT 2473
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Db 19 ATCGAGGGCGCTTTATTCT 1

RESULT 1040
LOCUS CQ779749/c 20 bp DNA linear PAT 14-JUN-2004
DEFINITION Sequence 19 from Patent WO2004046381.
ACCESSION CQ819706
VERSION CQ819706.1 GI:48715186
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM
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LOCUS CQ779749 20 bp DNA linear PAT 17-MAR-2004
DEFINITION Sequence 29 from Patent WO2004016812.
ACCESSION CQ779749
VERSION CQ779749.1 GI:45535917
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Clinton, M.
TITLE Avian sex determination method
JOURNAL Patent: WO 2004016812-A 29 26-FEB-2004;
ROSLIN INSTITUTE (EDINBURGH) (GB)
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1. .20
/organism="synthetic construct"
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/db_xref="taxon:32630"
/notes="Primer"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2455 ACCGAGGGCGCTTTGTCT 2473
      ||||| | ||||| |||||
Db 19 ATCGAGGGCGCTTTATTCT 1

RESULT 1041
LOCUS CQ786731 20 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 7 from Patent WO2004018507.
ACCESSION CQ786731
VERSION CQ786731.1 GI:45721746
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hanski, E., Moses, A.E. and Hidalgo-Graas, C.
TITLE Compositions and methods for treatment and prophylaxis of
infections caused by gram positive bacteria
JOURNAL Patent: WO 2004018507-A 7 04-MAR-2004;
YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW UNIVERS ITY OF
JERUSALEM (IL); HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT CO.
LTD. (IL)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Description of Artificial Sequence.Inverse PCR
primer from 5' of sila"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1995 CTTCAAGCAGCTGTGGAG 2013
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Db 2 CTTCAAGCAGCTGTATGG 20

RESULT 1042
LOCUS CQ819706 20 bp DNA linear PAT 14-JUN-2004
DEFINITION Sequence 19 from Patent WO2004046381.
ACCESSION CQ819706
VERSION CQ819706.1 GI:48715186
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM
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artificial sequences.
1
REFERENCE
AUTHORS Ralston,S.
TITLE Polymorphisms in th clcn7 gene as genetic markers for bone mass
JOURNAL Patent: WO 2004046381-A 19 03-JUN-2004;
The University Court of The University of Aberdeen (GB)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="Primer"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1099 AGGCTGTCTCTCAGGGAGG 1117
|||||
Db 1 AGGCTGTCTCTCAGATGGG 19
|||||

RESULT 1043
LOCUS C0821690 20 bp DNA linear PAT 21-JUN-2004
DEFINITION Sequence 35 from Patent WO2004048606.
ACCESSION C0821690
VERSION C0821690.1 GI:49019968
KEYWORDS synthetic construct
synthetic construct
artificial sequences.
ORGANISM
REFERENCE
AUTHORS J Rgensen,C.B., Cirera,S., Archibald,A., Andersson,L., Fredholm,M.
and Edfors-Lilja,I.
TITLE Porcine polymorphisms and methods for detecting them
JOURNAL Patent: WO 2004048606-A 35 10-JUN-2004;
Den KGL. Veterinaer- OG Landbohjskole (DK)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="lower primer related to gene RFC4"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 828 TGCCTGGCTGTGTGCTGCTG 846
|||||
Db 1 TGCTTAGCTGATGGTGTG 19
|||||

RESULT 1044
E02948/c
LOCUS E02948 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer sequence for cloning of acylamino acid releasing enzyme by
PCR.
ACCESSION E02948
VERSION E02948.1 GI:2171170
KEYWORDS JP 1991147787-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Isekawa,Y., MuneKawa,Y., Oshima,A., Mukai,H. and Katou,I.
TITLE NEW METHOD FOR CLONING DNA
JOURNAL Patent: JP 1991147787-A 2 24-JUN-1991;
TAKARA SHUZO CO LTD
COMMENT OS Artificial gene
OS Artificial sequence; Genes.
PN JP 1991147787-A/2

artificial sequences.
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REFERENCE
AUTHORS PD 24-JUN-1991
PF 31-OCT-1989 JP 1989281811
PI ISEKAWA YUJI, MUNEKAWA YOSHIHIRO, OSHIMA ATSUSHI, PI MUKAI
HIROYUKI,
PI KATOU IKUNOSHIN
PC C12N15/10//C07H21/04;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2940 TGGAGGGAGGCCGCCAGGG 2958
|||||
Db 19 TGGATGGAGTCCACAGGG 1
|||||

RESULT 1045
E04077
LOCUS E04077 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for amplifying envelope region of type C hepatitis virus.
ACCESSION E04077
VERSION E04077.1 GI:2172287
KEYWORDS JP 1992349885-A/2.
SOURCE synthetic construct
synthetic construct
artificial sequences.
ORGANISM
REFERENCE
AUTHORS Morinaga,T., Chayama,K., Kumada,H. and Ichikawa,Y.
TITLE NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
AND METHOD FOR DETECTING THE SAME
JOURNAL Patent: JP 1992349885-A 2 04-DEC-1992;
TEIJIN LTD
COMMENT OS Artificial gene
OS Artificial sequence; Genes.
PN JP 1992349885-A/2
PD 04-DEC-1992
PF 23-MAY-1991 JP 1991152169
PI MORINAGA TSUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU, PI
ICHIKAWA YATARO
PC C12N15/10,C12Q1/68,C12Q1/70//C12N15/11;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3664 AGGGCCATGGCTCAGGGTG 3682
|||||
Db 1 AGGGCCCTGGCGCATGGTG 19
|||||

RESULT 1046
E11000/c
LOCUS E11000 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for detecting human cytochrome P4501A2 polymorphism(one
member of a couple).
ACCESSION E11000

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VERSION E11000.1 GI:22024641
KEYWORDS JP 1996070897-A/18.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Fukui,T., Katsuragi,S., Kinoshita,M. and Shin,T.
TITLE DETECTION OF POLYMORPHISM OF HUMAN CYTOCHROME P4501A2 GENE
JOURNAL Patent: JP 1996070897-A 18 19-MAR-1996;
OTSUKA PHARMACEUT CO LTD
COMMENT OS None
OC Artificial sequences.
FN JP 1996070897-A/18
PD 19-MAR-1996
PF 06-JUL-1995 JP 1995170693
PR 06-JUL-1994 JP 94P 154571
PI FUKUI TAKASHI, KATSURAGI SHIYUKUTEN, KINOSHITA MORITOSHI, PI
SHIN TEIKIN
PC C12Q1/68,C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH key Location/Qualifiers
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FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3426 TGTGTCAGGTTCCGATGT 3444
DB 19 TGTGTCAGGTTCCAGCAGT 1

RESULT 1047
E13769/c
LOCUS 20 bp DNA linear PAT 27-APR-1998
DEFINITION PCR primer for discriminating genotype 6a of HCV (Hepatitis C virus).
ACCESSION E13769
VERSION E13769.1 GI:3252537
KEYWORDS JP 1997234072-A/21.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Ono,T., Mukaide,M., Hikichi,K. and Mizogami,M.
TITLE NEW OLIGONUCLEOTIDE, PRIMER FOR DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS COMPRISING THE SAME AND DISCRIMINATION IN GENOTYPE OF HEPATITIS C VIRUS BY USING THE PRIMER
JOURNAL Patent: JP 1997234072-A 21 09-SEP-1997;
S R L:KK
COMMENT OS None
OC Artificial sequences.
FN JP 1997234072-A/21
PD 09-SEP-1997
PF 01-FEB-1996 JP 1996038875
PR 01-FEB-1995 JP 95P 35997, 30-DEC-1995 JP 95P 352511 PI
ONO TOMOYOSHI, MUKAIDE MASAKAZU, HIKICHI KAZUMASA, PI MIZOGAMI MASAFUMI
PC C12N15/09,C07H21/04,C12Q1/68,C12Q1/70,(C12N15/09,C12R1:92); CC
strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: Yes;
FH key Location/Qualifiers
FH

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FT misc_feature 1..20 /note='Primer,OMM263'.
FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3189 GCGTCGCCCGAGCTGGAG 3207
DB 19 GCGTCGCCCTGGGCTGGCG 1

RESULT 1048
E29869/c
LOCUS 20 bp DNA linear PAT 18-JUN-2001
DEFINITION HIV cofactor inhibitor.
ACCESSION E29869
VERSION E29869.1 GI:13021264
KEYWORDS JP 1999292795-A/23.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Hiroshi,T., Naoki,Y., Toru,K., Kazuyuki,T. and Akira,W.
TITLE HIV cofactor inhibitor
JOURNAL Patent: JP 1999292795-A 23 26-OCT-1999;
YAMANOUCHI PHARMACEUT CO LTD
COMMENT OS Unidentified
FN JP 1999292795-A/23
PD 26-OCT-1999
PF 02-APR-1998 JP 1998125452
PR HIROSHI TAKAHISA,NAOKI YAMAMOTO,TORU KIMURA,KAZUYUKI TAKAI, PI
AKIRA WADA
PC A61K48/00,A61K31/70,A61K31/70,C12N15/09,C12N15/00 CC
FH key Location/Qualifiers
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FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1615 ATCCACAGGACCTGGCTG 1633
DB 19 ATCGATAGGTACCTGGCTG 1

RESULT 1049
E30661/c
LOCUS 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Immortalized human external trichilemmal cell and method for evaluating hair growth stimulant by using the same.
ACCESSION E30661
VERSION E30661.1 GI:13017227
KEYWORDS JP 200000089-A/14.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Jun.S., Eriko.T., Chika.H., Masahiro.T. and Hiroshi,H.

TITLE	Immortalized human external trichilemmal cell and method for evaluating hair growth stimulant by using the same
JOURNAL	Patent: JP 2000000089-A 14 07-JAN-2000; SHISEIDO CO LTD
COMMENT	OS Unidentified
PN	JP 2000000089-A/14
PD	07-JAN-2000
PF	15-JUN-1998 JP 1998181386
PR	
PI	JUN SUZUKI, ERIKO TAKEOKA, CHIKA HAMADA, MASASHIRO TAJIMA, PI HIROSHI HANDA
PC	C12N5/10, C12Q1/00//A61K7/06, C12N15/09, C12N5/00, C12N15/00 CC
Strandedness:	Single;
CC	Topology: Linear;
PH	Key
FT	source 1. .20
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	/mol_type='genomic DNA'
	/db_xref='taxon:32644'
Query Match	0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity	84.2%; Pred. No. 1.1e+03;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	758 ACCTCACCCTTTGAGGACGC 776
Db	20 ATGTAACCTTTTGAGGACGC 2
RESULT 1050	
E31396	
LOCUS	E31396 20 bp DNA linear PAT 18-JUN-2001
DEFINITION	Method for monitoring oil-contamination.
ACCESSION	E31396
VERSION	E31396.1 GI:13021550
KEYWORDS	JP 1999243967-A/24.
SOURCE	unidentified
ORGANISM	unidentified
REFERENCE	1 (bases 1 to 20)
AUTHORS	Hideo, K., Kazuya, W., Yuki, K. and Shigeaki, H.
TITLE	Method for monitoring oil-contamination
JOURNAL	Patent: JP 1999243967-A 24 14-SEP-1999;
COMMENT	MARINE BIOTECHNOLOGY INST CO LTD
	OS Unidentified
PN	JP 1999243967-A/24
PD	14-SEP-1999
PF	04-MAR-1998 JP 1998069399
PR	
PI	HIDEO KISHIRA, KAZUYA WATANABE, YUKI KASAI, SHIGEAKI HARAYAMA PC
PC	C12N15/09, C02F1/00, C12Q1/04, C12Q1/68//C12N1/20, C12Q1/04, PC
C12R1.01),	
PC	C12N15/00
CC	Strandedness: Single;
CC	Topology: Linear;
PH	Key
FT	source 1. .20
FEATURES	Location/Qualifiers
source	1. .20
	/organism='unidentified'
	/mol_type='genomic DNA'
	/db_xref='taxon:32644'
Query Match	0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity	84.2%; Pred. No. 1.1e+03;
Matches	16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	3272 GCTTTGCTCTTTTCAGGA 3290

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FEATURES
source
  Location/Qualifiers
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      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3272 GCTTGTCTCTTTTTCAGGA 3290
Db 1 GCTTTTCTCTTTGAGGA 19

RESULT 1053
LOCUS E59332 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59332
VERSION B59332.1 GI:18622509
KEYWORDS JP 2000342265-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose,K. and Yoshida,T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 13 12-DEC-2000;
TOAGOSEI CHEM IND CO LTD
COMMENT OS Artificial Sequence
PN JP 2000342265-A/13
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR KUNIHICO HIROSE,TADAO YOSHIDA
PC C12N15/09,B01D15/08,C12N15/00
CC
FH Key source Location/Qualifiers
FT source 1..20
  /organism="Artificial Sequence".

FEATURES
source
  Location/Qualifiers
    1..20
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2924 GGGCGTGGGGGGGGCGTGG 2942
Db 2 GGGCGGGGGGGGGGAGGG 20

RESULT 1054
LOCUS I12350/c 20 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 3 from patent US 542265.
ACCESSION I12350
VERSION I12350.1 GI:910373
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Civelli,O. and Van Tol,H.H.
TITLE DNA sequence for the human dopamine receptor D.sub.4 and expression thereof in mammalian cells
JOURNAL Patent: US 542265-A 3 06-JUN-1995;
FEATURES
source
  Location/Qualifiers
    1..20

FEATURES
source
  Location/Qualifiers
    1..20
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

Query Match
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  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3380 CTGTGTCTCCAGGCGG 3398
Db 2 CTGTGTCTCTGGGAGG 20

RESULT 1056
LOCUS I28186/c 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 559601.
ACCESSION I28186
VERSION I28186.1 GI:1818962
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Civelli,O.
TITLE Human dopamine receptor and its uses
JOURNAL Patent: US 559601-A 3 29-OCT-1996;
FEATURES
source
  Location/Qualifiers
    1..20
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 98 GCTGCGGCGAGCGGCTCAC 116
Db 19 GCGGCGGAGCGGCTCAC 1

RESULT 1057
LOCUS I33357 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 62 from patent US 5591623.
ACCESSION I33357
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Query Match	Score 14.2;	DB 1;	Length 20;
	0.4%		

REFERENCE 1 (bases 1 to 20)
AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and
Rosen,C.A.

TITLE Human DNA mismatch repair proteins
JOURNAL Patent: US 6416984-A 55 09-JUL-2002;
FEATURES Location/Qualifiers

source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795

Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1068

LOCUS AR217726/c 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 66 from patent US 6416984.
ACCESSION AR217726

VERSION AR217726.1 GI:23317597

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and
Rosen,C.A.

TITLE Human DNA mismatch repair proteins
JOURNAL Patent: US 6416984-A 66 09-JUL-2002;
FEATURES Location/Qualifiers

source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACACTCACC 1795

Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1069

LOCUS AR217729/c 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 69 from patent US 6416984.
ACCESSION AR217729

VERSION AR217729.1 GI:23317600

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Haseltine,W.A., Ruben,S.M., Wei,Y.-F., Adams,M.D.,
Fleischmann,R.D., Fraser,C.M., Fuldner,R.A., Kirkness,E.F. and
Rosen,C.A.

TITLE Human DNA mismatch repair proteins
JOURNAL Patent: US 6416984-A 69 09-JUL-2002;
FEATURES Location/Qualifiers

source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1777 GACCGAGTCTACACTCACC 1795

Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1070

LOCUS AR221053/c 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 106 from patent US 6426188.
ACCESSION AR221053

VERSION AR221053.1 GI:23327938

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Wyatt,J.
TITLE Antisense modulation of phosphorylase kinase alpha 1 expression
JOURNAL Patent: US 6426188-A 106 30-JUL-2002;
FEATURES Location/Qualifiers

source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.1e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 858 GGAGCTGTGTGGAGGTGAC 876

Db 19 GCAGCCGGTGGAGGATGAC 1

RESULT 1071

LOCUS AR223313/c 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6436393.
ACCESSION AR223313

VERSION AR223313.1 GI:23331464

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)

AUTHORS Bilbao,G., Curiel,D.T. and Contreras,J.L.
TITLE Adenoviral vector encoding anti-apoptotic Bcl-2 gene and uses
thereof

JOURNAL Patent: US 6436393-A 1 20-AUG-2002;
FEATURES Location/Qualifiers

source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 1.1e+03;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1013 AGATCTCCCGCTTCCGCT 1031

Db 19 ACATCTCCCGCATCCCACT 1

RESULT 1072

LOCUS AR223403/c 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from patent US 6436400.
ACCESSION AR223403

VERSION AR223403.1 GI:23331588

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Xu,W.-f., Presnell,S.R., Yee,D.P. and Foster,D.C.
TITLE Protease-activated receptor PAR4 ZCHEMR2
JOURNAL Patent: US 6436400-A 10 20-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2415 CCCGCTGCTGTGCACGG 2433
Db 20 CCATGCTGCTGTGCTACGG 2

RESULT 1073
LOCUS AR224513/c
DEFINITION Sequence 58 from patent US 6440737.
ACCESSION AR224513
VERSION AR224513.1 GI:23333353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Freier,S.M.
TITLE Antisense modulation of cellular apoptosis susceptibility gene
expression
JOURNAL Patent: US 6440737-A 58 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2235 AGCCACCTGCTGCTGGT 2253
Db 19 AGCTAACCTGCTGCTGTT 1

RESULT 1074
LOCUS AR225072
DEFINITION Sequence 38 from patent US 6441156.
ACCESSION AR225072
VERSION AR225072.1 GI:23334207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lerman,M.I., Latif,F., Wei,M.-H., Duh,F.-M., Minna,J.D., Sekido,Y.
and Gao,B.
TITLE Calcium channel compositions and methods of use thereof
JOURNAL Patent: US 6441156-A 38 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3706 TGGTGCCAGAGGTGTAC 3724

Unclassified.
REFERENCE 2 TGGTGCCACAGCAGTAC 20
Db 2 TGGTGCCACAGCAGTAC 20

RESULT 1075
LOCUS AR231256/c
DEFINITION Sequence 30 from patent US 6451763.
ACCESSION AR231256
VERSION AR231256.1 GI:27272168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tombran-Tink,J., Chader,G.J., Becerra,S.P., Rodriguez,I.R.,
Steele,P.R. and Johnson,L.V.
TITLE Retinal pigmented epithelium derived neurotrophic factor and
methods of use
JOURNAL Patent: US 6451763-A 30 17-SEP-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2585 GTGCGCTGGCCCTCCCA 2603
Db 20 GTTCGCTCGTCGCTCCCA 2

RESULT 1076
LOCUS AR242698/c
DEFINITION Sequence 10 from patent US 6473765.
ACCESSION AR242698
VERSION AR242698.1 GI:27289188
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Fink,R.
TITLE Matching/merging two data warehouse physical data models
JOURNAL Patent: US 6473765-A 10 29-OCT-2002;
FEATURES Location/Qualifiers
source 1..20
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2415 CCCGCTGCTGTGCACGG 2433
Db 20 CCATGCTGCTGTGCTACGG 2

RESULT 1077
LOCUS AR243570/c
DEFINITION Sequence 20 from patent US 6475797.
ACCESSION AR243570
VERSION AR243570.1 GI:27290935
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
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AUTHORS      Wyatt,J.
TITLE        Antisense modulation of SR-CYP expression
JOURNAL      Patent: US 6475797-A 20 05-NOV-2002;
FEATURES     Location/Qualifiers
source       1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3242 GGAGTGTGATCCAGTGAAG 3260
    |||||
Db 20 GGTGTGACTTCAGTGAAG 2

RESULT 1078
AR255972/c
LOCUS      AR255972      20 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 31 from patent US 6482644.
ACCESSION  AR255972
VERSION     AR255972.1 GI:27305231
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cowsett,L.M.
TITLE       Antisense modulation of dual specific phosphatase 8 expression
JOURNAL     Patent: US 6482644-A 31 19-NOV-2002;
FEATURES     Location/Qualifiers
source      1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 258 GAAGCTGCTGCGCGTGC 276
    |||||
Db 19 GAAGCTGCTGCGCGCCTG 1

RESULT 1079
AR268291/c
LOCUS      AR268291      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 83 from patent US 6498035.
ACCESSION  AR268291
VERSION     AR268291.1 GI:29698566
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Wyatt,J.
TITLE       Antisense modulation of MEK3 expression
JOURNAL     Patent: US 6498035-A 83 24-DEC-2002;
FEATURES     Location/Qualifiers
source      1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3377 TTGCTGTGTGTCGCCAGGCA 3395
    |||||
Db 19 TTGCTGCTTCGCCAGGCA 1

AUTHORS      Wyatt,J.
TITLE        Antisense modulation of SR-CYP expression
JOURNAL      Patent: US 6475797-A 20 05-NOV-2002;
FEATURES     Location/Qualifiers
source       1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3242 GGAGTGTGATCCAGTGAAG 3260
    |||||
Db 20 GGTGTGACTTCAGTGAAG 2

RESULT 1078
AR255972/c
LOCUS      AR255972      20 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 31 from patent US 6482644.
ACCESSION  AR255972
VERSION     AR255972.1 GI:27305231
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cowsett,L.M.
TITLE       Antisense modulation of dual specific phosphatase 8 expression
JOURNAL     Patent: US 6482644-A 31 19-NOV-2002;
FEATURES     Location/Qualifiers
source      1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 258 GAAGCTGCTGCGCGTGC 276
    |||||
Db 19 GAAGCTGCTGCGCGCCTG 1

RESULT 1079
AR268291/c
LOCUS      AR268291      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 83 from patent US 6498035.
ACCESSION  AR268291
VERSION     AR268291.1 GI:29698566
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Wyatt,J.
TITLE       Antisense modulation of MEK3 expression
JOURNAL     Patent: US 6498035-A 83 24-DEC-2002;
FEATURES     Location/Qualifiers
source      1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3377 TTGCTGTGTGTCGCCAGGCA 3395
    |||||
Db 19 TTGCTGCTTCGCCAGGCA 1

AUTHORS      Wyatt,J.
TITLE        Antisense modulation of syntaxin 4 interacting protein expression
JOURNAL      Patent: US 6503756-A 80 07-JAN-2003;
FEATURES     Location/Qualifiers
source       1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3026 GTATATTTGTAAAGCTATT 3044
    |||||
Db 19 GTATTTTGTAAACTTTT 1

RESULT 1080
AR272010/c
LOCUS      AR272010      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 80 from patent US 6503756.
ACCESSION  AR272010
VERSION     AR272010.1 GI:29703578
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Freier,S.M. and Wyatt,J.
TITLE       Antisense modulation of syntaxin 4 interacting protein expression
JOURNAL     Patent: US 6503756-A 80 07-JAN-2003;
FEATURES     Location/Qualifiers
source      1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3026 GTATATTTGTAAAGCTATT 3044
    |||||
Db 19 GTATTTTGTAAACTTTT 1

RESULT 1081
AR279110
LOCUS      AR279110      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 243 from patent US 6514694.
ACCESSION  AR279110
VERSION     AR279110.1 GI:29713753
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Milhausen,M.J.
TITLE       Methods for the detection of encysted parasites
JOURNAL     Patent: US 6514694-A 243 04-FEB-2003;
FEATURES     Location/Qualifiers
source      1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2850 TATGGAAGAGGAAAGGCT 2868
    |||||
Db 1 TGTGGCAGAGCAAAAGGCT 19

RESULT 1082
AR299882
LOCUS      AR299882      20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 11617 from patent US 6537751.
ACCESSION  AR299882
VERSION     AR299882.1 GI:31687166
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
JOURNAL     Patent: US 6537751-A 11617 25-MAR-2003;
FEATURES     Location/Qualifiers
source      1..20
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3377 TTGCTGTGTGTCGCCAGGCA 3395
    |||||
Db 19 TTGCTGCTTCGCCAGGCA 1
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 931 TTCATCCTGGTGGTGGCGG 949
||||| ||||| |||||
Db 19 TTATCGTGGTGATTCGGG 1

RESULT 1088
AR314448/c AR314448 20 bp DNA PAT 12-JUN-2003
LOCUS Sequence 4985 from patent US 6559294.
DEFINITION AR314448
ACCESSION AR314448
VERSION AR314448.1 GI:31707874
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 4985 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1644 GCTGGTGACCGAGGACAAC 1662
||||| ||||| |||||
Db 19 GCTTGTTACCAAGACAAC 1

RESULT 1089
AR315253 AR315253 20 bp DNA PAT 12-JUN-2003
LOCUS Sequence 5790 from patent US 6559294.
DEFINITION AR315253
ACCESSION AR315253
VERSION AR315253.1 GI:31708679
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5790 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1708 CTCGACTACTACAGACA 1726
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Db 2 CTCGCTCACTACAGACA 20

RESULT 1090
AR316159 AR316159 20 bp DNA PAT 12-JUN-2003
LOCUS Sequence 6696 from patent US 6559294.
DEFINITION AR316159
ACCESSION AR316159

VERSION AR316159.1 GI:31709585
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Hoiseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 6696 06-MAY-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2613 CTGAGCCTGCAGGAGCC 2631
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Db 2 CTGACCTTGCAGGAGATCC 20

RESULT 1091
AR342815/c AR342815 20 bp DNA PAT 17-AUG-2003
LOCUS Sequence 4 from patent US 6576468.
DEFINITION AR342815
ACCESSION AR342815
VERSION AR342815.1 GI:33738019
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Nicolaides, N.C., Grasso, L. and Sass, P.M.
TITLE Methods for obtaining microbe-resistant mammalian cells from hypermutable mammalian cells
JOURNAL Patent: US 6576468-A 4 10-JUN-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACCGAGTCTACCTCACC 1795
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Db 20 GACAGAGTCTTCACTAACC 2

RESULT 1092
AR361086/c AR361086 20 bp DNA PAT 17-AUG-2003
LOCUS Sequence 3 from patent US 6599695.
DEFINITION AR361086
ACCESSION AR361086
VERSION AR361086.1 GI:33768789
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gage, F.H. and Ray, J.
TITLE Method for assaying for early gene expression in neuroblasts
JOURNAL Patent: US 6599695-A 3 29-JUL-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;


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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 GACGAGTCTACACTCACC 1795
|||||
Db 20 GACAGAGTCTTCACTTACC 2

RESULT 1098
AR382950/c AR382950 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 190 from patent US 6610539.
ACCESSION AR382950
VERSION AR382950.1 GI:40091763
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences as inhibitors of microorganisms
JOURNAL Patent: US 6610539-A 190 26-AUG-2003;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2004 GCTGGTGGAGGACCTGGAC 2022
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Db 19 GCTGGTGGAGGACGAGTGGAC 1

RESULT 1099
AR408461/c AR408461 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 66 from patent US 6632607.
ACCESSION AR408461
VERSION AR408461.1 GI:40158627
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS De Beenhouwer, H., Portael, F., Machtelinckx, L., Jannes, G. and
Rossau, R.
TITLE Mycobacterium antibiotic resistance detection
JOURNAL Patent: US 6632607-A 66 14-OCT-2003;
FEATURES
source
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 355 GAGTTCGCGCGGAGCACC 373
|||||
Db 20 GAGTTCGCGGAGTGGAC 2

RESULT 1100
AR437052/c AR437052 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 104 from patent US 6656732.
ACCESSION AR437052
VERSION AR437052.1 GI:40200137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of src-c expression
JOURNAL Patent: US 6656732-A 104 02-DEC-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1533 GGAGCAGCTCAGCTTCAAG 1551
|||||
Db 20 GGAGCGGCCACCTTCGAG 2

RESULT 1101
AR437053 AR437053 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 105 from patent US 6656732.
ACCESSION AR437053
VERSION AR437053.1 GI:40200137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of src-c expression
JOURNAL Patent: US 6656732-A 105 02-DEC-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 736 CTAGAGGTTCTCTCCTTGC 754
|||||
Db 1 CTAGAGGTTCTCTCCCGGC 19

RESULT 1102
AR437098/c AR437098 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 150 from patent US 6656732.
ACCESSION AR437098
VERSION AR437098.1 GI:40200182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C.F. and Watt, A.T.
TITLE Antisense inhibition of src-c expression
JOURNAL Patent: US 6656732-A 150 02-DEC-2003;
FEATURES
source
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1100 AR437052 20 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 104 from patent US 6656732.
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1214 AGGCTGCTTCGGCCAGGT 1232
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Db 19 AGGTTGCTTCGGAGAGGT 1

RESULT 1103
AR451291/c
LOCUS AR451291 20 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9 from patent US 6673913.
ACCESSION AR451291
VERSION AR451291.1 GI:42682269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Sakaguchi, N. and Kuwahara, K.
TITLE GANP proteins
JOURNAL Patent: US 6673913-A 9 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 246 GCGATGGACAGAAGCTG 264
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Db 20 GCTTTGGACAGAAGCTG 2

RESULT 1104
AR488805
LOCUS AR488805 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 6 from patent US 6709817.
ACCESSION AR488805
VERSION AR488805.1 GI:47255003
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Zoghbi, H.Y., Van den Veyver, I.B., Amir, R. and Francke, U.
TITLE Method of screening Rett syndrome by detecting a mutation in MECP2
JOURNAL Patent: US 6709817-A 6 23-MAR-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2154 GCTGCCCGCCGCCACCC 2172
|||
Db 1 GTTCCCGCCGCCACCC 19

RESULT 1105
AR492019/c
LOCUS AR492019 20 bp mRNA linear PAT 15-MAY-2004
DEFINITION Sequence 233 from patent US 6716600.
ACCESSION AR492019
VERSION AR492019.1 GI:47260384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Johnson, E.M., Milbrandt, J.D., Kotzbauer, P.T., Lampe, P.A., Klein, R. and DeSautage, F.
TITLE Persephin and related growth factors
JOURNAL Patent: US 6716600-A 233 06-APR-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="mRNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3660 CTGCAGGCCATGGCTCAG 3678
|||||
Db 19 CTGCAGGCCAGGGCGAG 1

RESULT 1106
AR492377
LOCUS AR492377 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 76 from patent US 6716627.
ACCESSION AR492377
VERSION AR492377.1 GI:47260951
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dobie, K.W.
TITLE Antisense modulation of mucin 1, transmembrane expression
JOURNAL Patent: US 6716627-A 76 06-APR-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2380 CATCTTGCTTCAGGTGCA 2398
|||||
Db 1 CATTTTGCTCTGGTGCA 19

RESULT 1107
AR492685/c
LOCUS AR492685 20 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 55 from patent US 6716975.
ACCESSION AR492685
VERSION AR492685.1 GI:47262199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Wyatt, J.
TITLE Antisense modulation of EDG1 expression
JOURNAL Patent: US 6716975-A 55 06-APR-2004;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 933 CATCTTGGTGGCGGCT 951
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Db 19 CAGCCTGGTGTGTCGGGT 1

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RESULT 1108
AX080337
LOCUS AX080337 20 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 7 from Patent WO0107647.
ACCESSION AX080337
VERSION AX080337.1 GI:13159795
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Berlin, K.
TITLE Method for relative quantization of methylation of cytosin-type
bases in dna samples
JOURNAL Patent: WO 0107647-A 7 01-FEB-2001;
Epigenomics AG (DE)
FEATURES
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1. .20
/organism="Homo sapiens"
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/db_xref="taxon:9606"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2447 GCTGCAGCAGCGGGGCC 2465
Db 2 GCTGCAGCAGCTGGGGGCC 20
RESULT 1109
AX080338/c
LOCUS AX080338 20 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 8 from Patent WO0107647.
ACCESSION AX080338
VERSION AX080338.1 GI:13159796
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Berlin, K.
TITLE Method for relative quantization of methylation of cytosin-type
bases in dna samples
JOURNAL Patent: WO 0107647-A 8 01-FEB-2001;
Epigenomics AG (DE)
FEATURES
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1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2447 GCTGCAGCAGCGGGGCC 2465
Db 19 GCTGCAGCAGCTGGGGAGCC 1
RESULT 1110
AX148837/c
LOCUS AX148837 20 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 39 from Patent WO0136625.
ACCESSION AX148837
VERSION AX148837.1 GI:14347361
KEYWORDS

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groel and groes as
inhibitors of microorganisms
JOURNAL Patent: WO 0136625-A 39 25-MAY-2001;
Genesense Technologies Inc. (CA)
FEATURES
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1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Antisense oligonucleotide"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1298 AGATGCTGAAGAGCATGC 1316
Db 19 AGATGCTGAAGAGAGTTGC 1
RESULT 1111
AX149220
LOCUS AX149220 20 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 422 from Patent WO0136625.
ACCESSION AX149220
VERSION AX149220.1 GI:14347744
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Wright, J.A., Young, A.H. and Dugourd, D.
TITLE Antisense oligonucleotide sequences derived from groel and groes as
inhibitors of microorganisms
JOURNAL Patent: WO 0136625-A 422 25-MAY-2001;
Genesense Technologies Inc. (CA)
FEATURES
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/db_xref="taxon:32630"
/note="Antisense oligonucleotide"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3120 ATTTTAACTTATTGACAA 3138
Db 2 ATTTTCACTTTTGGAA 20
RESULT 1112
AX167126
LOCUS AX167126 20 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 13 from Patent WO0144455.
ACCESSION AX167126
VERSION AX167126.1 GI:14596614
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Beri, R.
TITLE Antisense oligonucleotides
JOURNAL Patent: WO 0144455-A 13 21-JUN-2001;
Astrazeneca AB (SE)

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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      /note="Antisense oligonucleotide"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3652 TTGCTTGCTCGAGGCGCA 3670
Db 1 TTTCGCCAGCAGCGGCGCA 19

RESULT 1113
AX224922
LOCUS AX224922 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 76 from Patent WO0161030.
ACCESSION AX224922
VERSION AX224922.1 GI:15554995
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gray, D.M. and Bollon, A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna
for control of gene expression
JOURNAL Patent: WO 0161030-A 76 23-AUG-2001; University of Texas at
Cytoclonal Pharmaceuticals, Inc. (US); Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES
source
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 529 CGGCCCATCTCGAGCGG 547
Db 1 CGCGCGAGCTGCGAGCGG 19

RESULT 1114
AX224927
LOCUS AX224927 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 81 from Patent WO0161030.
ACCESSION AX224927
VERSION AX224927.1 GI:15555000
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gray, D.M. and Bollon, A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna
for control of gene expression
JOURNAL Patent: WO 0161030-A 81 23-AUG-2001; University of Texas at
Cytoclonal Pharmaceuticals, Inc. (US); Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
Experimental Carcinogenesis, National Cancer Institute/NIH (US)
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source
  Location/Qualifiers
    1..20
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 529 CGGCCCATCTCGAGCGG 547
Db 1 CGCGCGAGCTGCGAGCGG 19

RESULT 1114
AX224927
LOCUS AX224927 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 81 from Patent WO0161030.
ACCESSION AX224927
VERSION AX224927.1 GI:15555000
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gray, D.M. and Bollon, A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna
for control of gene expression
JOURNAL Patent: WO 0161030-A 81 23-AUG-2001; University of Texas at
Cytoclonal Pharmaceuticals, Inc. (US); Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES
source
  Location/Qualifiers
    1..20
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 529 CGGCCCATCTCGAGCGG 547
Db 1 CGCGCGAGCTGCGAGCGG 19

RESULT 1115
AX295702/c
LOCUS AX295702 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 7464 from Patent WO0179548.
ACCESSION AX295702
VERSION AX295702.1 GI:17057391
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 7464 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
  Location/Qualifiers
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Hypothetical Probe Sequence"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1053 GTCCAACGGTCCATGAGC 1071
Db 20 GTCCAACGGTGCATCCGC 2

RESULT 1116
AX296663
LOCUS AX296663 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 8425 from Patent WO0179548.
ACCESSION AX296663
VERSION AX296663.1 GI:17058352
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 8425 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source
  Location/Qualifiers
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      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Hypothetical Probe Sequence"

Query Match
  Best Local Similarity 0.4%; Score 14.2; DB 1; Length 20;
  Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2327 GTGTGCGCTGTGTGTG 2345
Db 1 GTGCGTGCAGTCTGTGTG 19
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RESULT 1117
AX296746
LOCUS AX296746 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 8508 from Patent WO0179548.
ACCESSION AX296746
VERSION AX296746.1 GI:17058435
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Barany,P., Zirvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 8508 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2958 GTCTCACCCTGCAAGCAG 2976
Db 1 GTCTCAGCAGAAAGCAG 19

RESULT 1118
AX298596/c
LOCUS AX298596 20 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 230 from Patent WO0183749.
ACCESSION AX298596
VERSION AX298596.1 GI:17128586
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
TITLE Gene and sequence variation associated with sensing carbohydrate
compounds and other sweeteners
JOURNAL Patent: WO 0183749-A 230 08-NOV-2001;
WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
(US)
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/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 279 CGCCACACCTGCTCCCTTC 297
Db 19 CTCCACACTGCTCCCTTC 1

RESULT 1119
AX298894
LOCUS AX298894 20 bp DNA linear PAT 26-NOV-2001
DEFINITION Sequence 528 from Patent WO0183749.
ACCESSION AX298894

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VERSION AX298894.1 GI:17128884
KEYWORDS Mus sp.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1
AUTHORS Bachmanov,A.A., Beauchamp,G.K., Chatterjee,A., de Jong,P.J., Li,S.,
Li,X., Ohmen,J.D., Reed,D.R., Ross,D. and Tordoff,M.G.
TITLE Gene and sequence variation associated with sensing carbohydrate
compounds and other sweeteners
JOURNAL Patent: WO 0183749-A 528 08-NOV-2001;
WARNER-LAMBERT COMPANY (US) ; The Monell Chemical Senses Center
(US)
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/mol_type="unassigned DNA"
/db_xref="taxon:10095"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 824 ACTCTGCTGCTGCTGCTG 842
Db 2 ACTGTACGTGCTGCTGCTG 20

RESULT 1120
AX317742/c
LOCUS AX317742 20 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 3 from Patent WO0190313.
ACCESSION AX317742
VERSION AX317742.1 GI:17900627
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Feinberg,A.T., Strichman-Almashanu,L.T. and Jiang,S.C.
TITLE Methods for assaying gene imprinting and methylated cpg islands
JOURNAL Patent: WO 0190313-A 3 29-NOV-2001;
The Johns Hopkins University (US)
FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1346 CTGAGATGGAGATGATGAA 1364
Db 20 CTGAGATGGAGATGAACAA 2

RESULT 1121
AX342778
LOCUS AX342778 20 bp DNA linear PAT 12-JAN-2002
DEFINITION Sequence 45 from Patent WO0198474.
ACCESSION AX342778
VERSION AX342778.1 GI:18152134
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Delcours,J., Debyser,W., Gebruers,K., Goesaert,H., Fierens,K.,
Robben,J. and van Campenhout,S.

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Query Match	0.4%;	Score 14.2;	DB 1;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;		
Matches	16;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
Qy	622	CCCCACATCCAGTGGCTCA	640	
Db	2	CCCCACATACAGAGGCTAA	20	
RESULT 1124				
LOCUS	AX487048	20 bp	DNA	linear
DEFINITION	Sequence 4348 from Patent WO02053728.			
ACCESSION	AX487048			
VERSION	AX487048.1 GI:22321196			
KEYWORDS	Candida albicans			
SOURCE	Candida albicans			
ORGANISM	Candida albicans			
REFERENCE	1 Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.			
AUTHORS	Gene disruption methodologies for drug target discovery			
TITLE	Patent: WO 02053728-A 4348 11-JUL-2002;			
JOURNAL	Elitra Pharmaceuticals, Inc. (US)			
FEATURES	Location/Qualifiers			
source	1..20			
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	/db_xref="taxon:5476"			
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Best Local Similarity	84.2%;	Pred. No. 1.1e+03;		
Matches	16;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
Qy	1638	CAATGTCTCGTGACCGAG	1656	
Db	1	CAATGAGCTCGTGACCGTG	19	
RESULT 1125				
LOCUS	AX488257	20 bp	DNA	linear
DEFINITION	Sequence 5557 from Patent WO02053728.			
ACCESSION	AX488257			
VERSION	AX488257.1 GI:22322337			
KEYWORDS	Candida albicans			
SOURCE	Candida albicans			
ORGANISM	Candida albicans			
REFERENCE	1 Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L.			
AUTHORS	Gene disruption methodologies for drug target discovery			
TITLE	Patent: WO 02053728-A 5557 11-JUL-2002;			
JOURNAL	Elitra Pharmaceuticals, Inc. (US)			
FEATURES	Location/Qualifiers			
source	1..20			
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Query Match	0.4%;	Score 14.2;	DB 1;	Length 20;
Best Local Similarity	84.2%;	Pred. No. 1.1e+03;		
Matches	16;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
Qy	829	GCGTGGCTGGTGGCTGC	847	
Db	2	GAGTGGCTGGTGGTTGC	20	
RESULT 1126				

AX589229
LOCUS AX589229 20 bp DNA linear PAT 24-JAN-2003
DEFINITION Sequence 16 from Patent WO02084567.
ACCESSION AX589229
VERSION AX589229.1 GI:27900830
SOURCE Rattus rattus (black rat)
ORGANISM Rattus rattus
REFERENCE Rattus rattus
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
JOURNAL Rattus.
FEATURES
1 Soullou, J.P., Delsuc, M.A., Guillet, M., Sebille, F., Brouard, S.,
Gagne, K., Vanhove, B. and Pallier, A.
METHOD for analyzing T lymphocytes with the aid of T lymphocyte
receptors of an organism
PATENT: WO 02084567-A 16 24-OCT-2002;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:10117"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 326. CCTCCATCTCCTGGCTGAA 344
Db 2 CATCCATCTCCAGCTGAA 20
RESULT 1127
AX658511/c
LOCUS AX658511 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 427 from Patent WO03000928.
ACCESSION AX658511
VERSION AX658511.1 GI:29160868
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Poulsen, H.S., Pedersen, N., Mortensen, S., Sorensen, S.B.,
Petersen, M.W. and Elisner, H.I.
METHODS for identification of cancer cell surface molecules and
cancer specific promoters, and therapeutic uses thereof
PATENT: WO 03000928-A 427 03-JAN-2003;
JOURNAL Odin Medical A/S (DK)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 395 GGCATCAGCAGTGGAGCT 413
Db 20 GGCATCAGCAGTGGAGCT 2
RESULT 1128
AX665329
LOCUS AX665329 20 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 87 from Patent WO03002765.
ACCESSION AX665329
VERSION AX665329.1 GI:29290452

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Sellar, G.C. and Gabra, H.
JOURNAL Cancer
PATENT: WO 03002765-A 87 09-JAN-2003;
Cancer Research Technology Limited (GB)
FEATURES Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2101 GACACCCCGAGCTCCAGCT 2119
Db 2 GCGACCCCGAGCTCCAGCT 20
RESULT 1129
AX719302/c
LOCUS AX719302 20 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 17 from Patent WO03022298.
ACCESSION AX719302
VERSION AX719302.1 GI:29891742
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE Giraudo, P., Belin, M.F., Malcus, C., Colas, P., Antoine, J.C. and
Honorat, J.
TITLE Utilisation d'une proteine de la famille des crmps pour le
traitement des maladies liees au systeme immunitaire
PATENT: WO 03022298-A 17 20-MAR-2003;
JOURNAL INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
(FR)
FEATURES Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1989 GCCACCTTCAAGCAGCTG 2007
Db 20 GTCCACCTTCCAGCAGATG 2
RESULT 1130
AX743793/c
LOCUS AX743793 20 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 10 from Patent WO03031985.
ACCESSION AX743793
VERSION AX743793.1 GI:30722545
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE Akerblad, P. and Sigvardsson, M.
AUTHORS Method for identification of modulators of pre-adipocyte
TITLE differentiation

JOURNAL Patent: WO 0301985-A 10 17-APR-2003;

Astrazeneca AB (SE)

FEATURES Location/Qualifiers

source
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/notes="PCR Forward Primer mc/EB Prev"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2041 TCCACCGACGAGTACTGG 2059

Db 20 TTCAACGACGAGTCTCTGG 2

RESULT 1131

AX776233/c AX776233 20 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 3 from Patent WO03048362.

ACCESSION AX776233

VERSION AX776233.1 GI:32693889

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Farrar, G.J., Humphries, P., Millington-Ward, S. and Kenna, P.F.

TITLE Suppression of polymorphic alleles

JOURNAL Patent: WO 03048362-A 3 12-JUN-2003;

College of the Holy and Undivided Trinity of Queen Elizabeth (IE)

FEATURES Location/Qualifiers

source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' human rhodopsin primer over BstEII site"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1897 AAGGAGGGCCACCGCATGG 1915

Db 20 AAGGAGGTACCCGCATGG 2

RESULT 1132

AX804534/c AX804534 20 bp DNA linear PAT 25-NOV-2003
DEFINITION Sequence 702 from Patent WO03060160.

ACCESSION AX804534

VERSION AX804534.1 GI:38521675

KEYWORDS Oreochromis niloticus

SOURCE Oreochromis niloticus (Nile tilapia)

ORGANISM Oreochromis niloticus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidae; Cichlidae; Oreochromis.

REFERENCE 1

AUTHORS Lie, Y., Slettan, A., Hoeyum, M. and Lingaas, P.

TITLE Verification of food origin based on nucleic acid pattern

JOURNAL recognition

Patent: WO 03060160-A 702 24-JUL-2003;

Genomax ASA (NO)

FEATURES Location/Qualifiers

source
1..20
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/mol_type="unassigned DNA"
/db_xref="taxon:8128"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2676 TCCCGACCTCCAGGCTTTC 2694

Db 20 TCACACCTCCTGCTCTTC 2

RESULT 1133

AX923443 AX923443 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 20 from Patent WO03080816.

ACCESSION AX923443

VERSION AX923443.1 GI:40216492

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Andrews, P. and Draper, J.

TITLE Stem cell culture

JOURNAL Patent: WO 03080816-A 20 02-OCT-2003;

THE UNIVERSITY OF SHEFFIELD (GB)

FEATURES Location/Qualifiers

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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 174 TGACGAAGACGGGAGGAC 192

Db 2 TGACCAAGACTGAGAGGAC 20

RESULT 1134

AX938959 AX938959 20 bp DNA linear PAT 07-JAN-2004
DEFINITION Sequence 14 from Patent EP1362914.

ACCESSION AX938959

VERSION AX938959.1 GI:40733318

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Nakanishi, O. and Tatamiya, T.

TITLE Histone deacetylase inhibitor and use thereof

JOURNAL Patent: EP 1362914-A 14 19-NOV-2003;

Schering AG (DE)

FEATURES Location/Qualifiers

source
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/organism="synthetic construct"
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/db_xref="taxon:32630"

Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2117 GCTCCTCAGGGGACGACTC 2135

Db 2 GCTCCTCAGGGGACTGCC 20

RESULT 1135

AX958421/c

Best Local Similarity 84.4%; Pseud. NO.: 0; Gaps 0;
Matches 16; Conservative Mismatches 3; Indels

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QY 1812 CTTGGGGTCTGCTCTGG 1830
Db 19 CTGTGGTCCCTGCTCTGG 1

RESULT 1139
BD017353/c
LOCUS BD017353 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide modulation of protein kinase C-eta.
ACCESSION BD017353
VERSION BD017353.1 GI:22558529
KEYWORDS JP 2001231579-A/91.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, F.C., Boggs, R.T. and Dean, N.M.
TITLE Oligonucleotide modulation of protein kinase C-eta
JOURNAL Patent: JP 2001231579-A 91 28-AUG-2001;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001231579-A/91
PD 28-AUG-2001
PR 13-DEC-2000 JP 2000379234
PR 09-JUL-1993 US 08/089996, 22-FEB-1994 US 08/199779 PI
FRANK C BENNETT, RUSSELL T BOGGS, NICHOLAS M DEAN PC
C12N15/09, A61K31/711, A61K31/712, A61K48/00, A61P29/ PC
00, A61P35/00,
PC A61P43/00, C07H21/00, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, PC
G01N33/50,
PC G01N33/53, G01N33/566//C12N5/10, G01N33/68, C12N15/00, C12N5/00 CC
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FH Key Location/Qualifiers
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FT /organism='Artificial Sequence'.

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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1812 CTTGGGGTCTGCTCTGG 1830
Db 19 CTGTGGTCCCTGCTCTGG 1

RESULT 1140
BD074637
LOCUS BD074637 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotide composition and modulation method of JNK
protein.
ACCESSION BD074637
VERSION BD074637.1 GI:22620240
KEYWORDS JP 2001514905-A/61.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS McKay, R., Dean, N., Monia, B.P., Scott, P., Nero and Gaarde, W.A.
TITLE Antisense oligonucleotide composition and modulation method of JNK
JOURNAL Patent: JP 2001514905-A 61 18-SEP-2001;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2001514905-A/61
PD 18-SEP-2001
PR 07-AUG-1998 JP 2000509875
PR 13-AUG-1997 US 08/910629
PI ROBERT MCKAY, NICHOLAS DEAN, BRETT P MONIA, PAMELA SCOTT PI

NERO, WILLIAM A GAARDE
PC C12Q1/68, A61K31/7088, A61K48/00, A61P35/00, C12N15/09, C12P19/34,
PC C12N15/00
CC antisense sequence
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FT /organism='Artificial Sequence'.

FEATURES
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3379 GCTGTGTGTCGCCGAGCAGG 3397
Db 2 GCTGGGTTTCGCGAGCAGG 20

RESULT 1141
BD081247/c
LOCUS BD081247 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Persephin and related growth factors.
ACCESSION BD081247
VERSION BD081247.1 GI:22626850
KEYWORDS JP 2001516764-A/125.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Johnson, E.M., Milbrandt, J.D., Kotzbauer, P.T., Lampe, P.A., Klein, R.
and Desauvage, F.
TITLE Persephin and related growth factors
JOURNAL Patent: JP 2001516764-A 125 02-OCT-2001;
COMMENT WASHINGTON UNIVERSITY
OS Homo sapiens (human)
PN JP 2001516764-A/125
PD 02-OCT-2001
PR 15-SEP-1998 JP 2000511783
PR 16-SEP-1997 US 08/931858
PI EUGENE M JOHNSON, JEFFREY D MILBRANDT, PAUL
T KOTZBAUER, PATRICIA
PI A LAMPE,
PI ROBERT KLEIN, FRED DESAUVAGE
PC C07K14/475, A61K31/7088, A61K38/00, A61K48/00, C07K16/26, C12N1/21,
PC C12N5/10,
PC C12N15/09, C12P19/34, C12P21/02, C12Q1/68, G01N33/53, A61K37/02, PC
C12N5/00,
PC C12N15/00
CC Persephin and related growth factors
FH Key Location/Qualifiers
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FEATURES
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/mol_type="genomic DNA"
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3660 CTGCAGGCCATGGCTCAG 3678
Db 19 CTGCAGGCCAGGCGCAG 1

RESULT 1142

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BD123453/c
LOCUS BD123453 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of incubating microplate.
ACCESSION BD123453
VERSION BD123453.1 GI:23218398
KEYWORDS JP 2002022749-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ando,K.
TITLE Method of incubating microplate.
JOURNAL Patent: JP 2002022749-A 3 23-JAN-2002;
FUJIREBIO INC
COMMENT OS Artificial Sequence
PN JP 2002022749-A/3
PD 23-JAN-2002
PF 07-JUL-2000 JP 2000206033
PI KEN ANDO
PC GOIN35/00,GOIN1/28,GOIN33/543//C12M1/00,C12N15/09,GOIN1/28, PC
C12N15/00
CC Nucleic acid for probe hybridization assay (B probe) FH Key
FT source 1..20
FT Location/Qualifiers
/organism='Artificial Sequence'.
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 318 CCCCACTCCCTCCATCTCC 336
Db 20 CACCACCTTCCTCCATCTCC 2
RESULT 1143
BD140699
LOCUS BD140699 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Methods for the simultaneous identification of novel biological
targets and lead structures for drug development.
ACCESSION BD140699.1 GI:23235644
VERSION BD140699.1 GI:23235644
KEYWORDS JP 2002508507-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Heffner,D.L., Zepp,C.M., Gao,Y. and Jones,S.W.
TITLE Methods for the simultaneous identification of novel biological
targets and lead structures for drug development
JOURNAL Patent: JP 2002508507-A 1 19-MAR-2002;
SEPRACOR INC
COMMENT OS Artificial Sequence
PN JP 2002508507-A/1
PD 19-MAR-2002
PF 18-DEC-1998 JP 2000539165
PI DONALD L HEEFNER,CHARLES M ZEPP,YUN GAO,STEVEN W JONES PC
GOIN33/542,C12Q1/04,C12Q1/68,C12Q1/70,GOIN21/00,GOIN21/76, PC
GOIN33/53
PC GOIN33/566//C12N15/09,C12N15/00
CC Description of Artificial Sequence: construct FH Key
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source
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/organism='synthetic construct'

/mol_type='genomic DNA'
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Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 3463 TATATATATCTATATATAT 3481
Db 2 TATATGATTCATATATAT 20
RESULT 1144
BD167962
LOCUS BD167962 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of constructing mutation DNA library and utilization
thereof.
ACCESSION BD167962
VERSION BD167962.1 GI:27873774
KEYWORDS WO 0226964-A/9.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tsuji,T. and Yanagawa,H.
TITLE Method of constructing mutation DNA library and utilization thereof
JOURNAL Patent: WO 0226964-A 9 04-APR-2002;
MITSUBISHI CHEMICAL CORP,TORU TSUJI,HIROSHI YANAGAWA
COMMENT OS Artificial Sequence
PN WO 0226964-A/9
PD 04-APR-2002
PF 26-SEP-2001 WO 2001JP008387
PR 27-SEP-2000 JP 00P 293692,06-FEB-2001 JP 01P 029138 PI
TORU TSUJI,HIROSHI YANAGAWA
PC C12N15/09,C12P21/02
CC Description of Artificial Sequence:Synthesized FH Key
FT source 1..20
FT Location/Qualifiers
/organism='Artificial Sequence'.
FEATURES
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/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1679 ACTTCGGGCTGCCCGGGA 1697
Db 2 ACTTCGGGATGCCCCAGGA 20
RESULT 1145
BD271421/c
LOCUS BD271421 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Fab fragment libraries and method of using the same.
ACCESSION BD271421
VERSION BD271421.1 GI:33081189
KEYWORDS JP 2002543830-A/13.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hoogenboom,H.R.J.M.
TITLE Novel Fab fragment libraries and method of using the same
JOURNAL Patent: JP 2002543830-A 13 24-DEC-2002;
DVAX CORP
COMMENT OS Artificial Sequence
PN JP 2002543830-A/13
PD 24-DEC-2002
PF 18-MAY-2000 JP 2000618429

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PR 18-MAY-1999 EP 99201558.6
PI HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
C12N15/09,C07K16/34,G01N33/53,C12N15/00
CC Description of Artificial Sequence: Primer
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                    /db_xref="taxon:32630"
Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 23;
Matches 16; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 2098 CAGGACACCCAGCTCCAGCTC 2120
DB 23 CCRGWCTCCACGCTGCACCTC 1
RESULT 1146
LOCUS AR409907 23 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 20 from patent US 6635422.
ACCESSION AR409907
VERSION AR409907.1 GI:40161042
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
TITLE Methods for isolating and characterizing endogenous mRNA-protein
(mRNP) complexes
JOURNAL Patent: US 6635422-A 20 21-OCT-2003;
FEATURES
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                    /mol_type="unassigned RNA"
Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3115 TTTTAAATTTTAACTTATT 3133
DB 2 TTTTAAATTTTAAATTTT 20
RESULT 1147
AR264929
LOCUS AR264929 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 13 from patent US 6492121.
ACCESSION AR264929
VERSION AR264929.1 GI:29693316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokonaka,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6492121-A 13 10-DEC-2002;
FEATURES
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                    /mol_type="genomic DNA"
PR 18-MAY-1999 EP 99201558.6
PI HENDRICUS RENERUS JACOBUS MATTHEUS HOOGENBOOM PC
C12N15/09,C07K16/34,G01N33/53,C12N15/00
CC Description of Artificial Sequence: Primer
FH Key Location/Qualifiers
FT source 1..23
FT /organism='Artificial Sequence'.
FEATURES
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        1..23
            Location/Qualifiers
                1..23
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 30;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
DB 3 ATATATTTTTCCTTTTCCTTTT 29
RESULT 1148
AR478210
LOCUS AR478210 30 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 13 from patent US 6699661.
ACCESSION AR478210
VERSION AR478210.1 GI:47236858
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokonaka,T., Koyama,O. and Furusho,K.
TITLE Method for determining a concentration of target nucleic acid
molecules, nucleic acid probes for the method, and method for
analyzing data obtained by the method
JOURNAL Patent: US 6699661-A 13 02-MAR-2004;
FEATURES
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            Location/Qualifiers
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                    /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.4%; Score 14.2; DB 1; Length 30;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTTGCTTTCCTTTT 3285
DB 3 ATATATTTTTCCTTTTCCTTTT 29
RESULT 1149
BD072869
LOCUS BD072869 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method.
ACCESSION BD072869
VERSION BD072869.1 GI:22618472
KEYWORDS JP 2001286300-A/7.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
Yokonaka,T., Koyama,O. and Furusho,K.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor,
and method for analyzing data obtained by that method
JOURNAL Patent: JP 2001286300-A 7 16-OCT-2001;
JAPAN BIO INDUSTRY ASSOCIATION KANKYO ENG KK, DIRECTOR GENERAL OF
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT
OS Artificial Sequence
PN JP 2001286300-A/7
PD 16-OCT-2001
PF 20-APR-2000 JP 2000120097
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,VOICHI KAMAGATA,SHINYA PI
KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
PC C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
G01N33/566,
PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
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COMMENT
OS Artificial Sequence
PN JP 2002000275-A/10
PD 08-JAN-2002
PF 27-JUN-2000 JP 2000193133
PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI
    KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/34,C12Q1/68,C12Q1/68,C12N15/00 CC The base
sequence was prepared synthetically on the aim of CC
examining the
CC decrease in fluorescence emission of a nucleic acid probe CC
labeled with
CC BODIBY FL/C6 upon the hybridization of the
probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1..30
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FEATURES
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        Location/Qualifiers
        1..30
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        /db_xref="taxon:32630"
Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTGCTTTGTCCTTTT 3285
    ||||| ||| ||| ||| |||
DB 3 ATATATTTTTCCTTTTTCCTTTT 29
    ||||| ||| ||| ||| |||
RESULT 1154
BD145028
LOCUS
DEFINITION
    Method for assaying nucleic acid, nucleic acid probe used therefor,
    and method for analyzing data obtained by that method.
ACCESSION
    BD145028.1 GI:27850786
KEYWORDS
    JP 2002119291-A/9.
SOURCE
    synthetic construct
ORGANISM
    artificial sequences.
REFERENCE
    1 (bases 1 to 30)
AUTHORS
    Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
    Yamada,K. and Yokomaku,T.
TITLE
    Method for assaying nucleic acid, nucleic acid probe used therefor,
    and method for analyzing data obtained by that method
JOURNAL
    Patent: JP 2002119291-A 9 23-APR-2002;
    JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
    INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
    OS Artificial Sequence
    PN JP 2002119291-A/9
    PD 23-APR-2002
    PF 27-APR-2001 JP 2001133529
    PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
    TORIMURA,
    SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
    C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/
    53,
    G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
    PC G01N1/28,
    PC G01N1/28,
    CC The base sequence was prepared synthetically on the aim of CC
    decrease in fluorescence emission of
    a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
    hybridization of
    the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1..30
    /organism="Artificial Sequence".
FEATURES
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        Location/Qualifiers
        1..30
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match 0.4%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3259 AGATATTTTATTGCTTTGTCCTTTT 3285
    ||||| ||| ||| ||| |||
DB 3 ATATATTTTTCCTTTTTCCTTTT 29
    ||||| ||| ||| ||| |||
RESULT 1155
BD145028
LOCUS
DEFINITION
    Method for assaying nucleic acid, nucleic acid probe used therefor,
    and method for analyzing data obtained by that method.
ACCESSION
    BD145028.1 GI:27850786
KEYWORDS
    JP 2002119291-A/9.
SOURCE
    synthetic construct
ORGANISM
    artificial sequences.
REFERENCE
    1 (bases 1 to 30)
AUTHORS
    Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
    Yamada,K. and Yokomaku,T.
TITLE
    Method for assaying nucleic acid, nucleic acid probe used therefor,
    and method for analyzing data obtained by that method
JOURNAL
    Patent: JP 2002119291-A 9 23-APR-2002;
    JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
    INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT
    OS Artificial Sequence
    PN JP 2002119291-A/9
    PD 23-APR-2002
    PF 27-APR-2001 JP 2001133529
    PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI
    TORIMURA,
    SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
    C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/
    53,
    G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
    PC G01N1/28,
    PC G01N1/28,
    CC The base sequence was prepared synthetically on the aim of CC
    decrease in fluorescence emission of
    a nucleic acid probe labeled with BODIBY FL/C6 upon the CC
    hybridization of
    the probe with a target nucleic acid.
FH Key Location/Qualifiers

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JOURNAL Patent: JP 2002191372-A 109 09-JUL-2002;
 NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
 KANKYO ENGINEERING CO LTD
 COMMENT OS Artificial Sequence
 PN JP 2002191372-A/109
 PP 09-JUL-2002
 PP 26-SEP-2001 JP 2001295145
 PI RYUICHIRO KURANE, TAKAHIRO KANAGAWA, YOICHI KAMAGATA, MASAKI PI
 TORIMURA,
 PI SHINYA KURATA, KAZUTAKA YAMADA, TOYOKAZU YOKOMAKU PC
 C12N15/09, C12M1/00, C12Q1/68, G01N33/58, G01N33/53, G01N33/566, PC
 C12N15/00
 CC The base sequence was prepared synthetically on the aim of CC
 examining the
 CC decrease in fluorescence emission of a nucleic acid probe CC
 labeled with
 CC BODIBY Flr/C6 upon the hybridization of the
 probe with a target
 CC nucleic
 CC acid,
 CC and the base sequence was used as that of the probe. FH Key
 Location/Qualifiers
 FT source 1..30
 FT Location/Qualifiers
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 /organism='Artificial Sequence'.
 /organism="unidentified"
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 /db_xref="taxon:32644"
 Query Match 0.4%; Score 14.2; DB 1; Length 30;
 Best Local Similarity 70.4%; Pred. No. 1.5e+03;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 Qy 3259 AGATATTTATTTGCTTTGTCCTTTT 3285
 Db | | | | | | | | | | | | | | | | | | | |
 3 ATATATTTTATTTTGTGTTTGTGTTT 29
 RESULT 1157
 AX248879/c AX248879 31 bp DNA linear PAT 28-SEP-2001
 LOCUS Sequence 958 from Patent WO0166800.
 DEFINITION AX248879
 ACCESSION AX248879
 VERSION AX248879.1 GI:15863502
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
 TITLE Human single nucleotide polymorphisms
 JOURNAL Patent: WO 0166800-A 958 13-SEP-2001;
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
 FEATURES Location/Qualifiers
 source 1..31
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 0.4%; Score 14.2; DB 1; Length 31;
 Best Local Similarity 65.5%; Pred. No. 1.5e+03;
 Matches 19; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 Qy 486 CCGGCAGACGTCACGCTGGACGTGCTGG 514
 Db | | | | | | | | | | | | | | | | | | | |
 30 CCGGCAGCCCCCGCCVCGAGGATGGCCGG 2
 RESULT 1158
 AR222444/c AR222444 38 bp DNA linear PAT 26-SEP-2002
 LOCUS

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DEFINITION Sequence 2 from patent US 6429300.
ACCESSION AR222444
VERSION AR222444.1 GI:23329975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 38)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 2 06-AUG-2002;
FEATURES
source
    Location/Qualifiers
    1..38
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 38;
Best Local Similarity 62.9%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 3307 GGATTTTCTTAGGAGATTATTTTGGACTTC 3341
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Db 38 GGTATTTTCTTAGGAGATTATTTTGGACTTC 4
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RESULT 1159
LOCUS I31428 42 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 340 from patent US 5582979.
ACCESSION I31428
VERSION I31428.1 GI:1822219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 42)
AUTHORS Weber,J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 340 10-DEC-1996;
FEATURES
source
    Location/Qualifiers
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    /mol_type="unassigned DNA"

Query Match 0.4%; Score 14.2; DB 1; Length 42;
Best Local Similarity 62.9%; Pred. No. 1.6e+03;
Matches 22; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 598 TGAAGGTGTACAGTCACGACACACACACACATCCA 632
    |||||
Db 1 TGCCCGGCTACACACACACACACACACACACACA 35
    |||||

RESULT 1160
LOCUS BD185612 14 bp DNA linear PAT 17-JUN-2003
DEFINITION Analyses of double stranded nucleic acid using scanning probe microscope.
ACCESSION BD185612
VERSION BD185612.1 GI:131877812
KEYWORDS JP 2002360300-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Takeuchi,M.
TITLE Analyses of double stranded nucleic acid using scanning probe
JOURNAL OLYMPUS OPTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360300-A/1
PD 17-DEC-2002

DEFINITION Analyses of double stranded nucleic acid using scanning probe
PATENT: JP 2002360300-A 1 17-DEC-2002;
OLYMPUS OPTICAL CO LTD
OS Artificial Sequence
PN JP 2002360300-A/1
PD 17-DEC-2002

PF 06-JUN-2001 JP 2001171590
PI MINORU TAKEUCHI
PC C12Q1/68.C12N15/09.G01N33/483.G01N33/50.C12N15/00 CC
Analyses of double stranded nucleic acid using scanning probe CC

PF Key Location/Qualifiers
FT source 1..14
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FEATURES
source
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    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2328 TGTGTGCGTGTGTG 2341
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Db 1 TGTGTGCGTGTGTG 14
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RESULT 1161
LOCUS BD185613 14 bp DNA linear PAT 17-JUN-2003
DEFINITION Analyses of double stranded nucleic acid using scanning probe microscope.
ACCESSION BD185613
VERSION BD185613.1 GI:131877813
KEYWORDS JP 2002360300-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Takeuchi,M.
TITLE Analyses of double stranded nucleic acid using scanning probe
JOURNAL OLYMPUS OPTICAL CO LTD
COMMENT OS Artificial Sequence
PN JP 2002360300-A/2
PD 17-DEC-2002
PF 06-JUN-2001 JP 2001171590
PI MINORU TAKEUCHI
PC C12Q1/68.C12N15/09.G01N33/483.G01N33/50.C12N15/00 CC
Analyses of double stranded nucleic acid using scanning probe CC

PF Key Location/Qualifiers
FT source 1..14
    /organism="Artificial Sequence".

FEATURES
source
    Location/Qualifiers
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    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2328 TGTGTGCGTGTGTG 2341
    |||||
Db 14 TGTGTGCGTGTGTG 1
    |||||

RESULT 1162
LOCUS E32202 14 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32202
VERSION E32202.1 GI:13021735
KEYWORDS JP 2000060559-A/4.
SOURCE Hallotis discus discus

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ORGANISM  Haliotis discus discus
           Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
REFERENCE 1 (bases 1 to 14)
           Vetigastropoda; Haliotidae; Haliotidae; Haliotis.
AUTHORS   Hidaeki,T. and Masashi,S.
TITLE     Method for isolating satellite sequence
JOURNAL   Patent: JP 2000060559-A 4 29-FEB-2000;
COMMENT   NATL INST OF AGROBIOLOGICAL RESOURCES
           OS Haliotis discus discus
           PN JP 2000060559-A/4
           PD 29-FEB-2000
           PF 18-AUG-1998 JP 1998232153
           PR HIDEAKI TAKAHASHI,MASASHI SEKINO
           PC C12N15/09,C12Q1/68,C12N15/00
           CC Key
           FH Location/Qualifiers
           FT source
           FT 1..14
           FT /organism='Haliotis discus discus'.

FEATURES             Location/Qualifiers
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                     /organism="Haliotis discus discus"
                     /mol_type="genomic DNA"
                     /sub_species="discus"
                     /db_xref="taxon:91233"

     Query Match      0.4%; Score 14; DB 1; Length 14;
     Best Local Similarity 100.0%; Pred.No. 9.1e+02;
     Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2318 TGTGTGTGTGTGTG 2331
Db  14 TGTGTGTGTGTGTG 1

RESULT 1163
I31524/c  I31524 14 bp DNA linear PAT 06-FEB-1997
LOCUS     Sequence 436 from patent US 5582979.
DEFINITION I31524
ACCESSION I31524
VERSION   I31524.1 GI:1822315
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS   Weber,J.L.
TITLE     Length polymorphisms in (dc-da).sub.n.(dG-dT).sub.n sequences and
           method of using the same
JOURNAL   Patent: US 5582979-A 436 10-DEC-1996;
FEATURES   Location/Qualifiers
           source           1..14
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                           /mol_type="unassigned DNA"

     Query Match      0.4%; Score 14; DB 1; Length 14;
     Best Local Similarity 100.0%; Pred.No. 9.1e+02;
     Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2319 GTGTGTGTGTGTGTG 2332
Db  14 GTGTGTGTGTGTGTG 1

RESULT 1164
AX175251  AX175251 14 bp DNA linear PAT 03-JUL-2001
LOCUS     Sequence 15 from Patent WO0144465.
DEFINITION AX175251
ACCESSION AX175251
VERSION   AX175251.1 GI:14598619
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  synthetic construct

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artificial sequences.

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1
REFERENCE 1
AUTHORS   Phillips,N.C. and Filion,M.C.
TITLE     Therapeutically useful synthetic oligonucleotides
JOURNAL   Patent: WO 014465-A 15 21-JUN-2001;
           Bioniche Life Sciences Inc. (CA)
FEATURES   Location/Qualifiers
           source           1..14
                           /organism="synthetic construct"
                           /mol_type="unassigned DNA"
                           /db_xref="taxon:32630"

     Query Match      0.4%; Score 14; DB 1; Length 14;
     Best Local Similarity 100.0%; Pred.No. 9.1e+02;
     Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2318 TGTGTGTGTGTGTG 2331
Db  1 TGTGTGTGTGTGTG 14

RESULT 1165
AR241795  AR241795 15 bp DNA linear PAT 20-DEC-2002
LOCUS     Sequence 83 from patent US 6472154.
DEFINITION AR241795
ACCESSION AR241795
VERSION   AR241795.1 GI:27287607
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE     Polymorphic repeats in human genes
JOURNAL   Patent: US 6472154-A 83 29-OCT-2002;
FEATURES   Location/Qualifiers
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Db  1 ATATATATATATAA 14

RESULT 1166
BD234638  BD234638 16 bp DNA linear PAT 17-JUL-2003
LOCUS     Thymidine kinase mutants and fusion proteins having thymidine
DEFINITION kinase and guanylate kinase activities.
ACCESSION BD234638
VERSION   BD234638.1 GI:33044408
KEYWORDS  JP 2002516061-A/42.
SOURCE    unidentified
ORGANISM  unidentified.
REFERENCE 1 (bases 1 to 16)
AUTHORS   Black,M.E.
TITLE     Thymidine kinase mutants and fusion proteins having thymidine
           kinase and guanylate kinase activities
JOURNAL   Patent: JP 2002516061-A 42 04-JUN-2002;
           DARWIN MOLECULAR CORP
COMMENT   OS Unidentified
           PN JP 2002516061-A/42
           PD 04-JUN-2002
           PF 14-OCT-1998 JP 2000516019
           PR 14-OCT-1997 US 60/061812
           PI MARGARET E BLACK
           PC C12N15/09,A61K31/711,A61K35/76,A61K38/45,A61K48/00,A61K49/00,

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PC A61P31/00.
PC A61P35/00,C12N5/10,C12N9/12,C12N15/00,A61K37/52,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Thymidine kinase mutants and fusion proteins having thymidine
CC kinase and
CC guanylate kinase activities
FH Key Location/Qualifiers
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/db_xref='taxon:32644'
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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2677 CCCACCTCCAGGC 2690
Db 3 CCCACCTCCAGGC 16
RESULT 1167
AR230234
LOCUS 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 52 from patent US 6451571.
ACCESSION AR230234
VERSION AR230234.1 GI:27270289
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Loeb, I.A. and Black, M.E.
TITLE Thymidine kinase mutants
JOURNAL Patent: US 6451571-A 52 17-SEP-2002;
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Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2677 CCCACCTCCAGGC 2690
Db 3 CCCACCTCCAGGC 16
RESULT 1168
AR328665
LOCUS 16 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 6067 from patent US 6566127.
ACCESSION AR328665
VERSION AR328665.1 GI:33714473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6067 20-MAY-2003;
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Query Match 0.4%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2317 CTGTGTGTGTGTGT 2330
Db 3 CTGTGTGTGTGTGT 16
RESULT 1169
AR057463
LOCUS 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1667 from patent US 5837542.
ACCESSION AR057463
VERSION AR057463.1 GI:5983040
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
Draper, K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1667 17-NOV-1998;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 AGCTCTTCAAGCTG 15
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LOCUS 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1667 from patent US 6132967.
ACCESSION AR115221
VERSION AR115221.1 GI:14095543
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm, S., Stinchcomb, D.T., McSwiggen, J., Sullivan, S. and
Draper, K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1667 17-OCT-2000;
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Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1880 AGCTCTTCAAGCTG 1893
Db 2 AGCTCTTCAAGCTG 15
RESULT 1171
BD241576
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241576

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VERSION      BD241576.1 GI:33051346
KEYWORDS     JP 2002525127-A/523.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
AUTHORS      1 (bases 1 to 17)
TITLE        Methods and products related to genotyping and DNA analysis
JOURNAL      Patent: JP 2002525127-A 523 13-AUG-2002;
              MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT      OS Homo sapiens (human)
              EN JP 2002525127-A/523
              PD 13-AUG-2002
              PF 24-SEP-1999 JP 2000572407
              PR 25-SEP-1998 US 60/101757
              PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
              C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
              G01N37/00,
              PC C12N15/00
              CC Methods and products related to genotyping and DNA analysis FH
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              /mol_type="genomic DNA"
              /db_xref="taxon:9606"

Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 2327 GTGTGTCGGTGTGT 2340
DB 4 GTGTGTCGGTGTGT 17

RESULT 1172.
BD272846/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS      Cancer-susceptible mutation in BRCA2.
DEFINITION BD272846
ACCESSION  BD272846.1 GI:33082614
VERSION     JP 2002533054-A/15.
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   Lescallett,J.L., Lawrence,T., Allen,A.P., Olson,S.J., Thurber,D.B.
AUTHORS     and White,M.B.
TITLE       Cancer-susceptible mutation in BRCA2
JOURNAL     Patent: JP 2002533054-A 15 08-OCT-2002;
COMMENT     GENE LOGIC INC
OS Homo sapiens (human)
PN JP 2002533054-A/15
PD 08-OCT-2002
PF 02-DEC-1998 JP 2000523381
PR 02-DEC-1997 US 08/984034
PI JENNIFER L LSCALLETT, TAMMY LAWRENCE, ANTONETTE P ALLEN, SHERI J

PI OLSON,
PI DENISE B THURBER, MARGA B WHITE
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, C12Q1/68, G01N33/53, PC
G01N37/00,
PC C12N15/00, C12N15/00
CC Cancer-susceptible mutation in BRCA2
PH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FT Location/Qualifiers

VERSION      BD272846.1 GI:33082614
KEYWORDS     JP 2002533054-A/15.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    Lescallett,J.L., Lawrence,T., Allen,A.P., Olson,S.J., Thurber,D.B.
AUTHORS      and White,M.B.
TITLE        Cancer-susceptible mutation in BRCA2
JOURNAL      Patent: JP 2002533054-A 15 08-OCT-2002;
COMMENT      GENE LOGIC INC
OS Homo sapiens (human)
PN JP 2002533054-A/15
PD 08-OCT-2002
PF 02-DEC-1998 JP 2000523381
PR 02-DEC-1997 US 08/984034
PI JENNIFER L LSCALLETT, TAMMY LAWRENCE, ANTONETTE P ALLEN, SHERI J

PI OLSON,
PI DENISE B THURBER, MARGA B WHITE
PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, C12Q1/68, G01N33/53, PC
G01N37/00,
PC C12N15/00, C12N15/00
CC Cancer-susceptible mutation in BRCA2
PH Key Location/Qualifiers
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QY 3355 ATTTTCATCAAAAT 3368
DB 17 ATTTTCATCAAAAT 4

RESULT 1173.
AR483077 17 bp DNA linear PAT 14-MAY-2004
LOCUS      Sequence 523 from patent US 6703228.
DEFINITION AR483077
ACCESSION  AR483077
VERSION     AR483077.1 GI:47245600
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Landers,J., Jordan,B., Housman,D.E. and Charest,A.
TITLE       Methods and products related to genotyping and DNA analysis
JOURNAL     Patent: US 6703228-A 523 09-MAR-2004;
FEATURES    Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 0;

QY 2327 GTGTGTCGGTGTGT 2340
DB 4 GTGTGTCGGTGTGT 17

RESULT 1174.
AX634556 17 bp RNA linear PAT 21-FEB-2003
LOCUS      Sequence 1695 from Patent EP1260586.
DEFINITION AX634556
ACCESSION  AX634556
VERSION     AX634556.1 GI:28470170
KEYWORDS    unidentified
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
              Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
              Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
              Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
              Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
              genes
JOURNAL     Patent: EP 1260586-A 1695 27-NOV-2002;
              RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
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Matches 14; Conservative 0; Mismatches 0;

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Db 2 AGCTCTCAAGCTG 15
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DEFINITION Sequence 478 from Patent EPI281758.
ACCESSION AX687746
VERSION AX687746.1 GI:29410442
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 478 05-FEB-2003;
Neomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 4 TGGTGGAGGACCTG 17
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RESULT 1176
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LOCUS AX687747 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 479 from Patent EPI281758.
ACCESSION AX687747
VERSION AX687747.1 GI:29410443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 479 05-FEB-2003;
Neomica, Inc. (US)
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Db 3 TGGTGGAGGACCTG 16
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LOCUS AX687748 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 480 from Patent EPI281758.
ACCESSION AX687748

AX687748.1 GI:29410444
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 480 05-FEB-2003;
Neomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2006 TGGTGGAGGACCTG 2019
Db 2 TGGTGGAGGACCTG 15
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RESULT 1178
AX687749
LOCUS AX687749 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 481 from Patent EPI281758.
ACCESSION AX687749
VERSION AX687749.1 GI:29410445
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 481 05-FEB-2003;
Neomica, Inc. (US)
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source Location/Qualifiers
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Query Match 0.4%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2006 TGGTGGAGGACCTG 2019
Db 1 TGGTGGAGGACCTG 14
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RESULT 1179
AX687932
LOCUS AX687932 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 664 from Patent EPI281758.
ACCESSION AX687932
VERSION AX687932.1 GI:29410630
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

Query Match	0.4%; Score 14; DB 1; Length 17;	Best Local Similarity	100.0%; Pred. No. 1.1e+03;	Mismatches	0;	Indels	0;	Gaps	0;
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DEFINITION	Sequence 1077 from Patent EP1281758.								
ACCESSION	AX688345								
VERSION	AX688345.1 GI:29411045								
KEYWORDS	Homo sapiens (human)								
SOURCE	ORGANISM								
REFERENCE	1								
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.								
TITLE	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12								
JOURNAL	Patent: EP 1281758-A 1077 05-FEB-2003;								
LOCUS	AX688345	17 bp	DNA	linear					
DEFINITION	Sequence 668 from Patent EP1281758.								
ACCESSION	AX688345								
VERSION	AX688345.1 GI:29410634								
KEYWORDS	Homo sapiens (human)								
SOURCE	ORGANISM								
REFERENCE	1								
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.								
TITLE	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12								
JOURNAL	Patent: EP 1281758-A 668 05-FEB-2003;								
LOCUS	AX688344	17 bp	DNA	linear					
DEFINITION	Sequence 1076 from Patent EP1281758.								
ACCESSION	AX688344								
VERSION	AX688344.1 GI:29411044								
KEYWORDS	Homo sapiens (human)								
SOURCE	ORGANISM								
REFERENCE	1								
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.								
TITLE	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12								
JOURNAL	Patent: EP 1281758-A 1076 05-FEB-2003;								
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ACCESSION	AX688344								
VERSION	AX688344.1 GI:29411044								
KEYWORDS	Homo sapiens (human)								
SOURCE	ORGANISM								
REFERENCE	1								
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.								
TITLE	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12								
JOURNAL	Patent: EP 1281758-A 1076 05-FEB-2003;								
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DEFINITION	Sequence 1076 from Patent EP1281758.								
ACCESSION	AX688344								
VERSION	AX688344.1 GI:29411044								
KEYWORDS	Homo sapiens (human)								
SOURCE	ORGANISM								
REFERENCE	1								
AUTHORS	Shannon,M., Gu,Y. and Nguyen,C.T.								
TITLE	Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12								
JOURNAL	Patent: EP 1281758-A 1076 05-FEB-2003;								
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DEFINITION	Sequence 1076 from Patent EP1281758.								
ACCESSION	AX688344								

RESULT 1184
LOCUS AX688347/c 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1079 from Patent EP1281758.
ACCESSION AX688347
VERSION AX688347.1 GI:29411047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1079 05-FEB-2003;
Aeomica, Inc. (US)
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3657 TGCCTGCAGGGCCA 3670
Db 14 TGCCTGCAGGGCCA 1
RESULT 1185
LOCUS AX728804 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 438 from Patent WO03025175.
ACCESSION AX728804
VERSION AX728804.1 GI:30508147
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 438 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2566 CACCACGGGACATC 2579
Db 4 CACCACGGGACATC 17
RESULT 1186
LOCUS AX759001/c 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2322 from Patent WO03040369.
ACCESSION AX759001
VERSION AX759001.1 GI:32253617
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 2322 15-MAY-2003;
Molecular Engines Laboratories (FR)
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3388 CCCAGGCAGGGAGA 3401
Db 16 CCCAGGCAGGGAGA 3
RESULT 1187
LOCUS A31423 18 bp DNA linear PAT 08-NOV-1995
DEFINITION oligonucleotide from patent DE3731874.
ACCESSION A31423
VERSION A31423.1 GI:1249355
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS
JOURNAL Patent: DE 3731874-A 1 30-MAR-1989;
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source 1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3659 CCTGCAGGGCCATG 3672
Db 14 CCTGCAGGGCCATG 1
RESULT 1188
LOCUS A57884 18 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 7 from Patent EP0743367.
ACCESSION A57884
VERSION A57884.1 GI:3713655
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Fischer,A.D.
TITLE Gene expression analysis
JOURNAL Patent: EP 0743367-A 7 20-NOV-1996;
COMMENT MAX PLANCK GESELLSCHAFT (DE)
Other publication JP 8308598 961126
Other publication DE 19518505 961121.
FEATURES
source 1..18
Location/Qualifiers
/organism="unidentified"

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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GATGAAGATGATCGGAA 1376
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Db 1 GATGAAGMGATCGAGAA 18

RESULT 1189
LOCUS AX453148 18 bp DNA linear PAT 14-JUN-2004
DEFINITION Sequence 40 from Patent WO2004046377.
ACCESSION AX453148
VERSION AX453148.1 GI:48715894
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Casari,G., de Fusco,M. and Marconi,R.
TITLE alpha 2 subunit of the na, k pump
JOURNAL Diagnositic and therapeutic means for pathologies associated with
FONDAZIONE CENTRO SAN ROMANELLO DEL MONTE TABOR (IT)
PATENT: WO 2004046377-A 40 03-JUN-2004;
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 GGAGGAGCTGGTG 868
|||||:|||||
Db 4 GGAGGAGCTGGTG 17

RESULT 1190
LOCUS AX441362 18 bp DNA linear PAT 02-JUL-2002
DEFINITION Sequence 7 from Patent EP1209241.
ACCESSION AX441362
VERSION AX441362.1 GI:21690350
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Fischer,A.
TITLE Gene expression analysis
JOURNAL Patent: EP 1209241-A 7 29-MAY-2002;
Axaron Bioscience AG (DE)
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Sequenz P041"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GATGAAGATGATCGGAA 1376
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Db 1 GATGAAGMGATCGAGAA 18

RESULT 1191
LOCUS AX453148 18 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 27 from Patent WO0242444.
ACCESSION AX453148
VERSION AX453148.1 GI:21712655
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Yoder,O., Turgeon,B.G. and Lu,S.W.
TITLE Fungal gene cluster associated with pathogenesis
JOURNAL Patent: WO 0242444-A 27 30-MAY-2002;
Syngenta Participations AG (CH) ; CORNELL RESEARCH FOUNDATION, INC.
SYNGENTA PARTICIPATIONS AG (CH) ; Turgeon, Barbara G. (US) ; Lu, Shen-wen
(US) ; Yoder, Olen (US) ;
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2242 CCTGCTGCTGGTGC 2255
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Db 1 CCTGCTGCTGGTGC 14

RESULT 1192
LOCUS AX599908 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1248 from Patent WO02077272.
ACCESSION AX599908
VERSION AX599908.1 GI:28400058
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pelet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 1248 03-OCT-2002;
Epigenomics AG. (DE)
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for CDK 4"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2695 CCACCTCCACCCCT 2708
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Db 18 CCACCTCCACCCCT 5

RESULT 1193
LOCUS AX599910 18 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 1250 from Patent WO02077272.

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ACCESSION  AX599910
VERSION     AX599910.1  GI:28400060
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Berlin,K., Braun,A., Disler,J., Guetig,D., Howe,A., Mueller,J.,
            Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
            Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
            Pellet.C. and Ziebarth,H.
TITLE       Methods and nucleic acids for the analysis of hematopoietic cell
            proliferative disorders
JOURNAL     Patent: WO 02077272-A 1250 03-OCT-2002;
            Epigenomics AG (DE)
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Detection oligonucleotide for CDK 4"

Query Match      0.4%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2695 CCACCTCCACCCCT 2708
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Db 1 CCACCTCCACCCCT 14

RESULT 1194
LOCUS      A30762
DEFINITION Artificial DNA for oligonucleotide (TB-1).
ACCESSION  A30762
VERSION     A30762.1  GI:1567062
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     NUCLEOTIDIC SEQUENCES OF ACTINOMYCETALES, APPLICATIONS TO THE
            SYNTHESIS OR DETECTION OF NUCLEIC ACIDS, PRODUCTS OF EXPRESSION OF
            SUCH SEQUENCES AND APPLICATION AS IMMUNOGENIC COMPOSITIONS
            Patent: WO 9012875-A 16 01-NOV-1990;
JOURNAL     Patent: WO 9012875-A 16 01-NOV-1990;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3199 GAGCTGGAGGATCC 3212
      |||||
Db 7 GAGCTGGAGGATCC 20

RESULT 1195
LOCUS      A36727
DEFINITION Sequence 15 from Patent EP0586112.
ACCESSION  A36727
VERSION     A36727.1  GI:2293996
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis
            Mycobacterium tuberculosis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

tuberculosis complex.
1 (bases 1 to 20)
Tercero,J.C., Garcia,L.C., Ramos,J.A. and Alemany,J.C.
Control of PCR mediated detection of micro-organisms
Patent: EP 0586112-A 15 09-MAR-1994;
PHARMA GEN S A (ES)
Other publication JP 7087978 950404.
FEATURES    Location/Qualifiers
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            /db_xref="taxon:1773"

Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3199 GAGCTGGAGGATCC 3212
      |||||
Db 7 GAGCTGGAGGATCC 20

RESULT 1196
LOCUS      AR126637/C
DEFINITION Sequence 66 from patent US 6180353.
ACCESSION  AR126637
VERSION     AR126637.1  GI:14113230
KEYWORDS    .
SOURCE      Unknown.
            Unclasseified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dean,N.M. and Cowser,L.M.
TITLE       Antisense modulation of daxx expression
JOURNAL     Patent: US 6180353-A 66 30-JAN-2001;
FEATURES    Location/Qualifiers
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Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 AGATGACGAGGACG 184
      |||||
Db 16 AGATGACGAGGACG 3

RESULT 1197
LOCUS      BD270088
DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION  BD270088
VERSION     BD270088.1  GI:33079856
KEYWORDS    JP 2002537757-A/50.
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Valenzuela,D., Yuan,O., Hoffman,H., Hall,J. and Rapiejko,P.
TITLE       Secreted proteins and polynucleotides encoding them
JOURNAL     Patent: JP 2002537757-A 50 12-NOV-2002;
            ALPHAGEN INC
            OS Artificial Sequence
            PN JP 2002537757-A/50
            PD 12-NOV-2002
            PF 24-AUG-1999 JP 2000566287
            PR 24-AUG-1998 US 60/097638,24-AUG-1998 US 60/097659 PR
            09-SEP-1998 US 60/099618,28-SEP-1998 US 60/102092 PR
            25-NOV-1998 US 60/109978,23-DEC-1998 US 60/113645 PR
            23-DEC-1998 US 60/113646,23-AUG-1999 US 09/379246 PI DARIO

tuberculosis complex.
1 (bases 1 to 20)
Tercero,J.C., Garcia,L.C., Ramos,J.A. and Alemany,J.C.
Control of PCR mediated detection of micro-organisms
Patent: EP 0586112-A 15 09-MAR-1994;
PHARMA GEN S A (ES)
Other publication JP 7087978 950404.
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="Mycobacterium tuberculosis"
            /mol_type="unassigned DNA"
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Query Match      0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3199 GAGCTGGAGGATCC 3212
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Db 7 GAGCTGGAGGATCC 20

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VALENZUELA, OLIVE YUAN, HEIDI HOFFMAN, JEFF HALL, PETER PI RAPIJUKO
PC C12N15/09, A61K38/00, A61K48/00, A61P3/10, A61P11/06, A61P21/00, PC
A61P29/00,
PC A61P31/04, A61P31/10, A61P31/12, A61P31/18, A61P35/00, A61P37/00,
PC C07K14/47, C12N5/10, C12P21/02, G01N33/15, G01N33/50, C12N15/00, A61K37/02, PC
C12N5/00
CC oligonucleotide Location/Qualifiers
FH Key 1..20
FT source /organism="synthetic construct"
FT source /mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2005 CTGTGGAGGACCT 2018
Db 6 CTGTGGAGGACCT 19
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RESULT 1198
CQ818366/c
LOCUS CQ818366 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 8 from Patent WO2004044581.
ACCESSION CQ818366
VERSION CQ818366.1 GI:48427039
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Mackenzie, I., Rees, C.M., Nikitenko, L.L., Bicknell, R. and Smith, D.M.
TITLE Transcriptional regulation of cfrl and uses thereof
JOURNAL Patent: WO 2004044581-A 8 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTG 2329
Db 14 TCTGTGTGTGTGTG 1
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RESULT 1199
CQ818386/c
LOCUS CQ818386 20 bp DNA linear PAT 07-JUN-2004
DEFINITION Sequence 28 from Patent WO2004044581.
ACCESSION CQ818386
VERSION CQ818386.1 GI:48427059
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mackenzie, I., Rees, C.M., Nikitenko, L.L., Bicknell, R. and Smith, D.M.
TITLE Transcriptional regulation of cfrl and uses thereof
JOURNAL Patent: WO 2004044581-A 28 27-MAY-2004;
ISIS INNOVATION LIMITED (GB)
FEATURES
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/organism="synthetic construct"
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/db_xref="taxon:32630"

/organism="synthetic construct"
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Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTG 2329
Db 14 TCTGTGTGTGTGTG 1
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RESULT 1200
E30319
LOCUS E30319 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Gene participating in flower formation of plant.
ACCESSION E30319
VERSION E30319.1 GI:13017065
KEYWORDS JP 1999318462-A/6.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
AUTHORS Shinichiro, S. and Kiyotaka, O.
TITLE Gene participating in flower formation of plant
JOURNAL Patent: JP 1999318462-A 6 24-NOV-1999;
MITSUI GIYOUSAI SHOKUBUTSU BIO KENKYUSHO
COMMENT
OS Unidentified
PN JP 1999318462-A/6
PD 24-NOV-1999
PF 15-MAY-1998 JP 1998134095
PR
PI SHINICHIRO SAWA, KIYOTAKA OKADA
PC C12N15/09, A01H5/00, C07K14/415, C07K16/16, C12N1/21, C12N5/10, PC
C12P21/02
PC C12P21/08, G01N33/53//C12N1/21, C12R1/19, C12N5/10, C12R1/91),
PC C12P21/02, C12R1/91), C12N15/00, C12N5/00, (C12N5/00, C12R1/91) CC
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CC Topology: Linear;
FH Key Location/Qualifiers
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/organism="Unidentified".
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2108 CCAGCTCCAGCTCC 2121
Db 4 CCAGCTCCAGCTCC 17
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RESULT 1201
AR266079/c
LOCUS AR266079 20 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 86 from patent US 6492171.
ACCESSION AR266079
VERSION AR266079.1 GI:29694925
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 20)
TITLE Monia, B.P., Gaarde, W.A., Freier, S.M. and Wanciewicz, E.
JOURNAL Antisense modulation of TERT expression
Patent: US 6492171-A 86 10-DEC-2002;
FEATURES
source Location/Qualifiers

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source 1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTG 2331
Db 20 TGTGTGTGTGTGTG 7

RESULT 1202
AX149325/c
LOCUS AX149325 20 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 10 from Patent WO0136602.
ACCESSION AX149325
VERSION AX149325.1 GI:14347848
KEYWORDS synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Dahlberg,M., Moll,J. and Galvani,A.
TITLE Pak5 a member of the p21-activated kinase (pak) protein family,
nucleic acids and methods related to the same
JOURNAL Patent: WO 0136602-A 10 25-MAY-2001;
PHARMACIA & UPJOHN S.P.A. (IT)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notice="primer"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 1.2e+03;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1751 AGTGGATGGCGCTGAGG 1768
Db 19 AYTGGATGGCMCCWAGS 2

RESULT 1203
AX613800/c
LOCUS AX613800 20 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 4825 from Patent WO02072882.
ACCESSION AX613800
VERSION AX613800.1 GI:28409229
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Cullen,P. and Seedorf,U.
CORONARY chip
PATENT: WO 02072882-A 4825 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source 1. .20
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2098 CAGGACACCCCGAG 2111
Db 20 TGTGTGTGTGTGTG 7

RESULT 1204
BD013149/c
LOCUS BD013149 20 bp DNA linear PAT 02-AUG-2002
DEFINITION A gene encoding novel human secretory type phospholipase A2.
ACCESSION BD013149
VERSION BD013149.1 GI:22093338
KEYWORDS WO 0121775-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ishizaki,J., Suzuki,N. and Hanasaki,K.
TITLE A gene encoding novel human secretory type phospholipase A2
JOURNAL Patent: WO 0121775-A 22 29-MAR-2001;
SHIONOGI & CO LTD JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
COMMENT OS Artificial Sequence
PN WO 0121775-A/22
PD 29-MAR-2001
PF 18-SEP-2000 WO 2000JP006344
PR 21-SEP-1999 JP 99P 266616
PI JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
PC C12N9/20,C12N15/55,C12P21/02,C12P21/08,C07K16/40 CC
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1. .20
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/mol_type="genomic DNA"
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Query Match 0.4%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2438 CTGACTGTGTGTGTC 2451
Db 16 CTGACTGTGTGTGTC 3

RESULT 1205
BD167763/c
LOCUS BD167763 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Substance inhibiting binding of signal transducing molecule to
KDR/Flk-1 phosphorylated at tyrosine at the 1175-position and
method of using the same.
ACCESSION BD167763
VERSION BD167763.1 GI:27873575
KEYWORDS WO 0229090-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Shibuya,M., Takahashi,T., Furuya,A. and Shitara,K.
TITLE Substance inhibiting binding of signal transducing molecule to
KDR/Flk-1 phosphorylated at tyrosine at the 1175-position and
method of using the same
JOURNAL Patent: WO 0229090-A 3 11-APR-2002;
KYOWA HAKKO KOGYO CO LTD,MASABUMI SHIBUYA
COMMENT OS Artificial Sequence
PN WO 0229090-A/3
PD 11-APR-2002
PF 02-OCT-2001 WO 2001JP008684
PR 03-OCT-2000 JP 00P 303694
PI MASABUMI SHIBUYA,TOMOKO TAKAHASHI,AKIKO FURUYA,KENYA SHITARA
PC C12Q1/02,C12Q1/48,C12N15/09,C07K16/18,C07K14/47,A61K39/395, PC
A61P43/00,
PC A61P35/00,A61P9/00,A61K45/00,G01N33/15,G01N33/50 CC a primer
for replacing of human KDR/Flk-1 tyrosine residue at CC
position 801
CC for phenylalanine.
FH Key Location/Qualifiers
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FT source i. .20
 FT /organism='Artificial Sequence'
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 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 GATGGACAGAGC 262
 Db 19 GATGGACAGAGC 6

RESULT 1206
 AX103869
 LOCUS AX103869 22 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 61 from Patent WO0122972.
 ACCESSION AX103869
 VERSION AX103869.1 GI:13920066
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
 TITLE Immunostimulatory nucleic acids
 JOURNAL Patent: WO 0122972-A 61 05-APR-2001;
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
 GmbH (DE)
 FEATURES
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 1. .22
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"

Query Match 0.4%; Score 14; DB 1; Length 22;
 Best Local Similarity 77.3%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3264 TTTTATTTGCTTGTCTCTTTT 3285
 Db 1 TTTTATTTGCTTGTCTCTTTT 22

RESULT 1207
 AX546922
 LOCUS AX546922 22 bp DNA linear PAT 01-MAR-2003
 DEFINITION Sequence 61 from Patent WO02053141.
 ACCESSION AX546922
 VERSION AX546922.1 GI:25812066
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Bratzler, R.L.
 TITLE Inhibition of angiogenesis by nucleic acids
 JOURNAL Patent: WO 02053141-A 61 11-JUL-2002;
 Coley Pharmaceutical Group, Inc. (US)
 FEATURES
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 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic Sequence"

Query Match 0.4%; Score 14; DB 1; Length 22;
 Best Local Similarity 77.3%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3264 TTTTATTTGCTTGTCTCTTTT 3285
 Db 1 TTTTATTTGCTTGTCTCTTTT 22

RESULT 1208
 AX184223
 LOCUS AX184223 22 bp DNA linear PAT 06-AUG-2001
 DEFINITION Sequence 1976 from Patent WO0142511.
 ACCESSION AX184223
 VERSION AX184223.1 GI:15135567
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
 TITLE Ibd-related polymorphisms
 JOURNAL Patent: WO 0142511-A 1976 14-JUN-2001;
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Ellipsis
 Biotherapeutics Corporation (CA)
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.4%; Score 14; DB 1; Length 22;
 Best Local Similarity 93.3%; Pred. No. 1.3e+03;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2830 ACATATATATATATA 2844
 Db 6 ACATATATATATA 20

RESULT 1209
 I31174
 LOCUS I31174 39 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 86 from patent US 5582979.
 ACCESSION I31174
 VERSION I31174.1 GI:1821965
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 39)
 AUTHORS Weber, J.L.
 TITLE Length polymorphisms in (dC-dA).sub.n. (dG-dT).sub.n sequences and
 method of using the same
 JOURNAL Patent: US 5582979-A 86 10-DEC-1996;
 FEATURES
 source
 1. .39
 Location/Qualifiers
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 /mol_type="unassigned DNA"

Query Match 0.4%; Score 14; DB 1; Length 39;
 Best Local Similarity 60.5%; Pred. No. 1.6e+03;
 Matches 23; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 608 ACAGTACGACAGCCACATCCAGTGGCTCAAGCAC 645
 Db 1 ACACACACACACACACACATACACACACACACAC 38

RESULT 1210
 I31337
 LOCUS I31337 44 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 249 from patent US 5582979.
 ACCESSION I31337
 VERSION I31337.1 GI:1822128

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KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 44)
AUTHORS      Weber,J.L.
TITLE        Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and
              method of using the same
JOURNAL      Patent: US 5582979-A 249 10-DEC-1996;
FEATURES     Location/Qualifiers
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                /mol_type="unassigned DNA"

Query Match
Best Local Similarity 60.5%; Pred. No. 1.7e+03; Length 44;
Matches 23; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 608 ACAGTCACGACAGCCCATCCAGTCAGTGGTCAAGCAC 645
Db 5 ACACACACACACACACACACACACACACACACACACAC 42

RESULT 1211
AR046263
LOCUS      AR046263
DEFINITION Sequence 1056 from patent US 5817796.
ACCESSION AR046263
VERSION    AR046263.1 GI:5967728
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE        C-myb ribozymes having 2'-5'-linked adenylate residues
JOURNAL      Patent: US 5817796-A 1056 06-OCT-1998;
FEATURES     Location/Qualifiers
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Query Match
Best Local Similarity 88.2%; Pred. No. 1.1e+03; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3458 AAGTTTATATATCTA 3474
Db 1 AATTTTATATATATA 17

RESULT 1212
I53315
LOCUS      I53315
DEFINITION Sequence 1056 from patent US 5646042.
ACCESSION I53315
VERSION    I53315.1 GI:2474518
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE        C-myb targeted ribozymes
JOURNAL      Patent: US 5646042-A 1056 08-JUL-1997;
FEATURES     Location/Qualifiers
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Query Match
Best Local Similarity 88.2%; Pred. No. 1.1e+03; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3458 AAGTTTATATATCTA 3474
Db 1 AATTTTATATATATA 17

RESULT 1213
LOCUS      A02372/c
DEFINITION Oligonucleotide Lys320-Ala.
ACCESSION A02372
VERSION    A02372.1 GI:344633
KEYWORDS
SOURCE      synthetic construct
              ORGANISM synthetic construct
              artificial sequences.
REFERENCE    1 (bases 1 to 17)
AUTHORS
TITLE        ALTERED ANTIBODIES
JOURNAL      Patent: WO 8807089-A 14 22-SEP-1988;
FEATURES     Location/Qualifiers
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 588 GGAGTTCACACTGCAGG 604
Db 17 GGAGTTCGCTGCAGG 1

RESULT 1214
A06173/c
LOCUS      A06173
DEFINITION Oligonucleotide probe.
ACCESSION A06173
VERSION    A06173.1 GI:412792
KEYWORDS
SOURCE      synthetic construct
              ORGANISM synthetic construct
              artificial sequences.
REFERENCE    1 (bases 1 to 17)
AUTHORS
TITLE        GENE MODIFICATION
JOURNAL      Patent: WO 9001548-A 1 22-FEB-1990;
FEATURES     Location/Qualifiers
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Query Match
Best Local Similarity 88.2%; Pred. No. 1.1e+03; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1515 CACCTGCAGCCGCCG 1531
Db 17 CACCTGCTAGCCGCCG 1

RESULT 1215
AR039211
LOCUS      AR039211
DEFINITION Sequence 59 from patent US 5807743.
ACCESSION AR039211
VERSION    AR039211.1 GI:5958574
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
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Thu Oct 28 12:48:19 2004

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REFERENCE
  1 (bases 1 to 17)
  Stinchcomb,D.T. and McSwiggen,J.A.
  TITLE
  Interleukin-2 receptor gamma-chain ribozymes
  JOURNAL
  Patent: US 5807743-A 59 15-SEP-1998;
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    Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2699 TTCCACCTGCGCCCTC 2715
Db 1 TTTCCACTCGCCCTC 17

RESULT 1216
AR046566/c
LOCUS
  AR046566 17 bp DNA linear PAT 29-SEP-1999
  DEFINITION
  Sequence 1359 from patent US 5817796.
  ACCESSION
  AR046566
  VERSION
  AR046566.1 GI:5968031
  KEYWORDS
  Unknown.
  ORGANISM
  Unclassified.
  1 (bases 1 to 17)
  Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  AUTHORS
  C-myb ribozymes having 2'-5'-linked adenylate residues
  TITLE
  Patent: US 5817796-A 1359 06-OCT-1998;
  JOURNAL
  Patent: US 5817796-A 1359 06-OCT-1998;
  FEATURES
    source
      1..17
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      /mol_type="unassigned DNA"
  Query Match
    Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1346 CTGAGATCGAGATGATG 1362
Db 17 CTGAGATCGAGTGAGG 1

RESULT 1217
AR047368/c
LOCUS
  AR047368 17 bp DNA linear PAT 29-SEP-1999
  DEFINITION
  Sequence 2161 from patent US 5817796.
  ACCESSION
  AR047368
  VERSION
  AR047368.1 GI:5968833
  KEYWORDS
  Unknown.
  ORGANISM
  Unclassified.
  1 (bases 1 to 17)
  Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
  AUTHORS
  C-myb ribozymes having 2'-5'-linked adenylate residues
  TITLE
  Patent: US 5817796-A 2161 06-OCT-1998;
  JOURNAL
  Patent: US 5817796-A 2161 06-OCT-1998;
  FEATURES
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      /mol_type="unassigned DNA"
  Query Match
    Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2829 TACATATATATATATA 2845
Db 17 TACATATATATATATA 1

RESULT 1218
BD234970
LOCUS
  BD234970 17 bp DNA linear PAT 17-JUL-2003
  DEFINITION
  A method for stimulating the immune system.
  ACCESSION
  BD234970
  VERSION
  BD234970.1 GI:33044740
  KEYWORDS
  JP 2002517434-A/74.
  SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 17)
  Schlingsiepen,K.H., Schlingsiepen,R. and Brysch,W.
  AUTHORS
  A method for stimulating the immune system
  TITLE
  Patent: JP 2002517434-A 74 18-JUN-2002;
  JOURNAL
  BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK MBH
  COMMENT
  OS Homo sapiens (human)
  PN JP 2002517434-A/74
  PD 18-JUN-2002
  PF 10-JUN-1999 JP 2000553044
  PR 10-JUN-1998 EP 98110709.7,25-JUL-1998 EP 98113974.4 PI
  KARL HERMANN SCHLINGSIEPEN,REIMAR SCHLINGSIEPEN,WOLFGANG PI
  BRYSCH
  PC A61K45/06,A61K31/7089,A61K38/00,A61K39/395,A61K39/395,A61P31/
  PC 00,A61P35/00,
  PC A61P35/02,A61P37/02,C12N15/09,A61K37/02,C12N15/00 CC A
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  /db_xref='taxon:9606'
  Query Match
    Best Local Similarity 88.2%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2923 CGGGGGGGGGGGGGGGGG 2939
Db 1 CGGGGGGGGGGGGGGGGG 17

RESULT 1219
BD241250/c
LOCUS
  BD241250 17 bp DNA linear PAT 17-JUL-2003
  DEFINITION
  Methods and products related to genotyping and DNA analysis.
  ACCESSION
  BD241250
  VERSION
  BD241250.1 GI:33051020
  KEYWORDS
  JP 2002525127-A/197.
  SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 17)
  Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
  AUTHORS
  Methods and products related to genotyping and DNA analysis
  TITLE
  Patent: JP 2002525127-A 197 13-AUG-2002;
  JOURNAL
  MASSACHUSETTS INSTITUTE OF TECHNOLOGY
  COMMENT
  OS Homo sapiens (human)
  PN JP 2002525127-A/197
  PD 13-AUG-2002
  PF 24-SEP-1999 JP 2000572407
  PR 25-SEP-1998 US 60/101757
  PI JOHN E LANDERS,BARBARA JORDAN,DAVID E HOUSMAN,ALAIN CHAREST PC
  C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
  G01N37/00,
  PC C12N15/00
  CC Methods and products related to genotyping and DNA analysis FH

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Key          Location/Qualifiers
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FT           /organism='Homo sapiens (human)'.

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    /organism='Homo sapiens'
    /mol_type='genomic DNA'
    /db_xref='taxon:9606'

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1680 CTTGGGCTGGCCGGG 1696
Db 17 CTTCTGGCTGCCCAGG 1

RESULT 1220
BD241618
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Methods and products related to genotyping and DNA analysis.
ACCESSION     BD241618
VERSION       BD241618.1 GI:33051388
KEYWORDS      JP 2002525127-A/565.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 17)
Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
Methods and products related to genotyping and DNA analysis
Patent: JP 2002525127-A 565 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
OS Homo sapiens (human)
PN JP 2002525127-A/565
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS,BARBARA JORDAN,DAVID E HOUSMAN,ALAIN CHAREST PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
G01N37/00,
PC C12N15/00
CC Methods and products related to genotyping and DNA analysis FH
Key          Location/Qualifiers
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FT           /organism='Homo sapiens (human)'.

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    /mol_type='genomic DNA'
    /db_xref='taxon:9606'

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2326 TGTGTGTGGCTGTGTGT 2342
Db 1 TGTGTGTGGCTGTGTCT 17

RESULT 1221
BD253988/c
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION     BD253988
VERSION       BD253988.1 GI:33063758
KEYWORDS      JP 2002541795-A/1781.
SOURCE        unidentified
ORGANISM      unclassified.
1 (bases 1 to 17)
REFERENCE
AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
PN JP 2002541795-A/1782
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
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CC Regulation of repressor genes using nucleic acid molecules FH
Key          Location/Qualifiers
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    /db_xref='taxon:32644'

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2853 GGAAGAGGAAAGGCTG 2869
Db 17 GGGAGAGGAATAGGCTG 1

RESULT 1222
BD253989/c
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION     BD253989
VERSION       BD253989.1 GI:33063759
KEYWORDS      JP 2002541795-A/1782.
SOURCE        unidentified
ORGANISM      unclassified.
1 (bases 1 to 17)
REFERENCE
AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
PN JP 2002541795-A/1782
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key          Location/Qualifiers
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    /organism='unidentified'

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AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
PN JP 2002541795-A/1781
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
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CC Regulation of repressor genes using nucleic acid molecules FH
Key          Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2853 GGAAGAGGAAAGGCTG 2869
Db 17 GGGAGAGGAATAGGCTG 1

RESULT 1222
BD253989/c
LOCUS          17 bp DNA linear PAT 17-JUL-2003
DEFINITION    Regulation of repressor genes using nucleic acid molecules.
ACCESSION     BD253989
VERSION       BD253989.1 GI:33063759
KEYWORDS      JP 2002541795-A/1782.
SOURCE        unidentified
ORGANISM      unclassified.
1 (bases 1 to 17)
REFERENCE
AUTHORS      Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE        Regulation of repressor genes using nucleic acid molecules
JOURNAL      RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Eukaryote
PN JP 2002541795-A/1782
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key          Location/Qualifiers
FT source    1..17
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2852 TGGACGAGGAAAGGCT 2868
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DB 17 TGGACGAGGANTAGGCT 1

RESULT 1223
BD254375/c      17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION      Regulation of repressor genes using nucleic acid molecules.
ACCESSION      BD254375
VERSION        BD254375.1 GI:33064145
KEYWORDS       JP 2002541795-A/2168.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE         Regulation of repressor genes using nucleic acid molecules
JOURNAL       RIBOZYME PHARMACEUTICALS INC
COMMENT       OS Eukaryote
               PN JP 2002541795-A/2168
               PD 10-DEC-2002
               PF 11-APR-2000 JP 2000611654
               PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
               C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC
               C12P21/02,
               PC
               C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
               C12R1:91),
               PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
               PC A61K37/02,
               PC (C12N5/00,C12R1:91)
               CC Regulation of repressor genes using nucleic acid molecules FH
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2953 CAGGGCTCTACCCATG 2969
      ||||| ||| ||||| |||||
DB 17 CAGGGCTCTACCCATG 1

RESULT 1225
BD254752
LOCUS
DEFINITION      Regulation of repressor genes using nucleic acid molecules.
ACCESSION      BD254752
VERSION        BD254752.1 GI:33064522
KEYWORDS       JP 2002541795-A/2545.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE         Regulation of repressor genes using nucleic acid molecules
JOURNAL       RIBOZYME PHARMACEUTICALS INC
COMMENT       OS Eukaryote
               PN JP 2002541795-A/2545
               PD 10-DEC-2002
               PF 11-APR-2000 JP 2000611654
               PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
               C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
               C12P21/02,
               PC
               C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
               C12R1:91),
               PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
               PC A61K37/02,
               PC (C12N5/00,C12R1:91)
               CC Regulation of repressor genes using nucleic acid molecules FH
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 117 GCAGCGGCTACTGCGCC 133
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DB 17 GCAGCGGCTACTGCGCC 1

RESULT 1224
BD254495/c      17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION      Regulation of repressor genes using nucleic acid molecules.
ACCESSION      BD254495
VERSION        BD254495.1 GI:33064265
KEYWORDS       JP 2002541795-A/2288.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE         Regulation of repressor genes using nucleic acid molecules
JOURNAL       RIBOZYME PHARMACEUTICALS INC
COMMENT       OS Eukaryote
               PN JP 2002541795-A/2288
               PD 10-DEC-2002
               PF 11-APR-2000 JP 2000611654
               PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
               C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
               C12P21/02,
               PC
               C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
               C12R1:91),
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               PC A61K37/02,
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               CC Regulation of repressor genes using nucleic acid molecules FH
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QY 117 GCAGCGGCTACTGCGCC 133
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DB 17 GCAGCGGCTACTGCGCC 1

RESULT 1224
BD254495/c      17 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION      Regulation of repressor genes using nucleic acid molecules.
ACCESSION      BD254495
VERSION        BD254495.1 GI:33064265
KEYWORDS       JP 2002541795-A/2288.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS       Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE         Regulation of repressor genes using nucleic acid molecules
JOURNAL       RIBOZYME PHARMACEUTICALS INC
COMMENT       OS Eukaryote
               PN JP 2002541795-A/2288
               PD 10-DEC-2002
               PF 11-APR-2000 JP 2000611654
               PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
               C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
               C12P21/02,
               PC
               C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
               C12R1:91),
               PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
               PC A61K37/02,
               PC (C12N5/00,C12R1:91)
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QY 1563 CTGTGCTTACCAGGTGG 1579
DB 1 CGGTGCTTACCAGCGG 17

RESULT 1226
CQ617474
LOCUS      CQ617474
DEFINITION Sequence 2214 from Patent WO0192524.
ACCESSION  CQ617474
VERSION    CQ617474.1 GI:41667692
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
           Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2214 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 879 GCGGGGCGAGTGTGTATG 895
DB 1 GCGAGGCGAGTGTGTATG 17

RESULT 1227
CQ617930
LOCUS      CQ617930
DEFINITION Sequence 2670 from Patent WO0192524.
ACCESSION  CQ617930
VERSION    CQ617930.1 GI:41668148
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
           Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2670 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2917 CCTGGGCGGGCGGTGGG 2933
DB 1 CCTGGGCGGGCGGGGG 17

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1563 CTGTGCTTACCAGGTGG 1579
DB 1 CGGTGCTTACCAGCGG 17

RESULT 1228
CQ618036
LOCUS      CQ618036
DEFINITION Sequence 2776 from Patent WO0192524.
ACCESSION  CQ618036
VERSION    CQ618036.1 GI:41668254
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
           Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2776 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1987 AGCCACCTTCAAGCA 2003
DB 1 ACGGCCACCTTCAAGCA 17

RESULT 1229
CQ618038
LOCUS      CQ618038
DEFINITION Sequence 2778 from Patent WO0192524.
ACCESSION  CQ618038
VERSION    CQ618038.1 GI:41668256
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
           Shannon,M.E.
TITLE      Myosin-like gene expressed in human heart and muscle
JOURNAL    Patent: WO 0192524-A 2778 06-DEC-2001;
           Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1989 GCCCACCTTCAAGCAGC 2005
DB 1 GGCACCTTCAAGCACC 17

RESULT 1230
CQ623102
LOCUS      CQ623102
DEFINITION Sequence 7842 from Patent WO0192524.
ACCESSION  CQ623102
VERSION    CQ623102.1 GI:41673320
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7842 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1997 TCAAGCAGCTGGTGGAG 2013
Db 1 TGAAGCAGCAGGTGGAG 17
RESULT 1231
LOCUS CQ623258 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 7998 from Patent WO0192524.
ACCESSION CQ623258
VERSION CQ623258.1 GI:41673476
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 7998 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1994 CTTCAAGCAGCTGGTG 2010
Db 1 CCATCAAGCAGCTGGAG 17
RESULT 1232
LOCUS CQ623261 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8001 from Patent WO0192524.
ACCESSION CQ623261
VERSION CQ623261.1 GI:41673479
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8001 06-DEC-2001;
Aeomica, Inc. (US)

FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1997 TCAAGCAGCTGGTGGAG 2013
Db 1 TCAAGCAGCTGGAGCAG 17
RESULT 1233
LOCUS CQ623347 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8087 from Patent WO0192524.
ACCESSION CQ623347
VERSION CQ623347.1 GI:41673565
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8087 06-DEC-2001;
Aeomica, Inc. (US)
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 853 GAGGAGGAGCTGGTGA 869
Db 1 GAGGAGGAGACTGGAGA 17
RESULT 1234
LOCUS CQ623985 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 8725 from Patent WO0192524.
ACCESSION CQ623985
VERSION CQ623985.1 GI:41674203
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 8725 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

AUTHORS Poekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and Marx,A.

TITLE Method and nucleic acids for the improved treatment of breast cell proliferative disorders

JOURNAL Patent: WO 2004035803-A 195 29-APR-2004;
Epigenomics AG (DE)

FEATURES Location/Qualifiers

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2004 GCTGGTGGAGGACTGG 2020

Db 17 GCTGGTGGAGGACTGG 1

RESULT 1240

LOCUS I53618 17 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 1359 from patent US 5646042.

ACCESSION I53618

VERSION I53618.1 GI:2474821

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.

TITLE C-myb targeted ribozymes

JOURNAL Patent: US 5646042-A 1359 08-JUL-1997;

FEATURES Location/Qualifiers

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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1346 CTGAGATGGAGATGATG 1362

Db 17 CTGAGATGGAGGTGAGG 1

RESULT 1241

LOCUS I54420 17 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 2161 from patent US 5646042.

ACCESSION I54420

VERSION I54420.1 GI:2475623

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.

TITLE C-myb targeted ribozymes

JOURNAL Patent: US 5646042-A 2161 08-JUL-1997;

FEATURES Location/Qualifiers

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2829 TACATATATATATAA 2845

Db 17 TACATATATATAAAA 1

RESULT 1242

LOCUS AR187317/c 17 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 2805 from patent US 6346398.

ACCESSION AR187317

VERSION AR187317.1 GI:20233282

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6346398-A 2805 12-FEB-2002;

FEATURES Location/Qualifiers

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/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3250 TTCCAGTGAAGATATTT 3266

Db 17 TTCCATTGAAATATTT 1

RESULT 1243

LOCUS AR187357 17 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 2845 from patent US 6346398.

ACCESSION AR187357

VERSION AR187357.1 GI:20233322

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6346398-A 2845 12-FEB-2002;

FEATURES Location/Qualifiers

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Query Match 0.4%; Score 13.8; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3251 TCCAGTGAAGATATTT 3267

Db 1 TCCAGTGTAGATATATTT 17

RESULT 1244

LOCUS AR188717 17 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 4205 from patent US 6346398.

ACCESSION AR188717

VERSION AR188717.1 GI:20234682

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
AUTHORS
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1587 CATGGAGTCTTGGCCT 1603
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Db 1 CATGGAGTCTTGGCAT 17
RESULT 1245
AR188718 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 4206 from patent US 6346398.
ACCESSION AR188718
VERSION AR188718.1 GI:20234693
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
AUTHORS
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1588 ATGGAGTACTTGGCCTC 1604
|||||
Db 1 ATGGAGTCTTGGCATC 17
RESULT 1246
AR188755 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 4243 from patent US 6346398.
ACCESSION AR188755
VERSION AR188755.1 GI:20234720
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
AUTHORS
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1803 CGTCTGCTCTTTGGG 1819

Db 1 CGTCTGCTCTTTGGTG 17
RESULT 1247
AR190226 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 5714 from patent US 6346398.
ACCESSION AR190226
VERSION AR190226.1 GI:20236191
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
AUTHORS
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1288 GTAGCGGTGAAGATGCT 1304
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Db 1 GTAGCGGTGAAGATGTT 17
RESULT 1248
AR190240 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 5728 from patent US 6346398.
ACCESSION AR190240
VERSION AR190240.1 GI:20236205
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
AUTHORS
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1393 AACCTGCTGGCGCCTG 1409
|||||
Db 1 AACCTCTAGGCGCCTG 17
RESULT 1249
AR190291 17 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 5779 from patent US 6346398.
ACCESSION AR190291
VERSION AR190291.1 GI:20236256
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 5779 12-FEB-2002;
 FEATURES Location/Qualifiers
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 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1587 CATGGAGTCTTGGCGCT 1603
 Db 1 CATGGAGTCTTGGCAT 17
 RESULT 1250
 AR190292 17 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 5780 from patent US 6346398.
 DEFINITION AR190292
 ACCESSION AR190292
 VERSION AR190292.1 GI:20236257
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 5780 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..17
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 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1588 ATGGAGTCTTGGCGCTC 1604
 Db 1 ATGGAGTCTTGGCATC 17
 RESULT 1251
 AR190307 17 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 5795 from patent US 6346398.
 DEFINITION AR190307
 ACCESSION AR190307
 VERSION AR190307.1 GI:20236272
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 5795 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..17
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 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
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 QY 1680 CTTGGGCTTGGCCGG 1696
 Db 1 CTTGGGCTTGGCCGG 1696

Db 1 CTTGGGCTTGGCCGG 17
 RESULT 1252
 AR192109 17 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 7597 from patent US 6346398.
 DEFINITION AR192109
 ACCESSION AR192109
 VERSION AR192109.1 GI:20238074
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 7597 12-FEB-2002;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1296 GAAGATGCTGAAGACG 1312
 Db 1 GAAGATGCTGAAGAGG 17
 RESULT 1253
 AR261711 17 bp DNA linear PAT 29-JAN-2003
 LOCUS Sequence 195 from patent US 6322976.
 DEFINITION AR261711
 ACCESSION AR261711
 VERSION AR261711.1 GI:28072789
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Altman, T. J., Scott, J. and Stanton, L. W.
 TITLE Compositions and methods of disease diagnosis and therapy
 JOURNAL Patent: US 6322976-A 195 27-NOV-2001;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2575 ACATCAGCGGTGGCT 2591
 Db 1 ACATCATAGGGTGTGCT 17
 RESULT 1254
 AR286089 17 bp RNA linear PAT 10-APR-2003
 LOCUS Sequence 461 from patent US 6528640.
 DEFINITION AR286089
 ACCESSION AR286089
 VERSION AR286089.1 GI:29723685
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Beigelman, L., Burgin, A., Beaudry, A., Karpeisky, A.,
 Matulic-Adamic, J., Sweedler, D. and Zinnen, S.


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TITLE      Synthetic ribonucleic acids with RNase activity
JOURNAL    Patent: US 6528640-A 461 04-MAR-2003;
FEATURES   Location/Qualifiers
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           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      863  TGGTGGAGGCTGACGAG 879
Db      1    TGGTGGATGCTGAGGAG 17

RESULT 1255
AR286406  AR286406  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 778 from patent US 6528640.
ACCESSION AR286406
VERSION   AR286406.1 GI:29724002
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 778 04-MAR-2003;
FEATURES  Location/Qualifiers
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           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1744  CCGTGAAGTGGATGCG 1760
Db      1    CCGATCAAGTGGATGCG 17

RESULT 1256
AR286407  AR286407  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 779 from patent US 6528640.
ACCESSION AR286407
VERSION   AR286407.1 GI:29724003
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 779 04-MAR-2003;
FEATURES  Location/Qualifiers
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           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1751  AGTGGATGGCGCTGAG 1767
Db      1    AGTGGATGGCGCTGAG 17

RESULT 1257
AR286445  AR286445  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 817 from patent US 6528640.
ACCESSION AR286445
VERSION   AR286445.1 GI:29724041
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 817 04-MAR-2003;
FEATURES  Location/Qualifiers
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           /mol_type="unassigned RNA"

Query Match
Best Local Similarity  0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13    GGGCTGGTGGCCCTCGGA 29
Db      1    GGGCTGGAGCCCTCTGA 17

RESULT 1258
AR286463  AR286463  17 bp  RNA  linear  PAT 10-APR-2003
LOCUS
DEFINITION Sequence 835 from patent US 6528640.
ACCESSION AR286463
VERSION   AR286463.1 GI:29724059
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
           Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE     Synthetic ribonucleic acids with RNase activity
JOURNAL   Patent: US 6528640-A 835 04-MAR-2003;
FEATURES  Location/Qualifiers
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2149  GACCTGCTGCCCCCGGC 2165
Db      1    GACCTGCAGCCCCCAGC 17

RESULT 1259
AR317230  AR317230  17 bp  DNA  linear  PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 4 from patent US 6562624.
ACCESSION AR317230
VERSION   AR317230.1 GI:33696572
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS   Adachi,K., Hamer,J.E. and Hamer,L.
TITLE     Methods and materials for the rapid and high volume production of a
           gene knock-out library in an organism
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JOURNAL FEATURES source	Patent: US 6562624-A 4 13-MAY-2003; Location/Qualifiers 1. .17 /organism="unknown" /mol_type="genomic DNA"																								
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	RESULT 1260																								
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	LOCUS	DEFINITION	Sequence 1329 from patent US 6566127.																						
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JOURNAL FEATURES source	Unknown. Unclassified. 1 (bases 1 to 17) Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1329 20-MAY-2003;																								
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	Db	1	CATGGAGTCTTGGCAT 17																						
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	Db	17	TTCCATTGAAATATT 1																						
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JOURNAL FEATURES source	Unknown. Unclassified. 1 (bases 1 to 17) Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1369 20-MAY-2003;																								
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	AUTHORS																								
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	TITLE																								
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	Db	1	ATGGAGTCTTGGCATC 17																						
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	JOURNAL																								
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	source																								
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JOURNAL FEATURES source	Unknown. Unclassified. 1 (bases 1 to 17) Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 1369 20-MAY-2003;																								
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	JOURNAL																								
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	Db	1	ATGGAGTCTTGGCATC 17																						
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JOURNAL FEATURES source	Unknown. Unclassified. 1 (bases 1 to 17) 																								

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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1803 CGTCTGGTCTTTGGGG 1819
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Db 1 CGTCTGGTCTTTGGTG 17

RESULT 1265
AR325195 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 2597 from patent US 6566127.
ACCESSION AR325195
VERSION AR325195.1 GI:33711003
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2597 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1288 GTAGCGCTGAAGATGCT 1304
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Db 1 GTAGCGCTCAAGATGT 17

RESULT 1266
AR325206 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 2608 from patent US 6566127.
ACCESSION AR325206
VERSION AR325206.1 GI:33711014
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2608 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1393 AACCTGCTGGCGCCTG 1409
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Db 1 AACCTCTAGCGCGCTG 17

RESULT 1267

AR325259 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 2661 from patent US 6566127.
ACCESSION AR325259
VERSION AR325259.1 GI:33711067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 2661 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1680 CTTCGGCTGGCCCGG 1696
|||||
Db 1 CTTCGGCTGGCCCGG 17

RESULT 1268
AR325989 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 3391 from patent US 6566127.
ACCESSION AR325989
VERSION AR325989.1 GI:33711797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3391 20-MAY-2003;
FEATURES Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GAAGATGCTGAAGACG 1312
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Db 1 GAAGATGTTGAAGAGG 17

RESULT 1269
AR327329 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 4731 from patent US 6566127.
ACCESSION AR327329
VERSION AR327329.1 GI:33713137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4731 20-MAY-2003;
FEATURES Location/Qualifiers

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1296 GAAGATGCTGAAGAGC 1312
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Db 1 GAAATGCTGAAGAGG 17

RESULT 1270
AR327483 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR327483
DEFINITION Sequence 4885 from patent US 6566127.
ACCESSION AR327483
VERSION AR327483.1 GI:33713291
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 4885 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1950 GATCATGCGGAGTGCT 1966
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Db 1 GATCATGCTGGAGTGCT 17

RESULT 1271
AR328712 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR328712
DEFINITION Sequence 6114 from patent US 6566127.
ACCESSION AR328712
VERSION AR328712.1 GI:33714520
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6114 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 255 CAAGAAGCTGCTGCCG 271
||| ||||| ||||| |||||
Db 1 CAAGGTGCTGCTGCCG 17

RESULT 1272
AR329331 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR329331
DEFINITION Sequence 6733 from patent US 6566127.
ACCESSION AR329331
VERSION AR329331.1 GI:33715139
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6733 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1620 CAGGACCTGGTGGCC 1636
||| ||||| ||||| |||||
Db 1 CAGGACCTGGCGCAC 17

RESULT 1273
AR329361 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR329361
DEFINITION Sequence 6763 from patent US 6566127.
ACCESSION AR329361
VERSION AR329361.1 GI:33715169
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6763 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1804 GTCTGTCCTTTGGGT 1820
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Db 1 GTCTGTCCTTTGGGT 17

RESULT 1274
AR398079 17 bp RNA linear PAT 18-DEC-2003
LOCUS AR398079
DEFINITION Sequence 460 from patent US 6617438.
ACCESSION AR398079
VERSION AR398079.1 GI:40135600
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 460 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"
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Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 863 TGGTGGAGCTGACGAG 879
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Db 1 TGGTGGAGCTGACGAG 17

RESULT 1275
AR398396
LOCUS AR398396 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 777 from patent US 6617438.
ACCESSION AR398396
VERSION AR398396.1 GI:40136175
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 777 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1744 CCGTGAAGTGGATGCG 1760
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Db 1 CCGTGAAGTGGATGCG 17

RESULT 1276
AR398397
LOCUS AR398397 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 778 from patent US 6617438.
ACCESSION AR398397
VERSION AR398397.1 GI:40136177
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 778 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1751 AGTGATGGCGCTGAG 1767
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Db 1 AGTGATGGCGCTGAG 17

RESULT 1277
AR398435
LOCUS AR398435 17 bp RNA linear PAT 18-DEC-2003

DEFINITION Sequence 816 from patent US 6617438.
ACCESSION AR398435
VERSION AR398435.1 GI:40136245
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 816 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 GGGCTGGTGCCTCGGA 29
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Db 1 GGGCTGGAGCCTCTGA 17

RESULT 1278
AR398453
LOCUS AR398453 17 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 834 from patent US 6617438.
ACCESSION AR398453
VERSION AR398453.1 GI:40136278
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 834 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2149 GACCTGCTGCCCCGCG 2165
|||||
Db 1 GACCTGCAGCCCCCAGC 17

RESULT 1279
AR402298
LOCUS AR402298 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 638 from patent US 6623962.
ACCESSION AR402298
VERSION AR402298.1 GI:40149748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 638 23-SEP-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	
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QY 2324 TGTGTGTGTCGCTGTGT 2340
Db 1 TGTGTGTGTCAGTGTGT 17

RESULT 1285
AR458537 AR458537 17 bp DNA PAT 20-FEB-2004
LOCUS Sequence 2214 from patent US 6686188.
DEFINITION AR458537
ACCESSION AR458537
VERSION AR458537.1 GI:42693594
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2214 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 879 GCGGGCAGTGTGTATG 895
Db 1 GCGAGGCAGTGTGATG 17

RESULT 1286
AR458993 AR458993 17 bp DNA PAT 20-FEB-2004
LOCUS Sequence 2670 from patent US 6686188.
DEFINITION AR458993
ACCESSION AR458993
VERSION AR458993.1 GI:42694050
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2670 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2917 CCTGGGGGGGGCTGGG 2933
Db 1 CCTGGGGGGGGCTGGG 17

RESULT 1287
AR459099 AR459099 17 bp DNA PAT 20-FEB-2004
LOCUS Sequence 2776 from patent US 6686188.
DEFINITION AR459099
ACCESSION AR459099
VERSION AR459099.1 GI:42694156
KEYWORDS
SOURCE Unknown.
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2776 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1987 AGGCCACCTTCAAGCA 2003
Db 1 ACGGCCACCTTCAAGCA 17

RESULT 1288
AR459101 AR459101 17 bp DNA PAT 20-FEB-2004
LOCUS Sequence 2778 from patent US 6686188.
DEFINITION AR459101
ACCESSION AR459101
VERSION AR459101.1 GI:42694158
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2778 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1989 GCCCACCCTTCAAGCAGC 2005
Db 1 GCCCACCCTTCAAGCACC 17

RESULT 1289
AR464165 AR464165 17 bp DNA PAT 20-FEB-2004
LOCUS Sequence 7842 from patent US 6686188.
DEFINITION AR464165
ACCESSION AR464165
VERSION AR464165.1 GI:42699222
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed
predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 7842 03-FEB-2004;
FEATURES Location/Qualifiers
source 1..17
/mol_type="genomic DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1997 TCAAGCAGCTGGTGGAG 2013
 Db 1 TGAAGCAGCTGGTGGAG 17

RESULT 1290
 AR464321 AR464321 17 bp DNA PAT 20-FEB-2004
 LOCUS Sequence 7998 from patent US 6686188.
 DEFINITION AR464321
 ACCESSION AR464321
 VERSION AR464321.1 GI:42699378
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 7998 03-FEB-2004;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1994 CCTCAGCAGCTGGT 2010
 Db 1 CCATCAGCAGCTGGAG 17

RESULT 1291
 AR464324 AR464324 17 bp DNA PAT 20-FEB-2004
 LOCUS Sequence 8001 from patent US 6686188.
 DEFINITION AR464324
 ACCESSION AR464324
 VERSION AR464324.1 GI:42699381
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 8001 03-FEB-2004;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1997 TCAAGCAGCTGGTGGAG 2013
 Db 1 TCAAGCAGCTGGAGCAG 17

RESULT 1292
 AR464410 AR464410 17 bp DNA PAT 20-FEB-2004
 LOCUS Sequence 8087 from patent US 6686188.
 DEFINITION

AR464410 AR464410.1 GI:42699467
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 8087 03-FEB-2004;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 853 GAGGAGGAGCTGGTGA 869
 Db 1 GAGGAGGAGCTGGAGGA 17

RESULT 1293
 AR465048 AR465048 17 bp DNA PAT 20-FEB-2004
 LOCUS Sequence 8725 from patent US 6686188.
 DEFINITION AR465048
 ACCESSION AR465048
 VERSION AR465048.1 GI:42700105
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 8725 03-FEB-2004;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.1e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2049 CGAGTACCTGGACCTGT 2065
 Db 1 CGAGTACCTGGACACAGT 17

RESULT 1294
 AR465049 AR465049 17 bp DNA PAT 20-FEB-2004
 LOCUS Sequence 8726 from patent US 6686188.
 DEFINITION AR465049
 ACCESSION AR465049
 VERSION AR465049.1 GI:42700106
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 8726 03-FEB-2004;
 FEATURES Location/Qualifiers


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source 1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2050 GAGTACCTGGACCTGTC 2066
Db 1 GAGTACCTGGACAGTC 17

RESULT 1295
AR465670
LOCUS AR465670 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9347 from patent US 6686188.
ACCESSION AR465670
VERSION AR465670.1 GI:42700727
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9347 03-FEB-2004;
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source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 190 GACGAGGCTGGAGCAC 206
Db 1 GAAGAGGCTGGGACAC 17

RESULT 1296
AR466037/c
LOCUS AR466037 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9714 from patent US 6686188.
ACCESSION AR466037
VERSION AR466037.1 GI:42701094
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9714 03-FEB-2004;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2945 GGAGGCCCGGAGGTCT 2961
Db 17 GGAGGCCCGGAGGTCT 1

RESULT 1297
AR466184/c
LOCUS AR466184 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 9861 from patent US 6686188.
ACCESSION AR466184
VERSION AR466184.1 GI:42701241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 9861 03-FEB-2004;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 277 GCGCCCAACACCGTCG 293
Db 17 GCGCCCAACACCGTCG 1

RESULT 1298
AR482439
LOCUS AR482439 17 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 3 from patent US 6703200.
ACCESSION AR482439
VERSION AR482439.1 GI:47244871
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hamer, J.E. and Hamer, L.
TITLE Methods and materials for the rapid and high volume production of a gene knock-out library in an organism
JOURNAL Patent: US 6703200-A 3 09-MAR-2004;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2095 GGCCGAGGACCCCGCAG 2111
Db 1 GGCCGAGGAACTCCCGAG 17

RESULT 1299
AR482751/c
LOCUS AR482751 17 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 197 from patent US 6703228.
ACCESSION AR482751
VERSION AR482751.1 GI:47245274
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Landers, J., Jordan, B., Housman, D.E. and Charest, A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: US 6703228-A 197 09-MAR-2004;
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FEATURES
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Db 17 CTTCGGCTGGCCAGG 1

RESULT 1300
LOCUS AR483119 17 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 565 from patent US 6703228.
ACCESSION AR483119
VERSION AR483119.1 GI:47245642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 17)
  Landers,J., Jordan,B., Housman,D.E. and Charest,A.
  Methods and products related to genotyping and DNA analysis
  PATENT: US 6703228-A 565 09-MAR-2004;
JOURNAL
FEATURES
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Query Match
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QY 2326 TGTGTGTCGGTGTGT 2342
Db 1 TGTGTGTCGGTGTGTCT 17

RESULT 1301
LOCUS AX009041 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 74 from Patent WO963975.
ACCESSION AX009041
VERSION AX009041.1 GI:9996415
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
  A method for stimulating the immune system
  PATENT: WO 9963975-A 74 16-DEC-1999;
JOURNAL BIOGNOSTIK GBS (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES
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Query Match
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QY 2923 CGGGGGCTGGGGGGCG 2939
Db 1 CGGGGGCTGGGGGGCG 17

RESULT 1302
LOCUS AX216115 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1557 from Patent WO0159103.
ACCESSION AX216115
VERSION AX216115.1 GI:15526158
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
  1
  Blatt,L., McSwiggen,J. and Chowrira,B.M.
  Method and reagent for the modulation and diagnosis of cd20 and
  nogo gene expression
  Patent: WO 0159103-A 1557 16-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
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Query Match
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  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 502 CTGGACGTGCTGGAGCG 518
Db 1 CTGGAGGTGCTGGAGAG 17

RESULT 1303
LOCUS AX216149 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1591 from Patent WO0159103.
ACCESSION AX216149
VERSION AX216149.1 GI:15526192
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
  1
  Blatt,L., McSwiggen,J. and Chowrira,B.M.
  Method and reagent for the modulation and diagnosis of cd20 and
  nogo gene expression
  Patent: WO 0159103-A 1591 16-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
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QY 2932 GGGGGCGGTGGAGGAG 2948
Db 17 GGGGGCGGTGGAGGAG 1

RESULT 1304
LOCUS AX272795 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 364 from Patent WO0162911.
ACCESSION AX272795
VERSION AX272795.1 GI:16545532

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KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 364 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 831 GTGGCTGGTGGTGTGC 847
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Db 17 GTGGCTGGTGGTGTGC 1

RESULT 1305
AX272922
LOCUS AX272922 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 491 from Patent WO0162911.
ACCESSION AX272922
VERSION AX272922.1 GI:16545659
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 491 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATA 2840
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Db 1 ATATATACATATATCTA 17

RESULT 1306
AX273044
LOCUS AX273044 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 613 from Patent WO0162911.
ACCESSION AX273044
VERSION AX273044.1 GI:16545781
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid

JOURNAL Patent: WO 0162911-A 613 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

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Query Match 0.4%; Score 13.8; DB 1; Length 17;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2003 AGCTGGTGAGGACCTG 2019
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Db 1 AGGTGGTGAGGTCCTG 17

RESULT 1308
AX325317/c
LOCUS AX325317 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 1455 from Patent WO0192512.
ACCESSION AX325317
VERSION AX325317.1 GI:18096073
KEYWORDS
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 1455 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)

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QY	3241	TTGGAGGTGATTCACGTG	3257								
	17	TTGGAGGTGTTTCCAGTG	1								
DB											
RESULT 1309											
LOCUS		AX325318	17 bp	DNA	linear	PAT 02-SEP-2002					
DEFINITION		Sequence 1456 from Patent WO0192512.									
ACCESSION		AX325318									
VERSION		AX325318.1	GI:18096074								
KEYWORDS		Nicotiana tabacum (common tobacco)									
SOURCE		Nicotiana tabacum									
ORGANISM		Nicotiana tabacum									
REFERENCE		1 Nicotiana tabacum (common tobacco)									
AUTHORS		Kmiec, E.B., Gamber, H.B., Rice, M.C. and Kim, J.									
TITLE		Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides									
JOURNAL		Patent: WO 0192512-A 1456 06-DEC-2001;									
UNIVERSITY		OF DELAWARE (US)									
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Query Match		0.4%;	Score 13.8;					DB 1;	Length 17;		
Best Local Similarity		88.2%;	Pred. No. 1.1e+03;								
Matches		15;	Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;				
QY	3241	TTGGAGGTGATTCACGTG	3257								
	1	TTGGAGTGTTCACGTG	17								
DB											
RESULT 1310											
LOCUS		AX422231/c	17 bp	RNA	linear	PAT 18-JUN-2002					
DEFINITION		Sequence 567 from Patent WO0188124.									
ACCESSION		AX422231									
VERSION		AX422231.1	GI:21525613								
KEYWORDS		Homo sapiens (human)									
SOURCE		Homo sapiens									
ORGANISM		Homo sapiens									
REFERENCE		1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.									
AUTHORS		Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.									
TITLE		Method and reagent for the inhibition of erg									
JOURNAL		Patent: WO 0188124-A 567 22-NOV-2001;									
RIBOZYME		PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)									
FEATURES		Location/Qualifiers									
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Query Match		0.4%;	Score 13.8;					DB 1;	Length 17;		
Best Local Similarity		88.2%;	Pred. No. 1.1e+03;								
Matches		15;	Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;				
QY	1434	GCTGGTGGAGTACGCGG	1450								
	17	GCTGGAGGAGGACGCGG	1								
DB											
RESULT 1313											
LOCUS		AX475039/c	17 bp	DNA	linear	PAT 12-AUG-2002					
DEFINITION		Sequence 260 from Patent WO0224750.									
ACCESSION		AX475039									
VERSION		AX475039.1	GI:22214324								
KEYWORDS		Homo sapiens (human)									
SOURCE		Homo sapiens									

Query Match		0.4%;	Score 13.8;	DB 1;	Length 17;						
Best Local Similarity		88.2%;	Pred. No. 1.1e+03;								
Matches		15;	Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;				
QY	3241	TTGGAGGTGATTCACGTG	3257								
	17	TTGGAGGTGTTTCCAGTG	1								
DB											
RESULT 1311											
LOCUS		AX423119	17 bp	RNA	linear	PAT 18-JUN-2002					
DEFINITION		Sequence 1455 from Patent WO0188124.									
ACCESSION		AX423119									
VERSION		AX423119.1	GI:21526501								
KEYWORDS		Homo sapiens (human)									
SOURCE		Homo sapiens									
ORGANISM		Homo sapiens									
REFERENCE		1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.									
AUTHORS		Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.									
TITLE		Method and reagent for the inhibition of erg									
JOURNAL		Patent: WO 0188124-A 1455 22-NOV-2001;									
RIBOZYME		PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)									
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Best Local Similarity		88.2%;	Pred. No. 1.1e+03;								
Matches		15;	Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;				
QY	1568	CCTACCAGGTGGCCCGG	1584								
	1	CCGACGAGGTGGCCCGG	17								
DB											
RESULT 1312											
LOCUS		AX423120	17 bp	RNA	linear	PAT 18-JUN-2002					
DEFINITION		Sequence 1456 from Patent WO0188124.									
ACCESSION		AX423120									
VERSION		AX423120.1	GI:21526502								
KEYWORDS		Homo sapiens (human)									
SOURCE		Homo sapiens									
ORGANISM		Homo sapiens									
REFERENCE		1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.									
AUTHORS		Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.									
TITLE		Method and reagent for the inhibition of erg									
JOURNAL		Patent: WO 0188124-A 1456 22-NOV-2001;									
RIBOZYME		PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)									
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Best Local Similarity		88.2%;	Pred. No. 1.1e+03;								
Matches		15;	Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;				
QY	1571	ACGAGGTGGCCCGGGC	1587								
	1	ACGAGGTGGCCCGGGC	17								
DB											
RESULT 1313											
LOCUS		AX475039/c	17 bp	DNA	linear	PAT 12-AUG-2002					
DEFINITION		Sequence 260 from Patent WO0224750.									
ACCESSION		AX475039									
VERSION		AX475039.1	GI:22214324								
KEYWORDS		Homo sapiens (human)									
SOURCE		Homo sapiens									

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 024750-A 260 28-MAR-2002;
Aeomica, Inc. (US)
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Location/Qualifiers
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1527 GCCCGAGGAGCAGCTCA 1543
Db 17 GCCCGAGGTGCAGCTCA 1
RESULT 1314
AX530931
LOCUS AX530931 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 440 from Patent EP1239051.
ACCESSION AX530931
VERSION AX530931.1 GI:25253653
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 440 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 544 GCGGGGCTGCCGCCCAA 560
Db 1 GAGGCGCTGCCGCCCAA 17
RESULT 1315
AX530944
LOCUS AX530944 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 453 from Patent EP1239051.
ACCESSION AX530944
VERSION AX530944.1 GI:25253678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 453 11-SEP-2002;
Aeomica, Inc. (US)
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QY 2238 CCACCTGCTGCTGGTG 2254
Db 1 CCAACCTGCTGCTGGTG 17
RESULT 1316
AX530945
LOCUS AX530945 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 454 from Patent EP1239051.
ACCESSION AX530945
VERSION AX530945.1 GI:25253680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 454 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2239 CACCTGCTGCTGGTGC 2255
Db 1 CAACCTGCTGCTGGTGC 17
RESULT 1317
AX531999
LOCUS AX531999 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1508 from Patent EP1239051.
ACCESSION AX531999
VERSION AX531999.1 GI:25255764
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1508 11-SEP-2002;
Aeomica, Inc. (US)
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/db_xref="taxon:9606"
Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3671 TGGCTCAGGGTGTCTC 3687
Db 1 TGGCTCAGGGGTCTCTC 17
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RESULT 1318
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LOCUS AX544529 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 42 from Patent EP1243660.
ACCESSION AX544529
VERSION AX544529.1 GI:25809740
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Zhang, J., Gu, Y. and Nguyen, C.T.
AUTHORS Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 42 25-SEP-2002;
Aeomica, Inc. (US)
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/db_xref="taxon:9606"
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3697 CCCAGTGCATGGTGGCC 3713
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Db 1 CCCAGTCTGGTGGAC 17

RESULT 1319
AX544984/C
LOCUS AX544984 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 497 from Patent EP1243660.
ACCESSION AX544984
VERSION AX544984.1 GI:25810195
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Zhang, J., Gu, Y. and Nguyen, C.T.
AUTHORS Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 497 25-SEP-2002;
Aeomica, Inc. (US)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3697 CCCAGTGCATGGTGGCC 3713
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Db 1 CCCAGTCTGGTGGAC 17

RESULT 1320
AX578222
LOCUS AX578222 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 60 from Patent WO0211674.
ACCESSION AX578222
VERSION AX578222.1 GI:27647424
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.
AUTHORS Method and reagent for the inhibition of calcium activated chloride
TITLE Method and reagent for the inhibition of calcium activated chloride
JOURNAL Patent: WO 0211674-A 60 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3468 ATATCTATATATATAT 3484
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Db 1 ATCTGTATATATATAT 17

RESULT 1321
AX578223
LOCUS AX578223 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 61 from Patent WO0211674.
ACCESSION AX578223
VERSION AX578223.1 GI:27647425
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Thompson, J., Mcswiggen, J., Mckenzie, T., Ayers, D., Szymkowski, D.E.
AUTHORS Method and reagent for the inhibition of calcium activated chloride
TITLE Method and reagent for the inhibition of calcium activated chloride
JOURNAL Patent: WO 0211674-A 61 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3466 ATATCTATATATATAT 3482
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Db 1 ATATCTGTATATATAT 17

RESULT 1322
AX649233
LOCUS AX649233 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1073 from Patent EP1273660.
ACCESSION AX649233
VERSION AX649233.1 GI:29152051
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Gu, Y.
AUTHORS Human sodium-hydrogen exchanger like protein 1
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1073 08-JAN-2003;

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Db 1 GGCTGCGCGCCTAACAG 17

RESULT 1323
AX671977/c
LOCUS AX671977 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 422 from Patent WO03004526.
ACCESSION AX671977
VERSION AX671977.1 GI:293330325
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 422 16-JAN-2003;
Molecular Engines Laboratories (FR)
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QY 807 TATTGGCTTTCTCATC 823
Db 17 TATTGGCTTTCTGATC 1

RESULT 1324
AX676121/c
LOCUS AX676121 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 74 from Patent WO02059381.
ACCESSION AX676121
VERSION AX676121.1 GI:29333805
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Slaugenhaupt,S. and Gusella,J.F.
TITLE Gene for identifying individuals with familial dysautonomia
JOURNAL Patent: WO 02059381-A 74 01-AUG-2002;
The General Hospital Corporation (US)
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QY 1530 CGAGGAGCAGCTCACCT 1546
Db 17 CGGGGAGGAGCTCACCT 1

RESULT 1325
AX687732
LOCUS AX687732 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 464 from Patent EPI281758.
ACCESSION AX687732
VERSION AX687732.1 GI:29410428
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 464 05-FEB-2003;
Aeomica, Inc. (US)
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QY 1260 CAAGGACCGCGCGCCA 1276
Db 1 CAAGGCCCTGGCGGCCA 17

RESULT 1326
AX687796
LOCUS AX687796 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 528 from Patent EPI281758.
ACCESSION AX687796
VERSION AX687796.1 GI:29410492
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 528 05-FEB-2003;
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QY 3385 TGTCACGAGCAGGAGCA 3401
Db 1 TGCCACAGCAGGAGCA 17

RESULT 1327
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LOCUS AX687852 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 584 from Patent EP1281758.
ACCESSION AX687852
VERSION AX687852.1 GI:29410550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 584 05-FEB-2003;
Aeomica, Inc. (US)
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QY 381 AGGCATCAAGCTGGGC 397
Db 1 AGGCATCCAGCTGGGC 17
RESULT 1328
LOCUS AX688383 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1115 from Patent EP1281758.
ACCESSION AX688383
VERSION AX688383.1 GI:29411083
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 1115 05-FEB-2003;
Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
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QY 3 GGATGGCACAGGCTGG 19
Db 17 GGATGGCACAGGCTGG 1
RESULT 1329
LOCUS AX688727 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1459 from Patent EP1281758.
ACCESSION AX688727
VERSION AX688727.1 GI:29411431
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 1459 05-FEB-2003;
Aeomica, Inc. (US)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
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QY 3 GGATGGCACAGGCTGG 19
Db 17 GGATGGCACAGGCTGG 1
RESULT 1330
LOCUS AX690707 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3439 from Patent EP1281758.
ACCESSION AX690707
VERSION AX690707.1 GI:29413614
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 3439 05-FEB-2003;
Aeomica, Inc. (US)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 55 CTGCAGGTGCTGAATGC 71
Db 17 CTGCAGGTGCTGCCTGC 1
RESULT 1331
LOCUS AX722945 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 632 from Patent WO03025176.
ACCESSION AX722945
VERSION AX722945.1 GI:30423446
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE 1
AUTHORS Teleman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
JOURNAL reversion, apoptosis and/or virus resistance and their use as
PATENT: WO 03025176-A 632 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
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Location/Qualifiers

REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 1459 05-FEB-2003;
Aeomica, Inc. (US)
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RESULT 1330
LOCUS AX690707 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 3439 from Patent EP1281758.
ACCESSION AX690707
VERSION AX690707.1 GI:29413614
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 3439 05-FEB-2003;
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QY 3378 TGCTGTGTGTCAGGC 3394
Db 17 TGCTGTGTGTCAGGC 1
RESULT 1331
LOCUS AX722945 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 632 from Patent WO03025176.
ACCESSION AX722945
VERSION AX722945.1 GI:30423446
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE 1
AUTHORS Teleman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
JOURNAL reversion, apoptosis and/or virus resistance and their use as
PATENT: WO 03025176-A 632 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 249 GATGCACAAGAGCTGC 265
DB 1 GATGCACAAGAGCTGC 17

RESULT 1332
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DEFINITION Sequence 658 from Patent WO03025176.
ACCESSION AX722971
VERSION AX722971.1 GI:30423472
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 658 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2589 GCTCGGCCCTCCACACA 2605
DB 1 GATCGTCCCTCCACACA 17

RESULT 1333
AX724318
LOCUS AX724318 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2005 from Patent WO03025176.
ACCESSION AX724318
VERSION AX724318.1 GI:30503661
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 2005 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2944 GGGAGGCCCCAGGGGTC 2960
DB 17 GGGAGGCCCCAGGGGTC 1

RESULT 1336
AX727665
LOCUS AX727665 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5352 from Patent WO03025176.
ACCESSION AX727665
VERSION AX727665.1 GI:30507008
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5352 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2111 GCTCCAGCTCCTCAGGG 2127
DB 1 GATCCAGCTTCTCAGGG 17

RESULT 1334
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LOCUS AX727665 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5352 from Patent WO03025176.
ACCESSION AX727665
VERSION AX727665.1 GI:30507008
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
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JOURNAL Patent: WO 03025176-A 5352 27-MAR-2003;
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QY 2341 GTGTGTGTGTGCACATC 2357
DB 17 GTGTGTGTGTGAAGATC 1

RESULT 1335
AX729266/c
LOCUS AX729266 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 900 from Patent WO03025175.
ACCESSION AX729266
VERSION AX729266.1 GI:30508609
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 900 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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AX734014
LOCUS AX734014 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5648 from Patent WO03025175.
ACCESSION AX734014
VERSION AX734014.1 GI:30513357
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 5648 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Qy 2206 GGTCCCAACCAATGTGA 2222
Db 1 GATCCCAACCAATGTCA 17

RESULT 1337
AX734582
LOCUS AX734582 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 172 from Patent WO03025177.
ACCESSION AX734582
VERSION AX734582.1 GI:30513859
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 172 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3065 GTTCCCAACCCCAACA 3081
Db 1 GATCCCAACCCCAACA 17

RESULT 1338
AX735982
LOCUS AX735982 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1572 from Patent WO03025177.
ACCESSION AX735982
VERSION AX735982.1 GI:30515259
KEYWORDS Homo sapiens (human)
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ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 1572 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
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Qy 3741 GATTTTGTAAACCCAGC 3757
Db 1 GATCTTGTAAACCCATC 17

RESULT 1339
AX736612
LOCUS AX736612 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2202 from Patent WO03025177.
ACCESSION AX736612
VERSION AX736612.1 GI:30515900
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2202 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2314 GGTCTGTGTGTGTGTGT 2330
Db 1 GATCTGTGTGTGTGTGT 17

RESULT 1340
AX737215/c
LOCUS AX737215 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2805 from Patent WO03025177.
ACCESSION AX737215
VERSION AX737215.1 GI:30516503
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use

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Patent: WO 03025177-A 2805 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Query Match
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1314 TGCACCTGACAGGACC 1330
Db 17 TGCACGACAGGATC 1

RESULT 1341
AX737594/c
LOCUS AX737594 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3184 from Patent WO03025177.
ACCESSION AX737594
VERSION AX737594.1 GI:30516882
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03025177-A 3184 27-MAR-2003;
Amersham Biosciences SV Corp. (US)
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 501 GCTGACGCTGCTGAGC 517
Db 17 GCTGACCTGCTGGATC 1

RESULT 1342
AX733829/c
LOCUS AX733829 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 176 from Patent WO03037931.
ACCESSION AX733829
VERSION AX733829.1 GI:32166526
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 176 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
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            /db_xref="taxon:9606"

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Patent: WO 03025177-A 2805 27-MAR-2003;
Molecular Engines Laboratories (FR)
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2239 CACCCTGCTGCTGGTC 2255
Db 17 CCCCCCTGCTGCTTGC 1

RESULT 1343
AX753876/c
LOCUS AX753876 17 bp DNA linear PAT 23-JUN-2003
DEFINITION Sequence 223 from Patent WO03037931.
ACCESSION AX753876
VERSION AX753876.1 GI:32166573
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Shannon,M. and Phan,T.
TITLE Human angiomotin-like protein 1
JOURNAL Patent: WO 03037931-A 223 08-MAY-2003;
Amersham Biosciences SV Corp. (US)
FEATURES
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Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2432 GGTCTCTCTGACTGGTC 2448
Db 17 GGACTTCTGACTGGTC 1

RESULT 1344
AX759942
LOCUS AX759942 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3263 from Patent WO03040369.
ACCESSION AX759942
VERSION AX759942.1 GI:32254558
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3263 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
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            /db_xref="taxon:9606"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2747 GAGCCTTTACCTTTTAT 2763
Db 1 GATCCCTTGCCTTTTAT 17
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RESULT 1345
AX760079
LOCUS       AX760079             17 bp    DNA
DEFINITION   Sequence 3400 from Patent WO03040369.
ACCESSION   AX760079
VERSION     AX760079.1  GI:32254695
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 3400 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2206  GGTCCCCAACAAATGTGA 2222
Db    1  GATCCCCAACAAATGTCA 17

RESULT 1346
AX761940
LOCUS       AX761940             17 bp    DNA
DEFINITION   Sequence 5261 from Patent WO03040369.
ACCESSION   AX761940
VERSION     AX761940.1  GI:32256556
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Anson,R. and Tuijnder,M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 5261 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1068  GAGCTCCACACACACAC 1084
Db    1  GATCCCCAACACACAC 17

RESULT 1347
AX782224/c
LOCUS       AX782224             17 bp    DNA
DEFINITION   Sequence 555 from Patent WO03050284.
ACCESSION   AX782224
VERSION     AX782224.1  GI:32950073
KEYWORDS
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Guo,J.
TITLE       Human prostate cancer candidate protein 1
JOURNAL     Patent: WO 03050284-A 555 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES    Location/Qualifiers
            source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  3280  CTTTTCAGGAGAAATTA 3296
Db    17  CTTTTCAGGGGCATTA 1

RESULT 1348
AX783664
LOCUS       AX783664             17 bp    DNA
DEFINITION   Sequence 1995 from Patent WO03050284.
ACCESSION   AX783664
VERSION     AX783664.1  GI:32951513
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Guo,J.
TITLE       Human prostate cancer candidate protein 1
JOURNAL     Patent: WO 03050284-A 1995 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES    Location/Qualifiers
            source
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Query Match      0.4%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1222  TTCGCCAGGTGTCAT 1238
Db    1  TTCAGCCAGGAGTTCAT 17

RESULT 1349
AX783665
LOCUS       AX783665             17 bp    DNA
DEFINITION   Sequence 1996 from Patent WO03050284.
ACCESSION   AX783665
VERSION     AX783665.1  GI:32951514
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Guo,J.
TITLE       Human prostate cancer candidate protein 1
JOURNAL     Patent: WO 03050284-A 1996 19-JUN-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES    Location/Qualifiers
            source
            1..17
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Db      1  GCTGGGGTGCCTGCCG 17

RESULT 1353
DOGP36202/c
LOCUS   18 bp      DNA      linear      MAM 11-MAR-1996
DEFINITION
DOGP36202
ACCESSION
L24249.1 GI:401916
VERSION
PCR identification; PCR primer; STS.
SEGMENT
2 of 2
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 18)
Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
One hundred and one new simple sequence repeat-based markers for
the canine genome
Mamm. Genome 6 (3), 192-195 (1995)
JOURNAL
MEDLINE
95268214
PUBMED
7749226
COMMENT
Original source text: Canis familiaris (library: E. Ostrander, in
pBluescript+) adult spleen DNA.
Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EOstrander@bl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.
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/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/tissue_type="spleen"
/dev_stage="adult"
/tissue_lib="E. Ostrander, in pBluescript+"
primer_bind
complement(1..18)

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1948 ATGATCATGCGGGAGTG 1964
Db      17 ATGCTCATGCGGGAGTG 1

RESULT 1354
A88187/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 335 from Patent WO9833904.
ACCESSION
A88187
VERSION
A88187.1 GI:6736757
KEYWORDS
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
Brysch,W. and Schlingensiepen,K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 335 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
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/organism="unidentified"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1948 ATGATCATGCGGGAGTG 1964
Db      17 ATGCTCATGCGGGAGTG 1

RESULT 1355
A88187/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 335 from Patent WO9833904.
ACCESSION
A88187
VERSION
A88187.1 GI:6736757
KEYWORDS
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
Brysch,W. and Schlingensiepen,K.
AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
Patent: WO 9833904-A 335 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1948 ATGATCATGCGGGAGTG 1964
Db      17 ATGCTCATGCGGGAGTG 1

RESULT 1356
A90829/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 8 from Patent WO9830687.
ACCESSION
A90829
VERSION
A90829.1 GI:6739239
KEYWORDS
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
Poustka,A. and Mollenhauer,J.
PROTEIN CONTAINING AN SRCR DOMAIN
Patent: WO 9830687-A 8 16-JUL-1998;
DEUTSCHES KREBSFORSCH (DE); POUSTKA ANNEMARIE (DE)
FEATURES
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/organism="unidentified"
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/db_xref="taxon:32644"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1792 CACCAGAGTGACGTCTG 1808
Db      17 CACCAGAGTGATGTGTG 1

RESULT 1357
A90154/c
LOCUS   18 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION
Sequence 335 from Patent EP0856579.
ACCESSION
A90154
VERSION
A90154.1 GI:6738668
KEYWORDS
unidentified
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
Brysch,W.D. and Schlingensiepen,K.D.
An antisense oligonucleotide preparation method
Patent: EP 0856579-A 335 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1792 CACCAGAGTGACGTCTG 1808
Db      17 CACCAGAGTGATGTGTG 1

/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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A91171/c
LOCUS A91171 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 5 from Patent WO9827206.
ACCESSION A91171
VERSION A91171.1 GI:6740207
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Icard-Liepkalns, C., Mallet, J. and Corresponding, N.A.
JOURNAL Patent: WO 9827206-A 5 25-JUN-1998;
ICARD LIEPKALNS CHRISTINE (FR); MALLET JACQUES (FR)
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2092 GGTGGCCAGCACCC 2108
Db 18 GGTGGCCAGCACCCG 2

RESULT 1358
AR036682/c
LOCUS AR036682 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5800811.
ACCESSION AR036682
VERSION AR036682.1 GI:5954538
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hall, F.L., Nimni, M.E., Tuan, T.-L., Wu, L. and Cheung, D.T.
TITLE Artificial skin prepared from collagen matrix containing
transforming growth factor-beta, having a collagen binding site
JOURNAL Patent: US 5800811-A 21 01-SEP-1998;
FEATURES
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGATGAT 1370
Db 18 GTGATGATGATGAT 2

RESULT 1359
AR062605/c
LOCUS AR062605 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5843738.
ACCESSION AR062605
VERSION AR062605.1 GI:5990296
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.Frank, and Mirabelli, C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5843738-A 5 01-DEC-1998;
FEATURES
source 1..18
Location/Qualifiers

A91171/c
LOCUS A91171 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 5 from Patent WO9827206.
ACCESSION A91171
VERSION A91171.1 GI:6740207
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Icard-Liepkalns, C., Mallet, J. and Corresponding, N.A.
JOURNAL Patent: WO 9827206-A 5 25-JUN-1998;
ICARD LIEPKALNS CHRISTINE (FR); MALLET JACQUES (FR)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2092 GGTGGCCAGCACCC 2108
Db 18 GGTGGCCAGCACCCG 2

RESULT 1358
AR036682/c
LOCUS AR036682 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 21 from patent US 5800811.
ACCESSION AR036682
VERSION AR036682.1 GI:5954538
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hall, F.L., Nimni, M.E., Tuan, T.-L., Wu, L. and Cheung, D.T.
TITLE Artificial skin prepared from collagen matrix containing
transforming growth factor-beta, having a collagen binding site
JOURNAL Patent: US 5800811-A 21 01-SEP-1998;
FEATURES
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGATGAT 1370
Db 18 GTGATGATGATGAT 2

RESULT 1359
AR062605/c
LOCUS AR062605 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5843738.
ACCESSION AR062605
VERSION AR062605.1 GI:5990296
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.Frank, and Mirabelli, C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5843738-A 5 01-DEC-1998;
FEATURES
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Location/Qualifiers

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Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2690 CTTTCCCACTTCCACC 2706
Db 18 CTTTCCCACTGCCATC 2

RESULT 1360
AR078582/c
LOCUS AR078582 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 8 from patent US 5962672.
ACCESSION AR078582
VERSION AR078582.1 GI:10005328
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Coswert, L.M.
TITLE Antisense modulation of RhoB expression
JOURNAL Patent: US 5962672-A 8 05-OCT-1999;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1998 CAAGCAGCTGTGGAGG 2014
Db 17 CAAGCAGCTGTGGTGG 1

RESULT 1361
AR080699
LOCUS AR080699 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 4 from patent US 5968826.
ACCESSION AR080699
VERSION AR080699.1 GI:10007429
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.Frank., Condon, T.P. and Coswert, L.M.
TITLE Antisense inhibition of integrin, alpha.4 expression
JOURNAL Patent: US 5968826-A 4 19-OCT-1999;
FEATURES
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1965 CTGGCATGCCGCCCT 1981
Db 2 CTGGCATGCCGCCACT 18

RESULT 1362
AR082993
LOCUS AR082993 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 19 from patent US 5976798.
ACCESSION AR082993

VERSION AR082993.1 GI:10009783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Parker W.Davis., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
TITLE Methods for detecting mitochondrial mutations diagnostic for Alzheimer's disease and methods for determining heteroplasmy of mitochondrial nucleic acid
JOURNAL Patent: US 5976798-A 19 02-NOV-1999;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2075 TCGAGCAGTACTCCCG 2091
Db 2 TCGAGTAGTACTCCCG 18
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RESULT 1363
AR104708/c
LOCUS AR104708 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6093811.
ACCESSION AR104708
VERSION AR104708.1 GI:12817416
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank, and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 6093813-A 5 25-JUL-2000;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2690 CTTTCCCACTTCCACC 2706
Db 18 CTTTCCCACTGCCATC 2
|||||
|

RESULT 1364
AR105530/c
LOCUS AR105530 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6096722.
ACCESSION AR105530
VERSION AR105530.1 GI:12819127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank., Mirabelli,C.K. and Baker,B.
TITLE Antisense modulation of cell adhesion molecule expression and treatment of cell adhesion molecule-associated diseases
JOURNAL Patent: US 6096722-A 5 01-AUG-2000;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2690 CTTTCCCACTTCCACC 2706
Db 18 CTTTCCCACTGCCATC 2
|||||
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RESULT 1364
AR105530/c
LOCUS AR105530 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 5 from patent US 6096722.
ACCESSION AR105530
VERSION AR105530.1 GI:12819127
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank., Mirabelli,C.K. and Baker,B.
TITLE Antisense modulation of cell adhesion molecule expression and treatment of cell adhesion molecule-associated diseases
JOURNAL Patent: US 6096722-A 5 01-AUG-2000;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2690 CTTTCCCACTTCCACC 2706
Db 18 CTTTCCCACTGCCATC 2
|||||
|

RESULT 1365
AR119310/c
LOCUS AR119310 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 73 from patent US 6150104.
ACCESSION AR119310
VERSION AR119310.1 GI:14101220
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Splawski,I. and Keating,M.T.
TITLE Homozygous mutation in KVLQT1 which causes Jervell and Lange
Nielsen syndrome
JOURNAL Patent: US 6150104-A 73 21-NOV-2000;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 969 GCGCAGCCCCCACAAGA 985
Db 18 GCGCAGCCGCCCCACA 2
|||||
|

RESULT 1366
AR121140/c
LOCUS AR121140 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 36 from patent US 6159697.
ACCESSION AR121140
VERSION AR121140.1 GI:14104716
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia,B.P. and Cowsert,L.M.
TITLE Antisense modulation of Smad7 expression
JOURNAL Patent: US 6159697-A 36 12-DEC-2000;
FEATURES Location/Qualifiers
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2284 GCAGATGGAGACACGC 2300
Db 17 GCAGATGGGAGACAC 1
|||||
|

RESULT 1367
AR123192/c
LOCUS AR123192 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6169079.
ACCESSION AR123192
VERSION AR123192.1 GI:14108158
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide inhibition of cell adhesion
JOURNAL Patent: US 619079-A 5 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2690 CTTTCCCACTCCACC 2706
Db 18 CTTTCCCACTGCCATC 2

RESULT 1368
ARI138072
LOCUS ARI138072 18 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 82 from patent US 6197584.
ACCESSION ARI138072
VERSION ARI138072.1 GI:14479581
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Cowsert,L.M.
TITLE Antisense modulation of CD40 expression
JOURNAL Patent: US 6197584-A 82 06-MAR-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2132 ACTCCGTGTTGCCAC 2148
Db 2 ACTGCCGTGTTGCCAC 18

RESULT 1369
ARI145511
LOCUS ARI145511 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6217858.
ACCESSION ARI145511
VERSION ARI145511.1 GI:15108700
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Galun,E., Nahor,O. and Blum,H.E.
TITLE Pharmaceutical composition for treating hepatitis B virus (HBV) infection
JOURNAL Patent: US 6217858-A 10 17-APR-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 588 GGAGTTCCTCACTGCAAG 604
Db 1 GGAATTCCTCACTGCATG 17

RESULT 1370
ARI162682
LOCUS ARI162682 18 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6258790.
ACCESSION ARI162682
VERSION ARI162682.1 GI:16229996
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank., Condon,T.P. and Cowsert,L.M.
TITLE Antisense modulation of integrin.alpha.4 expression
JOURNAL Patent: US 6258790-A 4 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1965 CTGGCATCGCGCCCT 1981
Db 2 CTGGCATCGCGCCACT 18

RESULT 1371
BD178738/c
LOCUS BD178738 18 bp DNA linear PAT 16-APR-2003
DEFINITION Gene panel for genes involving liver regeneration.
ACCESSION BD178738
VERSION BD178738.1 GI:30016005
KEYWORDS WO 02077222-A/76.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Yokoya,F., Okutsu,T., Mori,M., Yoshiyuki, Takahara, Fukuda,H., Aburatani,H. and Sonaka,I.
TITLE Gene panel for genes involving liver regeneration
JOURNAL Patent: WO 02077222-A 76 03-OCT-2002;
COMMENT AJINOMOTO CO INC,FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI, YOSHIYUKI TAKAHARA,HISAO FUKUDA,HIROYUKI ABURATANI,ICHIRO SONAKA
OS Artificial Sequence
PN WO 02077222-A/76
PD 03-OCT-2002
PF 13-MAR-2002 WO 2002JP002372
PR 13-MAR-2001 JP 01P 070940
PI FUMIHIKO YOKOYA,TOMOHISA OKUTSU,MAIKO MORI,YOSHIYUKI PI TAKAHARA,HISAO FUKUDA,
FI HIROYUKI ABURATANI,ICHIRO SONAKA
PC C12N15/09,C12Q1/68,G01N33/15,G01N33/50,G01N37/00 CC
Description of Artificial Sequence: primer
FH Key Location/Qualifiers
FT source 1..18
/organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1339 CTGGTCTCTGAGATGGA 1355
 DB 18 CTGGTGGCTGGGATGGA 2

RESULT 1372
 BD226623 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Antisense modulation of CD40 expression.
 DEFINITION BD226623
 ACCESSION BD226623
 VERSION BD226623.1 GI:33036393
 KEYWORDS JP 2002513593-A/82.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,C.F. and Cowsert,L.M.
 TITLE Antisense modulation of CD40 expression
 JOURNAL Patent: JP 2002513593-A 82 14-MAY-2002;
 ISIS PHARMACEUTICALS INC
 OS Unidentified
 PN JP 2002513593-A/82
 PD 14-MAY-2002
 PF 22-APR-1999 JP 2000547271
 PR 01-MAY-1998 US 09/071433
 PI C FRANK BENNETT,LEX M COWSERT
 PC C12N15/09,A61K9/10,A61K45/00,A61K48/00,A61P1/00,A61P11/06, PC
 A61P17/06,
 PC A61P29/00,A61P35/00,A61P37/02,A61P37/06,A61P43/00,C12P19/34,
 PC C12Q1/68,
 PC C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Antisense modulation of CD40 expression
 FH Key Location/Qualifiers
 FT source 1..18
 FT /organism='Unidentified'.
 FEATURES source
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 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2132 ACTCCGTGTTGCCAC 2148
 DB 2 ACTGCGCTGTTGCCAC 18

RESULT 1373
 BD227742 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Antisense modulation of integrin alph 4 expression.
 DEFINITION BD227742
 ACCESSION BD227742
 VERSION BD227742.1 GI:33037512
 KEYWORDS JP 2002526555-A/4.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Bennett,F.C., Condon,T.P. and Cowsert,L.M.
 TITLE Antisense modulation of integrin alph 4 expression
 JOURNAL Patent: JP 2002526555-A 4 20-AUG-2002;
 ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2002526555-A/4
 PD 20-AUG-2002
 PF 19-AUG-1999 JP 2000574727
 PR 05-OCT-1998 US 09/166203
 PI FRANK C BENNETT,THOMAS P CONDON,LEX M COWSERT PC

C07H21/04,A61K31/7115,A61K31/712,A61K31/7125,A61K48/00,A61P1/ PC
 00,A61P11/16,
 PC A61P3/00,A61P11/06,A61P25/28,A61P29/00,A61P29/00,A61P35/00, PC
 A61P35/04,
 PC A61P37/06,A61P43/00,C12N15/09,C12Q1/02,C12Q1/68,C12N15/00 CC
 antisense sequence Location/Qualifiers
 FH Key 1..18
 FT source /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1965 CTGGCATCGCGCCCT 1981
 DB 2 CTGGCATCGCGCCACT 18

RESULT 1374
 BD250528 18 bp DNA linear PAT 17-JUL-2003
 LOCUS Identification of genetic targets for modulation by
 DEFINITION oligonucleotides and generation of oligonucleotides for gene
 modulation.
 ACCESSION BD250528
 VERSION BD250528.1 GI:33060298
 KEYWORDS JP 2002511276-A/82.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Cowsert,L.M., Baker,B.F., Mcneil,J., Freier,S.M., Sasmor,H.M.,
 Brooks,D.G., Ohasi,C., Wyatt,J.R., Borchers,A.H. and Vikkars,T.A.
 TITLE Identification of genetic targets for modulation by
 oligonucleotides and generation of oligonucleotides for gene
 modulation
 JOURNAL Patent: JP 2002511276-A 82 16-APR-2002;
 ISIS PHARMACEUTICALS INC
 OS Artificial Sequence
 PN JP 2002511276-A/82
 PD 16-APR-2002
 PF 13-APR-1999 JP 2000543647
 PR 13-APR-1998 US 60/081483,28-APR-1998 US 09/067638 PI
 LEX M COWSERT,BRENDA F BAKER,JOHN MCNEIL,SUSAN M FREIER,HENRI PI
 M SASMOR,
 PI DOUGLAS G BROOKS,CARA OHASI,JACQUELINE R WYATT,ALEXANDER H PI
 BORCHERS,
 PI TIMOTHY A VIKKARS
 PC C12N15/09,C07B61/00,C07B61/00,C12Q1/68,G06F17/30,G06F17/50, PC
 C12N15/00
 CC Antisense Oligonucleotide
 FH Key Location/Qualifiers
 FT source 1..18
 FT /organism='Artificial Sequence'.
 FEATURES source
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 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2132 ACTCCGTGTTGCCAC 2148
 DB 2 ACTGCGCTGTTGCCAC 18

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RESULT 1375
CQ788499/c
LOCUS          CQ788499          18 bp    DNA          linear          PAT 24-MAR-2004
DEFINITION     Sequence 76 from Patent WO2004020619.
ACCESSION      CQ788499
VERSION        CQ788499.1 GI:45723264
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1
AUTHORS        Constien,R., Mudde,G., Schroeder,A., Yu,P. and Hanke,P.
TITLE          Modified phospholipase C-gamma-2, expression products, and
               non-human animal models comprising said genes, and therapeutic uses
JOURNAL        Patent: WO 2004020619-A 76 11-MAR-2004;
               Ingenium Pharmaceuticals AG (DE)
FEATURES       Location/Qualifiers
               1..18
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="primer p1cg2-60"
Query Match    0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2305 CAGAGCTTTCGTCTGTG 2321
Db 18 CAGTCTTTCGTCTGTG 2

RESULT 1376
E05446/c
LOCUS          E05446          18 bp    DNA          linear          PAT 29-SEP-1997
DEFINITION     DNA sequence of synthetic terminator.
ACCESSION      E05446
VERSION        E05446.1 GI:2173635
KEYWORDS       JP 1993244940-A/6.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Yamaguchi,T., Fukushi,H., Hirai,K., Aoyama,S., Yamaguchi,T.,
               Iritani,K., Hayashi,K., Yoneda,Y., Okawa,S. and Kamogawa,K.
TITLE          RECOMBINANT AVIPOX VIRUS AND VACCINE COMPOSED THEREOF
JOURNAL        Patent: JP 1993244940-A 6 24-SEP-1993;
               NIPPON ZEON CO LTD, SHIONOGI & CO LTD
COMMENT        OS Artificial Gene
               OC Artificial sequence; Genes.
               PN JP 1993244940-A/6
               PD 24-SEP-1993
               PF 04-MAR-1992 JP 1992082800
               PR 09-AUG-1991 JP 91P 224868
               PI YAMAGUCHI TAKESHI, FUKUSHI HIDEOTO, HIRAI KATSUYA, PI Aoyama
               SHIGEMI.
               YASUHIRO.
               YASUHIRO.
               PI OKAWA SETSUKO, KAMOGAWA KOICHI
               PC C12N7/01,A61K39/275,C12N15/40,C12N15/86//C12P21/02,(C12P21/02,
               PC C12R1:92);
               CC strandedness: Double;
               CC topology: Linear;
               CC hypothetical: No;
               CC anti-sense: No.
               Location/Qualifiers
               1..18
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

FEATURES       source
               1..18
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match    0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2305 CAGAGCTTTCGTCTGTG 2321
Db 18 CAGTCTTTCGTCTGTG 2

RESULT 1377
E39158/c
LOCUS          E39158          18 bp    DNA          linear          PAT 18-JUN-2001
DEFINITION     DNA encoding novel fused protein and process for producing useful
               protein mediating the expression thereof.
ACCESSION      E39158
VERSION        E39158.1 GI:13019232
KEYWORDS       JP 1999341991-A/3.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Seiji,S., Masahiko,H., Toshiyuki,K. and Masaaki,K.
TITLE          DNA encoding novel fused protein and process for producing useful
               protein mediating the expression thereof
JOURNAL        Patent: JP 1999341991-A 3 14-DEC-1999;
               ITO HAM KK, JUZO UDAKA
COMMENT        OS Artificial Sequence
               PN JP 1999341991-A/3
               PD 14-DEC-1999
               PF 30-MAR-1999 JP 1999089488
               PR
               PI SEIJI SATO,MASAHIKO HIGASHIKUJI,TOSHIYUKI KUDO,MASAAKI KONDO
               PC C12N15/09,C12N1/21,C12P21/02,C12P21/02//C07K14/605,C07K14/62,
               PC C07K14/655
               PC C07K19/00,(C12N15/09,C12R1:08),(C12N1/21,C12R1:08),(C12P21/02,
               PC C12R1:08),
               PC C12N15/00,(C12N15/00,C12R1:08)
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               FH Key
               FT source
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               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match    0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAGATGAT 1370
Db 18 GTGATGATGATGATGAT 2

RESULT 1378
E39158/c
LOCUS          E39158          18 bp    DNA          linear          PAT 18-JUN-2001
DEFINITION     DNA encoding novel fused protein and process for producing useful
               protein mediating the expression thereof.
ACCESSION      E39158
VERSION        E39158.1 GI:13019232
KEYWORDS       JP 1999341991-A/4.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Seiji,S., Masahiko,H., Toshiyuki,K. and Masaaki,K.
TITLE          DNA encoding novel fused protein and process for producing useful
               protein mediating the expression thereof
JOURNAL        Patent: JP 1999341991-A 4 14-DEC-1999;
               ITO HAM KK, JUZO UDAKA

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COMMENT OS Artificial Sequence
PN JP 1999341991-A/4
PD 14-DEC-1999
PF 30-MAR-1999 JP 1999089488
PR SEIJI SATO,MASAHKO HIGASHIKUJI,TOSHIYUKI KUDO,MASAAKI KONDO
PC C12N15/09,C12N1/21,C12P21/02,C12P21/02//C07K14/605,C07K14/62,
PC C07K14/655
PC C07K19/00,(C12N15/09,C12R1:08),(C12N1/21,C12R1:08),(C12P21/02,
PC C12R1:08),
PC C12N15/00,(C12N15/00,C12R1:08)
CC
EH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
FT Location/Qualifiers
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source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1354 GAGATGATGATGATGAT 1370
Db 1 GTGATGATGATGATGAT 17
RESULT 1379
I18339
LOCUS 18 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 12 from patent US 5495009.
ACCESSION I18339
VERSION I18339.1 GI:1598694
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matteucci,M., Jones,B. and Lin,K.-Y.
TITLE Oligonucleotide analogs containing thioformacetal linkages
JOURNAL Patent: US 5495009-A 12 27-FEB-1996;
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3269 TTTCCTTTGTCCTTTT 3285
Db 1 TTTTCTTTCCTTTT 17
RESULT 1380
I20607/c
LOCUS 18 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 5 from patent US 5514788.
ACCESSION I20607
VERSION I20607.1 GI:1600962
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5514788-A 5 07-MAY-1996;
FEATURES
Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3269 TTTCCTTTGTCCTTTT 3285
Db 1 TTTTCTTTCCTTTT 17
RESULT 1381
I33300/c
LOCUS 18 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 5 from patent US 5591623.
ACCESSION I33300
VERSION I33300.1 GI:1824091
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5591623-A 5 07-JAN-1997;
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2690 CTTTCCCACTTCCACC 2706
Db 18 CTTTCCCACTGCCATC 2
RESULT 1382
I57038/c
LOCUS 18 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 39 from patent US 5650553.
ACCESSION I57038
VERSION I57038.1 GI:2477451
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Ecker,J., Rothenberg,M., Lehman,A. and Roman,G.
TITLE Plant genes for sensitivity to ethylene and pathogens
JOURNAL Patent: US 5650553-A 39 22-JUL-1997;
FEATURES
Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 543 GGCGGGGCTGCCGCCA 559
Db 18 GGCGGGGCTGCCGCCA 2
RESULT 1383
I92477
LOCUS 18 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 7 from patent US 5728523.
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ACCESSION 192477
VERSION 192477.1 GI:3936947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Vogelstein,B. and Kinzler,K.W.
TITLE Polymerase delta mutations in colorectal tumors with replication errors
JOURNAL Patent: US 5728523-A 7 17-MAR-1998;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 657 TGGCAGCAAGGTGGGCC 673
Db 1 TGTGAGCATGGTGGGCC 17

RESULT 1384
AR193175/c
LOCUS AR193175 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 9 from patent US 6346606.
ACCESSION AR193175
VERSION AR193175.1 GI:20239140
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Mollenhauer,J. and Poustka,A.
TITLE Protein containing a scavenger receptor cysteine rich domain
JOURNAL Patent: US 6346606-A 9 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1148 AGCTGCTCGCGACCC 1164
Db 17 AGCTGCTCGCAGACCAC 1

RESULT 1385
AR198571/c
LOCUS AR198571 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 21 from patent US 6352972.
ACCESSION AR198571
VERSION AR198571.1 GI:20248420
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Nimni,M.E., Hall,F.L., Wu,L., Han,B. and Shors,E.C.
TITLE Bone morphogenetic proteins and their use in bone growth
JOURNAL Patent: US 6352972-A 21 05-MAR-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1148 AGCTGCTCGCGACCC 1164
Db 17 AGCTGCTCGCAGACCAC 1

RESULT 1386
AR198571/c
LOCUS AR198571 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 21 from patent US 6352972.
ACCESSION AR198571
VERSION AR198571.1 GI:20248420
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Nimni,M.E., Hall,F.L., Wu,L., Han,B. and Shors,E.C.
TITLE Bone morphogenetic proteins and their use in bone growth
JOURNAL Patent: US 6352972-A 21 05-MAR-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1148 AGCTGCTCGCGACCC 1164
Db 17 AGCTGCTCGCAGACCAC 1

RESULT 1387
AR214545/c
LOCUS AR214545 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 10 from patent US 6410009.
ACCESSION AR214545
VERSION AR214545.1 GI:23312417
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Galun,E., Nahor,O. and Blum,H.E.
TITLE Pharmaceutical composition for treating hepatitis B virus (HBV) infection
JOURNAL Patent: US 6410009-A 10 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 543 GCGCGGCGTCCGCCCA 559
Db 18 GCGGTGGTGCAGCCA 2

RESULT 1387
AR214545/c
LOCUS AR214545 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 10 from patent US 6410009.
ACCESSION AR214545
VERSION AR214545.1 GI:23312417
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Galun,E., Nahor,O. and Blum,H.E.
TITLE Pharmaceutical composition for treating hepatitis B virus (HBV) infection
JOURNAL Patent: US 6410009-A 10 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..18
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 543 GCGCGGCGTCCGCCCA 559
Db 18 GCGGTGGTGCAGCCA 2

RESULT 1388
AR215521/c
LOCUS AR215521 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 69 from patent US 6410323.
ACCESSION AR215521
VERSION AR215521.1 GI:23313777
KEYWORDS
SOURCE Unknown.
```

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Roberts,M.L. and Cowse,L.M.
TITLE Antisense modulation of human Rho family gene expression
JOURNAL Patent: US 6410323-A 69 25-JUN-2002;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1998 CAAGCAGCTGGTGAGG 2014
Db 17 CAAGAGCTGGTGAGG 1

RESULT 1389
AR274624/c
LOCUS AR274624 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 8 from patent US 6506595.
ACCESSION AR274624
VERSION AR274624.1 GI:29707158
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sato,S., Higashikuni,N., Kudo,T. and Kondo,M.
TITLE DNAs encoding new fusion proteins and processes for preparing useful polypeptides through expression of the DNAs
JOURNAL Patent: US 6506595-A 8 14-JAN-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAGATGAT 1370
Db 18 GTGATGATGATGATGAT 2

RESULT 1390
LOCUS AR274625 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 9 from patent US 6506595.
ACCESSION AR274625
VERSION AR274625.1 GI:29707159
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sato,S., Higashikuni,N., Kudo,T. and Kondo,M.
TITLE DNAs encoding new fusion proteins and processes for preparing useful polypeptides through expression of the DNAs
JOURNAL Patent: US 6506595-A 9 14-JAN-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 GAGATGATGAGATGAT 1370
Db 1 GTGATGATGATGATGAT 17

RESULT 1391
AR293143/c
LOCUS AR293143 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4878 from patent US 6537751.
ACCESSION AR293143
VERSION AR293143.1 GI:31680427
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4878 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 AGCAGCTCACCTTCAAG 1551
Db 17 AGCAGCTCAAGTTCAG 1

RESULT 1392
AR294845/c
LOCUS AR294845 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6580 from patent US 6537751.
ACCESSION AR294845
VERSION AR294845.1 GI:31682129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 6580 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2016 CCTGACCGTGCTCTTA 2032
Db 18 CCTGTACCTTGCTCTTA 2

RESULT 1393
AR295340
LOCUS AR295340 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7075 from patent US 6537751.
ACCESSION AR295340
VERSION AR295340.1 GI:31682624
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7075 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7075 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2996 GCACCGCAGTTTGTCTT 3012
||||| |||||
Db 1 GCACCGCATTGTGAT 17

RESULT 1394
AR296057
LOCUS AR296057 18 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7792 from patent US 6537751.
ACCESSION AR296057
VERSION AR296057.1 GI:31693341
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7792 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 53 GGCTGCGAGTGCTGAAT 69
||||| ||||| |||||
Db 1 GGCTTCAGGTGCTAAAT 17

RESULT 1395
AR370530/c
LOCUS AR370530 18 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 5 from patent US 6300491.
ACCESSION AR370530
VERSION AR370530.1 GI:34607283
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C.F. and Mirabelli, C.K.
TITLE Oligonucleotide inhibition of cell adhesion
JOURNAL Patent: US 6300491-A 5 09-OCT-2001;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2690 CTTTCCCACTTCCACC 2706
||||| ||||| |||||

Db 18 CTTTCCCACTGCCCATC 2

RESULT 1396
AR390575
LOCUS AR390575 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 445 from patent US 6610839.
ACCESSION AR390575
VERSION AR390575.1 GI:40112501
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Morin, G.B. and Andrews, W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 445 26-AUG-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 458 GCGTCGTGGAGACAAG 474
||||| ||||| |||||
Db 1 GCGACATGGAGACAAG 17

RESULT 1397
AR393189
LOCUS AR393189 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 445 from patent US 6617110.
ACCESSION AR393189
VERSION AR393189.1 GI:40118483
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B., Harley, C.B. and Andrews, W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in drug screening
JOURNAL Patent: US 6617110-A 445 09-SEP-2003;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 458 GCGTCGTGGAGACAAG 474
||||| ||||| |||||
Db 1 GCGACATGGAGACAAG 17

RESULT 1398
AX060284
LOCUS AX060284 18 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 8 from Patent WO0100831.
ACCESSION AX060284
VERSION AX060284.1 GI:12405773
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Conklin, D.C. and Gao, Z.

TITLE Helical polypeptide zalpha29
JOURNAL Patent: WO 010831-A 8 04-JAN-2001;
ZymoGenetics, Inc. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide primer ZC21,720"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1857 GTACCCCGGATCCCTG 1873
Db 2 GTACCCCGGATCACAG 18

RESULT 1399
AX060757
LOCUS AX060757 18 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 45 from Patent WO0078972.
ACCESSION AX060757
VERSION AX060757.1 GI:12406144
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Lawn, R.M., Wade, D. and Garvin, M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 45 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ABC1 sequencing primer"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2100 GGACACCCCGAGTCCA 2116
Db 2 GGACACCCCGAGCTTCA 18

RESULT 1400
AX060936
LOCUS AX060936 18 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 45 from Patent WO0078971.
ACCESSION AX060936
VERSION AX060936.1 GI:12406311
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
TITLE ATP binding cassette transporter protein abc1 polypeptides
JOURNAL Patent: WO 0078971-A 45 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ABC1 sequencing primer"

Query Match 0.4%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2100 GGACACCCCGAGTCCA 2116
Db 2 GGACACCCCGAGCTTCA 18

RESULT 1401
AX082556
LOCUS AX082556 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 7 from Patent WO0111047.
ACCESSION AX082556
VERSION AX082556.1 GI:13184666
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bowman, B.M. and Wang, K.
TITLE Dna sequences isolated from human colonic epithelial cells
JOURNAL Patent: WO 0111047-A 7 15-FEB-2001;
Bayer Corporation (US)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3411 GGGAGGGCGCGCCCTG 3427
Db 1 GGGAGGAGCCAGCCCTG 17

RESULT 1402
AX082560
LOCUS AX082560 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 11 from Patent WO0111047.
ACCESSION AX082560
VERSION AX082560.1 GI:13184670
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bowman, B.M. and Wang, K.
TITLE Dna sequences isolated from human colonic epithelial cells
JOURNAL Patent: WO 0111047-A 11 15-FEB-2001;
Bayer Corporation (US)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3411 GGGAGGGCGCGCCCTG 3427
Db 1 GGGAGGAGCCAGCCCTG 17

RESULT 1403
AX082562
LOCUS AX082562 18 bp DNA linear PAT 28-FEB-2001

DEFINITION Sequence 13 from Patent WO0111047.
ACCESSION AX082562
VERSION AX082562.1 GI:13184672
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE
AUTHORS Bowman, B.M. and Wang, K.
TITLE Dna sequences isolated from human colonic epithelial cells
JOURNAL Patent: WO 0111047-A 13 15-FEB-2001;
Bayer Corporation (US)
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3411 GGGAGGGCGCGCCCTG 3427
||||| ||||| ||||| |||||
Db 1 GGGAGGAGCCAGCCCTG 17

RESULT 1404
AX101276
LOCUS AX101276 18 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 17 from Patent WO0121791.
ACCESSION AX101276
VERSION AX101276.1 GI:13620066
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL
FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 428 TGGTGGCCCTCGACCGC 444
||||| ||||| ||||| |||||
Db 2 TGGTGGCATCGACCGC 18

RESULT 1405
AX110441
LOCUS AX110441 18 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 1174 from Patent WO0123604.
ACCESSION AX110441
VERSION AX110441.1 GI:13926733
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
TITLE Picard, F.J. and Roy, P.H.
JOURNAL Highly conserved genes and their use to generate probes and primers

for detection of microorganisms
Patent: WO 0123604-A 1174 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1660 AACGTGATGAAGATCGC 1676
||||| ||||| ||||| |||||
Db 2 AACGTGATGAAGTTCGC 18

RESULT 1406
AX111434/c
LOCUS AX111434 18 bp DNA linear PAT 29-MAY-2002
DEFINITION Sequence 2167 from Patent WO0123604.
ACCESSION AX111434
VERSION AX111434.1 GI:13927726
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
TITLE Picard, F.J. and Roy, P.H.
JOURNAL Highly conserved genes and their use to generate probes and primers
JOURNAL for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2167 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 CCGCTGCCCGCCGCGCTG 313
||||| ||||| ||||| |||||
Db 17 CCGCGCCCGCCGCGCTG 1

RESULT 1407
AX233412
LOCUS AX233412 18 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 55 from Patent WO0162788.
ACCESSION AX233412
VERSION AX233412.1 GI:15592750
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Olaveson, M., Lench, N., Allen, M. and Tazi-Ahmini, R.U.
TITLE Corneodesmosin based test and model for inflammatory disease
JOURNAL Patent: WO 0162788-A 55 30-AUG-2001;
Oxagen Limited (GB)
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 319 CCCACTCCCTCCATCTC 335
 Db 1 CCCACCCCTCCACCTC 17

RESULT 1408
 LOCUS AX599395/c 18 bp DNA linear PAT 14-FEB-2003
 DEFINITION Sequence 735 from Patent WO02077272.
 ACCESSION AX599395
 VERSION AX599395.1 GI:28399539
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.
 TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
 JOURNAL Patent: WO 02077272-A 735 03-OCT-2002;
 Epigenomics AG (DE)
 FEATURES
 source Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Detection oligonucleotide for DAPK1"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTCCGAAATAT 3778
 Db 17 AATTTCCGAAATAT 1

RESULT 1409
 LOCUS AX599440/c 18 bp DNA linear PAT 14-FEB-2003
 DEFINITION Sequence 780 from Patent WO02077272.
 ACCESSION AX599440
 VERSION AX599440.1 GI:28399584
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.
 TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
 JOURNAL Patent: WO 02077272-A 780 03-OCT-2002;
 Epigenomics AG (DE)
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Detection oligonucleotide for MLH1"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
 Db 18 ATACTTAACACTTCTCA 2

RESULT 1410
 LOCUS AX599728 18 bp DNA linear PAT 14-FEB-2003
 DEFINITION Sequence 1068 from Patent WO02077272.
 ACCESSION AX599728
 VERSION AX599728.1 GI:28399876
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Berlin, K., Braun, A., Distler, J., Guetig, D., Howe, A., Mueller, J., Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E., Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T., Pelet, C. and Ziebarth, H.
 TITLE Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
 JOURNAL Patent: WO 02077272-A 1068 03-OCT-2002;
 Epigenomics AG (DE)
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Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3481 TAATTTATGAGTGT 3497
 Db 1 TAATTTATGAGTGT 17

RESULT 1411
 LOCUS AX659428/c 18 bp DNA linear PAT 22-MAR-2003
 DEFINITION Sequence 30 from Patent WO02102824.
 ACCESSION AX659428
 VERSION AX659428.1 GI:29161658
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Beinfuhr, C. and Snajdr, J.
 TITLE Method for specific fast detection of relevant bacteria in drinking water
 JOURNAL Patent: WO 02102824-A 30 27-DEC-2002;
 Vermicon AG (DE)
 FEATURES
 source Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="oligonucleotide"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1222 TTCGGCCAGGTGGTCAT 1238
 Db 17 TTCGGCTAGGGGTCTAT 1

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RESULT 1412
AX695098/c
LOCUS AX695098 18 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 725 from Patent WO03008583.
ACCESSION AX695098
VERSION AX695098.1 GI:29418216
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Morris,D.W. and Engelhard,E.K.
TITLE Novel compositions and methods for cancer
JOURNAL Patent: WO 03008583-A 725 30-JAN-2003;
Sagres Discovery (US)
FEATURES
source Location/Qualifiers
1. .18
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2334 CGTGTGTGTGTGTGT 2350
Db 18 CATGTGTGTGTGTGT 2

RESULT 1413
AX705489/c
LOCUS AX705489 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 158 from Patent WO03014388.
ACCESSION AX705489
VERSION AX705489.1 GI:29562154
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Distler,J., Model,F. and Taubert,H.
TITLE Method and nucleic acids for the analysis of colon cancer
JOURNAL Patent: WO 03014388-A 158 20-FEB-2003;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for p21"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 17 AACCTCGCTACTACAA 1

RESULT 1414
AX705491
LOCUS AX705491 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 160 from Patent WO03014388.
ACCESSION AX705491
VERSION AX705491.1 GI:29562156
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lymphoid cell
JOURNAL Patent: WO 03044226-A 458 30-MAY-2003;
Epigenomics AG (DE)
FEATURES
source Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for p21"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 17 AACCTCGCTACTACAA 1

RESULT 1416
AX767810/c
LOCUS AX767810 18 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 458 from Patent WO03044226.
ACCESSION AX767810
VERSION AX767810.1 GI:32436496
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
AUTHORS Burger,M., Caldwell,C., Genc,B., Becker,E., Maier,S. and
Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lymphoid cell
JOURNAL Patent: WO 03044226-A 458 30-MAY-2003;
Epigenomics AG (DE)
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source Location/Qualifiers
1. .18
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Detection oligonucleotide for CDKN1A"

Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1705 AACCTCGACTACTACAA 1721
Db 17 AACCTCGCTACTACAA 1
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/db_xref="taxon:32630"
/note="Detection oligonucleotide for MLH1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1419
AX796279/c 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 622 from Patent WO03052135.
ACCESSION AX796279
VERSION AX796279.1 GI:37516945
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell
JOURNAL proliferative disorder
Patent: WO 03052135-A 622 26-JUN-2003;
Epigenomics AG (DE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTCCGAAATAA 3778
Db 17 AATTTCCGAAACAA 1

RESULT 1418
AX796334/c 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 677 from Patent WO03052135.
ACCESSION AX796334
VERSION AX796334.1 GI:37517000
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell
JOURNAL proliferative disorder
Patent: WO 03052135-A 677 26-JUN-2003;
Epigenomics AG (DE)
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1420
AX823043/c 18 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 935 from Patent EP1340818.
ACCESSION AX823043
VERSION AX823043.1 GI:39749679
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 935 03-SEP-2003;
Epigenomics AG (DE)
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1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTCCGAAATAA 3778
Db 17 AATTTCCGAAACAA 1

RESULT 1417
AX796279/c 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 622 from Patent WO03052135.
ACCESSION AX796279
VERSION AX796279.1 GI:37516945
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell
JOURNAL proliferative disorder
Patent: WO 03052135-A 622 26-JUN-2003;
Epigenomics AG (DE)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1419
AX822802/c 18 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 694 from Patent EP1340818.
ACCESSION AX822802
VERSION AX822802.1 GI:39749438
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 694 03-SEP-2003;
Epigenomics AG (DE)
FEATURES
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for MLH1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1420
AX823043/c 18 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 935 from Patent EP1340818.
ACCESSION AX823043
VERSION AX823043.1 GI:39749679
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 935 03-SEP-2003;
Epigenomics AG (DE)
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/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTCCGAAATAA 3778
Db 17 AATTTCCGAAACAA 1

RESULT 1417
AX796279/c 18 bp DNA linear PAT 04-OCT-2003
LOCUS
DEFINITION Sequence 622 from Patent WO03052135.
ACCESSION AX796279
VERSION AX796279.1 GI:37516945
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Burger,M., Field,J.K., Genc,B., Liloglou,T., Lipscher,E., Maier,S.
and Nimmrich,I.
TITLE Method and nucleic acids for the analysis of a lung cell
JOURNAL proliferative disorder
Patent: WO 03052135-A 622 26-JUN-2003;
Epigenomics AG (DE)
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/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1419
AX822802/c 18 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 694 from Patent EP1340818.
ACCESSION AX822802
VERSION AX822802.1 GI:39749438
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 694 03-SEP-2003;
Epigenomics AG (DE)
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Detection oligonucleotide for MLH1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3516 AGACTTAACACTTCTTA 3532
Db 18 ATACTTAACACTTCTCA 2

RESULT 1420
AX823043/c 18 bp DNA linear PAT 11-DEC-2003
LOCUS
DEFINITION Sequence 935 from Patent EP1340818.
ACCESSION AX823043
VERSION AX823043.1 GI:39749679
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 935 03-SEP-2003;
Epigenomics AG (DE)
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/note="Detection oligonucleotide for DAPK1"

Query Match      0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3762 AACTTCCGAAATAA 3778
Db 17 AATTTCCGAAACAA 1

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RESULT 1421
AX826442/c
LOCUS AX826442 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 694 from Patent WO03072821.
ACCESSION AX826442
VERSION AX826442.1 GI:39751956
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1.
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: WO 03072821-A 694 04-SEP-2003;
Epigenomics AG (DE)
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1. .18
/organism="synthetic construct"
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/note="Detection oligonucleotide for MLH1"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3516 AGACTTAACACTTCTTA 3532
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Db 18 ATACTTAACACTTCTCA 2

RESULT 1422
AX826683/c
LOCUS AX826683 18 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 935 from Patent WO03072821.
ACCESSION AX826683
VERSION AX826683.1 GI:39752197
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1.
AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,
Rujan,T. and Schmitt,A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: WO 03072821-A 935 04-SEP-2003;
Epigenomics AG (DE)
FEATURES
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1. .18
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/db_xref="taxon:32630"
/note="Detection oligonucleotide for DAPK1"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3762 AACTTTCGAAATATAA 3778
| ||||| ||||| |||||
Db 17 AAATTCGAAATACAA 1

RESULT 1423
BD023630/c
LOCUS BD023630 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Polypeptide belonging to the family of basic helix-loop-helix
(BHLH) family and nucleic acid sequence corresponding thereto.
ACCESSION BD023630
VERSION BD023630.1 GI:22564853
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KEYWORDS JP 2001510464-A/5.
SOURCE Rattus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
REFERENCE
1 (bases 1 to 18)
AUTHORS Liepkalns,C.I., Mallet,J. and Ravassard,P.
TITLE Polypeptide belonging to the family of basic helix-loop-helix
(BHLH) family and nucleic acid sequence corresponding thereto
JOURNAL Patent: JP 2001510464-A 5 31-JUL-2001;
RHONE-POULENC RORER SA
COMMENT PN JP 2001510464-A/5
PD 31-JUL-2001
PF 19-DEC-1997 JP 1998527415
PR 19-DEC-1996 FR 96/15651
PI CHRISTINE ICARD LIEPKALNS,JACQUES MALLET,PHILIPPE RAVASSARD PC
C07K14/47,A61K31/711,A61K35/76,A61K38/00,A61K48/00,A61P25/00, PC
C12N15/09,
PC C12N15/00,A61K37/02
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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1. .18
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/mol_type="genomic DNA"
/db_xref="taxon:10118"
Query Match 0.4%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2092 GGTGGCCAGGACACCCC 2108
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Db 18 GGTGGCCAGGACACCCG 2

RESULT 1424
BD064969/c
LOCUS BD064969 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Protein containing an SRCR domain.
ACCESSION BD064969
VERSION BD064969.1 GI:22610572
KEYWORDS JP 2001509667-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 18)
AUTHORS Mollenhauer,J. and Poustka,A.
TITLE Protein containing an SRCR domain
JOURNAL Patent: JP 2001509667-A 7 24-JUL-2001;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS
COMMENT OS Artificial Sequence
PN JP 2001509667-A/7
PD 24-JUL-2001
PF 09-JAN-1998 JP 1998530469
PR 09-JAN-1997 DE 197 00 519.5,18-JUL-1997 DE 197 30 997.6 PI
JAN MOLLENHAUER,ANNEMARIE POUSTKA
PC C12N15/12,C12N15/70,C12N1/21,C12Q1/68,C07K14/47,C07K16/18, PC
A61K38/17,
PC A61K48/00,G01N33/50
CC Description of Artificial Sequence: primer sequence for CC
amplifying a DNA
encoding a protein containing SRCR domain.
FH Key Location/Qualifiers
FT source
1. .18
/organism="Artificial Sequence".
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1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1148 AGCTGCTGCGACCC 1164
 Db 17 AGCTGCTGCGACCC 1

RESULT 1425
 BD065700/c 18 bp DNA linear PAT 27-AUG-2002
 LOCUS An antisense oligonucleotide preparation method.
 DEFINITION
 ACCESSION BD065700
 VERSION BD065700.1 GI:22611303
 KEYWORDS JP 2001511000-A/335.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Schlingsiepen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 335 07-AUG-2001;
 BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MEH

COMMENT OS Unknown
 PN JP 2001511000-A/335
 PD 07-AUG-2001
 PR 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGSIEPEN,WOLFGANG BRYSCH
 PC C12N15/11,C07H21/04,A61K31/70
 CC An antisense oligonucleotide preparation method FH Key
 FT source 1.18
 FT Location/Qualifiers
 /organism='Unknown'

FEATURES
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 /db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1792 CACCAGGTGACGTCTG 1808
 Db 17 CACCAGGTGATGTGTG 1

RESULT 1426
 BD070462 18 bp DNA linear PAT 27-AUG-2002
 LOCUS Methods for detecting mitochondrial mutations diagnostic for
 DEFINITION Alzheimer's disease and methods for determining heteroplasmy of
 mitochondrial nucleic acid.
 ACCESSION BD070462
 VERSION BD070462.1 GI:22616065
 KEYWORDS JP 2001514500-A/19.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Parkes,W.D., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
 TITLE Methods for detecting mitochondrial mutations diagnostic for
 Alzheimer's disease and methods for determining heteroplasmy of
 mitochondrial nucleic acid
 JOURNAL Patent: JP 2001514500-A 19 11-SEP-2001;
 MITOKOR
 COMMENT OS Unidentified
 PN JP 2001514500-A/19
 PD 11-SEP-2001

PF 27-FEB-1998 JP 1998537738
 PR 28-FEB-1997 US 08/810599
 PI WILLIAM DAVIS PARKER,CORINNA HERRNSTADT,SOUMITRA GHOSH,BOIN D
 PI FAHY
 PC C12Q1/68,C07H21/04
 CC Strandedness: Double;
 CC Topology: Linear;
 CC Methods for detecting mitochondrial mutations diagnostic for
 CC Alzheimer's
 CC disease and methods for determining heteroplasmy of CC
 mitochondrial nucleic
 CC acid
 FH Key Location/Qualifiers
 FT source 1.18
 FT /organism='Unidentified'

FEATURES
 source
 1.18
 Location/Qualifiers
 /organism='unidentified'
 /mol_type='genomic DNA'
 /db_xref='taxon:32644'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2075 TCGAGCAGTACTCCCG 2091
 Db 2 TCGAGTAGTACTCCCG 18

RESULT 1427
 BD089937 18 bp DNA linear PAT 27-AUG-2002
 LOCUS A method of arraying genome clone.
 DEFINITION
 ACCESSION BD089937
 VERSION BD089937.1 GI:22635547
 KEYWORDS JP 2001321190-A/2181.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Soeda,E.
 TITLE A method of arraying genome clone
 JOURNAL Patent: JP 2001321190-A 2181 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
 GENOTECHS

COMMENT OS Artificial Sequence
 PN JP 2001321190-A/2181
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EIICHI SOEDA
 PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
 C12N15/00,
 PC C12N15/00
 CC Description of Artificial Sequence:Synthetic DNA FH Key
 CC Location/Qualifiers
 FT source 1.18
 FT /organism='Artificial Sequence'

FEATURES
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 1.18
 Location/Qualifiers
 /organism='synthetic construct'
 /mol_type='genomic DNA'
 /db_xref='taxon:32630'

Query Match 0.4%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2101 GACACCCCGCTCCAG 2117
 Db 2 GACACCCCGCTCCAG 18

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RESULT 1428
SSAJ787/c
LOCUS          SSAJ787          19 bp  mRNA          linear          MAM 29-JUL-1997
DEFINITION     Sus scrofa EST 3'UTR SSCIG2 forward primer.
ACCESSION      AJ000787
VERSION        AJ000787.1  GI:2286010
KEYWORDS       PCR primer.
SOURCE         Sus scrofa (pig)
ORGANISM       Sus scrofa
               Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Fridolfsson,A.K., Hori,T., Wintero,A.K., Fredholm,M., Yerle,M.,
               Robic,A., Andersson,L. and Ellegren,H.
TITLE          Expansion of the pig comparative map by expressed sequence tags
               (EST) mapping
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 19)
AUTHORS        Fridolfsson,A.K.
TITLE          Direct Submission
JOURNAL        Submitted (27-JUL-1997) Fridolfsson A.K., Animal Breeding and
               Genetics, Swedish University of Agricultural Sciences, Biomedical
               Center, Box 597, S-751 24 Uppsala, SWEDEN
FEATURES       Location/Qualifiers
               source
               1..19
               /organism="Sus scrofa"
               /mol_type="mRNA"
               /db_xref="taxon:9823"
               /chromosome="1"
               /map="1q"
Query Match    0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1565 GTGCTTACCGAGTGGCC 1581
Db 17 GTGCTTCCAGGTGGCC 1

RESULT 1429
A36743/c
LOCUS          A36743          19 bp  DNA          linear          PAT 05-MAR-1997
DEFINITION     Sequence 9 from Patent EP0584023.
ACCESSION      A36743
VERSION        A36743.1  GI:2294010
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unidentified
               unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Mabilat,C. and Pechere,J.
TITLE          Mycobacteria DNA fragments, amplification primers, hybridization
               probes, reagents and detection process of mycobacteria
JOURNAL        Patent: EP 0584023-A 9 23-FEB-1994;
               BIO MERIEUX (FR)
COMMENT        Other publication CA 2103933 940213
               Other publication FR 2694754 940218.
FEATURES       Location/Qualifiers
               source
               1..19
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
Query Match    0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 242 CCGAGCGGATGGACAAG 258
Db 19 CCGAGCGGATGGACAAG 3

RESULT 1430
SSAJ787/c
LOCUS          SSAJ787          19 bp  mRNA          linear          MAM 29-JUL-1997
DEFINITION     Sus scrofa EST 3'UTR SSCIG2 forward primer.
ACCESSION      AJ000787
VERSION        AJ000787.1  GI:2286010
KEYWORDS       PCR primer.
SOURCE         Sus scrofa (pig)
ORGANISM       Sus scrofa
               Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Fridolfsson,A.K., Hori,T., Wintero,A.K., Fredholm,M., Yerle,M.,
               Robic,A., Andersson,L. and Ellegren,H.
TITLE          Expansion of the pig comparative map by expressed sequence tags
               (EST) mapping
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 19)
AUTHORS        Fridolfsson,A.K.
TITLE          Direct Submission
JOURNAL        Submitted (27-JUL-1997) Fridolfsson A.K., Animal Breeding and
               Genetics, Swedish University of Agricultural Sciences, Biomedical
               Center, Box 597, S-751 24 Uppsala, SWEDEN
FEATURES       Location/Qualifiers
               source
               1..19
               /organism="Sus scrofa"
               /mol_type="mRNA"
               /db_xref="taxon:9823"
               /chromosome="1"
               /map="1q"
Query Match    0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1565 GTGCTTACCGAGTGGCC 1581
Db 17 GTGCTTCCAGGTGGCC 1

RESULT 1431
A36743/c
LOCUS          A36743          19 bp  DNA          linear          PAT 05-MAR-1997
DEFINITION     Sequence 9 from Patent EP0584023.
ACCESSION      A36743
VERSION        A36743.1  GI:2294010
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unidentified
               unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Mabilat,C. and Pechere,J.
TITLE          Mycobacteria DNA fragments, amplification primers, hybridization
               probes, reagents and detection process of mycobacteria
JOURNAL        Patent: EP 0584023-A 9 23-FEB-1994;
               BIO MERIEUX (FR)
COMMENT        Other publication CA 2103933 940213
               Other publication FR 2694754 940218.
FEATURES       Location/Qualifiers
               source
               1..19
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
Query Match    0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 242 CCGAGCGGATGGACAAG 258
Db 19 CCGAGCGGATGGACAAG 3

RESULT 1432
A36744/c
LOCUS          A36744          19 bp  DNA          linear          PAT 29-SEP-1999
DEFINITION     Sequence 10 from Patent EP0584023.
ACCESSION      A36744
VERSION        A36744.1  GI:2294011
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unidentified
               unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Mabilat,C. and Pechere,J.
TITLE          Mycobacteria DNA fragments, amplification primers, hybridization
               probes, reagents and detection process of mycobacteria
JOURNAL        Patent: EP 0584023-A 10 23-FEB-1994;
               BIO MERIEUX (FR)
COMMENT        Other publication CA 2103933 940213
               Other publication FR 2694754 940218.
FEATURES       Location/Qualifiers
               source
               1..19
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
Query Match    0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTAATTTTAACTT 17

RESULT 1433
A36744/c
LOCUS          A36744          19 bp  DNA          linear          PAT 29-SEP-1999
DEFINITION     Sequence 10 from Patent EP0584023.
ACCESSION      A36744
VERSION        A36744.1  GI:2294011
KEYWORDS       unidentified
SOURCE         unidentified
ORGANISM       unidentified
               unclassified.
REFERENCE      1 (bases 1 to 19)
AUTHORS        Mabilat,C. and Pechere,J.
TITLE          Mycobacteria DNA fragments, amplification primers, hybridization
               probes, reagents and detection process of mycobacteria
JOURNAL        Patent: EP 0584023-A 10 23-FEB-1994;
               BIO MERIEUX (FR)
COMMENT        Other publication CA 2103933 940213
               Other publication FR 2694754 940218.
FEATURES       Location/Qualifiers
               source
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               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"
Query Match    0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTAATTTTAACTT 17
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TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 4 19-JAN-1999;
FEATURES   Location/Qualifiers
            source
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            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1433
AR030974
LOCUS      AR030974      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5861501.
ACCESSION AR030974
VERSION    AR030974.1 GI:5944188
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 6 19-JAN-1999;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1434
AR030975
LOCUS      AR030975      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5861501.
ACCESSION AR030975
VERSION    AR030975.1 GI:5944189
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 7 19-JAN-1999;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1435
AR030976
LOCUS      AR030976      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5861501.
ACCESSION AR030976
VERSION    AR030976.1 GI:5944190
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 8 19-JAN-1999;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1436
AR030977
LOCUS      AR030977      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5861501.
ACCESSION AR030977
VERSION    AR030977.1 GI:5944191
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 9 19-JAN-1999;
FEATURES   Location/Qualifiers
            source
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            /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17

RESULT 1437
AR030978
LOCUS      AR030978      19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5861501.
ACCESSION AR030978
VERSION    AR030978.1 GI:5944192
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE      Capped synthetic RNA, analogs, and aptamers
JOURNAL    Patent: US 5861501-A 10 19-JAN-1999;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3114 GTTTTAATTTTAACTT 3130
Db      1 GTTTTATTTTAAATT 17
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Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1438
AR030981
LOCUS AR030981 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 13 from patent US 5861501.
ACCESSION AR030981
VERSION AR030981.1 GI:5944195
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 13 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1439
AR030982
LOCUS AR030982 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5861501.
ACCESSION AR030982
VERSION AR030982.1 GI:5944196
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 14 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1440
AR030983
LOCUS AR030983 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5861501.
ACCESSION AR030983
VERSION AR030983.1 GI:5944197
KEYWORDS

SOURCE Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 15 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1441
AR030984
LOCUS AR030984 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5861501.
ACCESSION AR030984
VERSION AR030984.1 GI:5944198
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 5861501-A 16 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1442
AR066286/c
LOCUS AR066286 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5849901.
ACCESSION AR066286
VERSION AR066286.1 GI:5996502
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Mablat,C. and Pechere,J.-C.
TITLE DNA fragments of mycobacteria, amplification primers hybridization
probes, reagents and method for the detection of mycobacteria
JOURNAL Patent: US 5849901-A 9 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 242 CCGAGCGGATGGACAAG 258
Db 19 CCGAGCGGATGGACAAG 3

RESULT 1443
LOCUS AR066287 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5849901.
ACCESSION AR066287
VERSION AR066287.1 GI:5996503
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Mabilat,C. and Pechere,J.-C.
TITLE DNA fragments of mycobacteria, amplification primers hybridization
JOURNAL probes, reagents and method for the detection of mycobacteria
FEATURES Patent: US 5849901-A 10 15-DEC-1998;
source Location/Qualifiers
1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 242 CCGAGCGGATGGACAAG 258
Db 1 CCGAGCGGATGGACAAG 17

RESULT 1444
LOCUS AR066714/c 19 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 62 from patent US 5851760.
ACCESSION AR066714
VERSION AR066714.1 GI:5997936
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Evans,G.A. and Smith,M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 62 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 872 CTGACGAGGGGGGAGT 888
Db 17 CTGACGAGGGGGGAGT 1

RESULT 1445
LOCUS AR083027 19 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 53 from patent US 5976798.
ACCESSION AR083027
VERSION AR083027.1 GI:10009817
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)

Parker,W.Davis., Herrstadt,C., Ghosh,S. and Fahy,E.D.
Methods for detecting mitochondrial mutations diagnostic for
Alzheimer's disease and methods for determining heteroplasmy of
mitochondrial nucleic acid
Patent: US 5976798-A 53 02-NOV-1999;
Location/Qualifiers
1..19
/mol_type="unassigned DNA"

AUTHORS
TITLE
JOURNAL
FEATURES source
1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1932 CACACACGACCTGTACA 1948
Db 3 CACACACGACCTGTCCA 19

RESULT 1446
LOCUS AR108814 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6111095.
ACCESSION AR108814
VERSION AR108814.1 GI:12824301
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 1 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTAATTTTAAATT 17

RESULT 1447
LOCUS AR108817 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 4 from patent US 6111095.
ACCESSION AR108817
VERSION AR108817.1 GI:12824304
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 4 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..19
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTAATTTTAAATT 17
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RESULT 1448
AR108819
LOCUS AR108819 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 6 from patent US 6111095.
ACCESSION AR108819
VERSION AR108819.1 GI:12824306
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 6 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1450
AR108821
LOCUS AR108821 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 8 from patent US 6111095.
ACCESSION AR108821
VERSION AR108821.1 GI:12824308
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 9 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1449
AR108820
LOCUS AR108820 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6111095.
ACCESSION AR108820
VERSION AR108820.1 GI:12824307
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 7 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1452
AR108823
LOCUS AR108823 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 10 from patent US 6111095.
ACCESSION AR108823
VERSION AR108823.1 GI:12824310
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 10 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
||||| |||||||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1453
AR108826
LOCUS AR108826 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6111095.
ACCESSION AR108826
VERSION AR108826.1 GI:12824309
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 9 29-AUG-2000;
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 GTTTTATTTTAAATTT 17

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Query Match 0.4%; Score 13.8; DB 1; Length 19;
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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

RESULT 1451
AR108822
LOCUS AR108822 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6111095.
ACCESSION AR108822
VERSION AR108822.1 GI:12824309
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 9 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
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Db 1 GTTTTATTTTAAATTT 17

source 1..19
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
||||| |||||||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1450
AR108821
LOCUS AR108821 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 8 from patent US 6111095.
ACCESSION AR108821
VERSION AR108821.1 GI:12824308
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 9 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
||||| |||||||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1449
AR108820
LOCUS AR108820 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6111095.
ACCESSION AR108820
VERSION AR108820.1 GI:12824307
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 7 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
||||| |||||||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1452
AR108823
LOCUS AR108823 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 10 from patent US 6111095.
ACCESSION AR108823
VERSION AR108823.1 GI:12824310
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 10 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
||||| |||||||
Db 1 GTTTTATTTTAAATTT 17

RESULT 1453
AR108826
LOCUS AR108826 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6111095.
ACCESSION AR108826
VERSION AR108826.1 GI:12824309
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 19)
AUTHORS Benseler,F., Cole,J.L., Olsen,D.B. and Kuo,L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6111095-A 9 29-AUG-2000;
FEATURES
source
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3114 GTTTAAATTTTAACTT 3130
||||| |||||||
Db 1 GTTTTATTTTAAATTT 17
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ACCESSION AR108826
VERSION AR108826.1 GI:12824313
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler, F., Cole, J.L., Olsen, D.B. and Kuo, L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 611095-A 13 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..19
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAAATTTTAACTT 3130
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Db 1 GTTTTAAATTTTAAATTT 17

RESULT 1454
AR108827
LOCUS AR108827 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 611095.
ACCESSION AR108827
VERSION AR108827.1 GI:12824314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler, F., Cole, J.L., Olsen, D.B. and Kuo, L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 611095-A 14 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..19
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAAATTTTAACTT 3130
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Db 1 GTTTTAAATTTTAAATTT 17

RESULT 1454
AR108827
LOCUS AR108827 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 611095.
ACCESSION AR108827
VERSION AR108827.1 GI:12824314
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler, F., Cole, J.L., Olsen, D.B. and Kuo, L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 611095-A 14 29-AUG-2000;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAAATTTTAACTT 3130
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Db 1 GTTTTAAATTTTAAATTT 17

RESULT 1455
AR108828
LOCUS AR108828 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 15 from patent US 611095.
ACCESSION AR108828
VERSION AR108828.1 GI:12824315
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler, F., Cole, J.L., Olsen, D.B. and Kuo, L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 611095-A 15 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAAATTTTAACTT 3130
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Db 1 GTTTTAAATTTTAAATTT 17

RESULT 1456
AR108829
LOCUS AR108829 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 16 from patent US 611095.
ACCESSION AR108829
VERSION AR108829.1 GI:12824316
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Benseler, F., Cole, J.L., Olsen, D.B. and Kuo, L.C.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 611095-A 16 29-AUG-2000;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAAATTTTAACTT 3130
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Db 1 GTTTTAAATTTTAAATTT 17

RESULT 1457
BD196756/c
LOCUS BD196756 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Prostatic cancer gene.
ACCESSION BD196756
VERSION BD196756.1 GI:33006526
KEYWORDS JP 2002516657-A/345.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen, D., Blumenfeld, M., Chumakov, I. and Bougueleret, L.
TITLE Prostatic cancer gene
JOURNAL Patent: JP 2002516657-A 345 11-JUN-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002516657-A/345
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306, 09-SEP-1998 US 60/099658 PI
DANIEL COHEN, MARTA BLUMENFELD, ILYA CHUMAKOV, LYDIE BOUGUELERET, PC
C12N15/09, C12N15/09, A01K67/027, C07K14/47, C07K16/18, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12N5/10, C12P21/08, C12Q1/68, G01N33/50 PC
C12N15/00, C12N5/00,
PC C12N5/00, C12N15/00
CC upstream amplification primer for SEQ 250, SEQ 327 FH Key
Location/Qualifiers
FT primer bind 1..19.
Location/Qualifiers
source 1..19
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/db_xref="taxon:9606"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2751 CTTTACCTTTTATGCAA 2767
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 Db 17 CTATACCTTTTGTGCAA 1

RESULT 1458
 BD226482
 LOCUS 19 bp DNA linear PAT 17-JUL-2003
 DEFINITION Method and probes for the detection of chromosome aberrations.
 ACCESSION BD226482
 VERSION BD226482.1 GI:33036252
 KEYWORDS JP 2002513587-A/28.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dongen,J.J.M.V., Pluzek,K.J., Nielsen,K.V. and Adelhörst,K.
 TITLE Method and probes for the detection of chromosome aberrations
 JOURNAL Patent: JP 2002513587-A 28 14-MAY-2002;
 DAKO AS

COMMENT
 OS Artificial Sequence
 PN JP 2002513587-A/28
 PD 14-MAY-2002
 PF 04-MAY-1999 JP 2000547260
 PR 04-MAY-1998 DK 0615/98
 PI JACOBS JOHANNES MARIA VAN DONGEN,KARL JOHAN PLUZEK,KIRSTEN PI
 VANG NIELSEN,
 PI KIM ADELHORST
 PC C12N15/09,C07H21/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
 Description of Artificial Sequence:PNA probe, mbr, exon 28, CC
 position

CC 411-393
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 FT source 1..19
 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
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FEATURES
 source
 Query Match 0.4%; Score 13.8; DB 1; Length 19;
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QY 3558 CTGGACTGCTTCTTC 3574
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 Db 3 CTGGACTGCTTCTTC 19

RESULT 1459
 BD232821
 LOCUS 19 bp DNA linear PAT 17-JUL-2003
 DEFINITION Diagnostic method based on the quantification of extramitochondrial
 DNA
 ACCESSION BD232821
 VERSION BD232821.1 GI:33042591
 KEYWORDS JP 2002518023-A/49.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Herrnstadt,C., Ghosh,S.S., Clevenger,W., Fahy,E.D. and Davis,R.E.
 TITLE Diagnostic method based on the quantification of extramitochondrial
 JOURNAL Patent: JP 2002518023-A 49 25-JUN-2002;
 MITOKOR

COMMENT
 OS Artificial Sequence
 PN JP 2002518023-A/49
 PD 25-JUN-2002
 PF 14-JUN-1999 JP 2000554883
 PR 15-JUN-1998 US 09/098079,15-JUN-1998 US 09/097889 PR

30-APR-1999 US 09/302681
 PI CORINNA HERRNSTADT,SOUMITRA S GHOSH,WILLIAM CLEVENGER,EWIN D
 FAHY,
 PI ROBERT E DAVIS
 PC C12Q1/68,A61K45/00,A61P25/28,A61P43/00,C12N15/09//A61P3/00, PC
 A61P3/10,
 PC A61P25/00,A61P25/14,A61P25/16,A61P25/18,C12N15/00 CC
 Oligonucleotide primer corresponding to cytochrome c oxidase CC
 encoding
 CC mitochondrial DNA
 FH Key Location/Qualifiers
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 FT /organism='Artificial Sequence'.
 FT Location/Qualifiers
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 /db_xref="taxon:32630"

QY 1932 CACACACGACCTGTACA 1948
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 Db 2 CACACACGACCTGTCCA 18

RESULT 1460
 BD232822
 LOCUS 19 bp DNA linear PAT 17-JUL-2003
 DEFINITION Diagnostic method based on the quantification of extramitochondrial
 DNA
 ACCESSION BD232822
 VERSION BD232822.1 GI:33042592
 KEYWORDS JP 2002518023-A/50.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Herrnstadt,C., Ghosh,S.S., Clevenger,W., Fahy,E.D. and Davis,R.E.
 TITLE Diagnostic method based on the quantification of extramitochondrial
 JOURNAL Patent: JP 2002518023-A 50 25-JUN-2002;
 MITOKOR

COMMENT
 OS Artificial Sequence
 PN JP 2002518023-A/50
 PD 25-JUN-2002
 PF 14-JUN-1999 JP 2000554883
 PR 15-JUN-1998 US 09/098079,15-JUN-1998 US 09/097889 PR
 30-APR-1999 US 09/302681
 PI CORINNA HERRNSTADT,SOUMITRA S GHOSH,WILLIAM CLEVENGER,EWIN D
 FAHY,
 PI ROBERT E DAVIS
 PC C12Q1/68,A61K45/00,A61P25/28,A61P43/00,C12N15/09//A61P3/00, PC
 A61P3/10,
 PC A61P25/00,A61P25/14,A61P25/16,A61P25/18,C12N15/00 CC
 Oligonucleotide primer corresponding to cytochrome c oxidase CC
 encoding
 CC mitochondrial DNA
 FH Key Location/Qualifiers
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 FT Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

FEATURES
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 Query Match 0.4%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1932 CACACACGACCTGTACA 1948

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Db          3 CACACACCACTGTCCA 19
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RESULT 1461
I33095/c
LOCUS      19 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 9 from patent US 5589585.
ACCESSION  I33095
VERSION    I33095.1 GI:1823886
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Mabilat,C. and Pechere,J.-C.
TITLE     DNA fragments, probes and amplification primers of the 65 kd
          antigen of mycobacteria
JOURNAL   Patent: US 5589585-A 9 31-DEC-1996;
FEATURES  Location/Qualifiers
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          /mol_type="unassigned DNA"
Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 242 CCGAGCGGATGGACAAG 258
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Db 19 CCGAGCGGATGGACAAG 3

RESULT 1462
I33096
LOCUS      19 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 10 from patent US 5589585.
ACCESSION  I33096
VERSION    I33096.1 GI:1823887
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Mabilat,C. and Pechere,J.-C.
TITLE     DNA fragments, probes and amplification primers of the 65 kd
          antigen of mycobacteria
JOURNAL   Patent: US 5589585-A 10 31-DEC-1996;
FEATURES  Location/Qualifiers
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          1..19
          /organism="unknown"
          /mol_type="unassigned DNA"
Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 242 CCGAGCGGATGGACAAG 258
||||| ||||| ||||| ||
Db 19 CCGAGCGGATGGACAAG 3

RESULT 1463
I62823
LOCUS      19 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 560989.
ACCESSION  I62823
VERSION    I62823.1 GI:2480531
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)

AUTHORS   Cole,J.L., Kuo,L.C. and Olsen,D.B.
TITLE     DNA polymerase extension assay for influenza virus endonuclease
JOURNAL   Patent: US 5660989-A 1 26-AUG-1997;
FEATURES  Location/Qualifiers
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          /organism="unknown"
          /mol_type="unassigned DNA"
Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
||||| ||||| ||||| ||
Db 1 GTTTTAATTTTAACTT 17

RESULT 1464
AR205763
LOCUS      19 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6369208.
ACCESSION  AR205763
VERSION    AR205763.1 GI:21503428
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
TITLE     Capped synthetic RNA, analogs, and aptamers
JOURNAL   Patent: US 6369208-A 1 09-APR-2002;
FEATURES  Location/Qualifiers
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          /organism="unknown"
          /mol_type="unassigned DNA"
Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
||||| ||||| ||||| ||
Db 1 GTTTTAATTTTAACTT 17

RESULT 1465
AR205766
LOCUS      19 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 4 from patent US 6369208.
ACCESSION  AR205766
VERSION    AR205766.1 GI:21503432
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS   Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
TITLE     Capped synthetic RNA, analogs, and aptamers
JOURNAL   Patent: US 6369208-A 4 09-APR-2002;
FEATURES  Location/Qualifiers
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          /mol_type="unassigned DNA"
Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
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Db 1 GTTTTAATTTTAACTT 17
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RESULT 1466
AR205768
LOCUS AR205768 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6369208.
ACCESSION AR205768
VERSION AR205768.1 GI:21503434
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 6 09-APR-2002;
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATTT 17

RESULT 1467
AR205769
LOCUS AR205769 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6369208.
ACCESSION AR205769
VERSION AR205769.1 GI:21503435
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 7 09-APR-2002;
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATTT 17

RESULT 1468
AR205770
LOCUS AR205770 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 8 from patent US 6369208.
ACCESSION AR205770
VERSION AR205770.1 GI:21503437
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 8 09-APR-2002;
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATTT 17

RESULT 1469
AR205771
LOCUS AR205771 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 9 from patent US 6369208.
ACCESSION AR205771
VERSION AR205771.1 GI:21503438
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 9 09-APR-2002;
FEATURES
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Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATTT 17

RESULT 1470
AR205772
LOCUS AR205772 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 10 from patent US 6369208.
ACCESSION AR205772
VERSION AR205772.1 GI:21503439
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cole,J.L., Kuo,L.C., Olsen,D.B. and Benseler,F.
TITLE Capped synthetic RNA, analogs, and aptamers
JOURNAL Patent: US 6369208-A 10 09-APR-2002;
FEATURES
    Location/Qualifiers
        source
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                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3114 GTTTTAATTTTAACTT 3130
Db 1 GTTTTATTTTAAATTT 17

RESULT 1471
AR205775
LOCUS AR205775 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 13 from patent US 6369208.
ACCESSION AR205775
VERSION AR205775.1 GI:21503443
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TITLE Diagnostic method based on quantification of extramitochondrial DNA
JOURNAL Patent: US 6441149-A 50 27-AUG-2002;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1932 CACACGACCGCTGACA 1948
Db 3 CACACACCGCTGTCCA 19

RESULT 1477
AR241182/c 19 bp DNA linear PAT 20-DEC-2002

LOCUS AR241182
DEFINITION Sequence 9 from patent US 6468983.
ACCESSION AR241182
VERSION AR241182.1 GI:27286412
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.
TITLE RNase L activators and antisense oligonucleotides effective to
treat telomerase-expressing malignancies
JOURNAL Patent: US 6468983-A 9 22-OCT-2002;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2558 TGCCTTGCACACCGGG 2574
Db 18 TGCATTGCACCCCGGG 2

RESULT 1478
AR241929 19 bp DNA linear PAT 20-DEC-2002

LOCUS AR241929
DEFINITION Sequence 217 from patent US 6472154.
ACCESSION AR241929
VERSION AR241929.1 GI:27287741
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 217 29-OCT-2002;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2832 ATATATATATATACAT 2848
Db 1 ATATATATATATATAT 17

RESULT 1479
AR279766 19 bp RNA linear PAT 10-APR-2003

LOCUS AR279766
DEFINITION Sequence 12 from patent US 6518017.
ACCESSION AR279766
VERSION AR279766.1 GI:29714911
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Riley,T.A., Brown,B.D. and Arnold,L.J.
TITLE Combinatorial antisense library
JOURNAL Patent: US 6518017-A 12 11-FEB-2003;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1434 GCTGGTGGAGTACGCGG 1450
Db 1 GCTGGTTGAGTACTCGG 17

RESULT 1480
AR279780 19 bp RNA linear PAT 10-APR-2003

LOCUS AR279780
DEFINITION Sequence 26 from patent US 6518017.
ACCESSION AR279780
VERSION AR279780.1 GI:29714925
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Riley,T.A., Brown,B.D. and Arnold,L.J.
TITLE Combinatorial antisense library
JOURNAL Patent: US 6518017-A 26 11-FEB-2003;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1434 GCTGGTGGAGTACGCGG 1450
Db 1 GCTGGTTGAGTACTCGG 17

RESULT 1481
AR292645/c 19 bp DNA linear PAT 12-JUN-2003

LOCUS AR292645
DEFINITION Sequence 4380 from patent US 6537751.
ACCESSION AR292645
VERSION AR292645.1 GI:31679929
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 4380 25-MAR-2003;
FEATURES Location/Qualifiers
source
1..19

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/organism="unknown"
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2751 CTTTACCTTTTATGCAA 2767
Db 17 CTATACCTTTTGTGCAA 1

RESULT 1482
LOCUS AR293082/c 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4817 from patent US 6537751.
ACCESSION AR293082
VERSION AR293082.1 GI:31680366
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 4817 25-MAR-2003;
Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 887 GTGTGTATGCAGGCATC 903
Db 19 GTGTGTATGTAGTCATC 3

RESULT 1483
LOCUS AR293964/c 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5699 from patent US 6537751.
ACCESSION AR293964
VERSION AR293964.1 GI:31681248
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 5699 25-MAR-2003;
Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1347 TCAGATGGAGATGATCA 1363
Db 17 TGAGATGAAGATGAAGA 1

RESULT 1484
LOCUS AR294605 19 bp DNA linear PAT 12-JUN-2003

/organism="unknown"
/mol_type="genomic DNA"

Sequence 6340 from patent US 6537751.
AR294605 GI:31681889
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
JOURNAL disequilibrium map of the human genome
FEATURES Patent: US 6537751-A 6340 25-MAR-2003;
Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3449 AGATGTTACAGTTTAT 3465
Db 18 AGATGTAACAGGTTTAT 2

RESULT 1485
LOCUS AR451358 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6673917.
ACCESSION AR451358
VERSION AR451358.1 GI:42682383
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense IAP nucleic acids and uses thereof
JOURNAL Patent: US 6673917-A 3 06-JAN-2004;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2831 CATATATATATATAACA 2847
Db 1 CAGATATATATGTAACA 17

RESULT 1486
LOCUS AX039732 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 121 from Patent WO0063441.
ACCESSION AX039732
VERSION AX039732.1 GI:11229761
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hernstadt,C. and Davis,R.E.
TITLE Single nucleotide polymorphisms in mitochondrial genes that segregate with alzheimer's disease
JOURNAL Patent: WO 0063441-A 121 26-OCT-2000;
FEATURES MITOKOR (US)
source 1..19
Location/Qualifiers
/mol_type="synthetic construct"
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LOCUS AX130618 19 bp DNA linear PAT 15-MAY-2001
 DEFINITION Sequence 1836 from Patent WO0130362.
 ACCESSION AX130618
 VERSION AX130618.1 GI:14136923
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Robbins,J.M. and Tritz,R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
 JOURNAL Patent: WO 0130362-A 1836 03-MAY-2001;
 IMMUSOL, INC. (US)
 FEATURES
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 1..19
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="Cyclin D1 ribozyme binding site"
 Query Match 0.4%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1830 GGAGATCTTCACGCTGG 1846
 |||||
 Db 2 GGAGGTCTTCCGCTGG 18
 |||||
 RESULT 1492
 LOCUS AX130619 19 bp DNA linear PAT 15-MAY-2001
 DEFINITION Sequence 1837 from Patent WO0130362.
 ACCESSION AX130619
 VERSION AX130619.1 GI:14136924
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Robbins,J.M. and Tritz,R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
 JOURNAL Patent: WO 0130362-A 1837 03-MAY-2001;
 IMMUSOL, INC. (US)
 FEATURES
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 Location/Qualifiers
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="Cyclin D1 ribozyme binding site"
 Query Match 0.4%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1830 GGAGATCTTCACGCTGG 1846
 |||||
 Db 1 GGAGGTCTTCCGCTGG 17
 |||||
 RESULT 1493
 LOCUS AX130906 19 bp DNA linear PAT 15-MAY-2001
 DEFINITION Sequence 2124 from Patent WO0130362.
 ACCESSION AX130906
 VERSION AX130906.1 GI:14137211
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Robbins,J.M. and Tritz,R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
 JOURNAL Patent: WO 0130362-A 2124 03-MAY-2001;
 IMMUSOL, INC. (US)
 FEATURES
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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 /note="Cyclin E ribozyme binding site"
 Query Match 0.4%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3490 GAGTTTTCACAGATGT 3506
 |||||
 Db 17 GAGTTTTCACACATT 1
 |||||
 RESULT 1494
 LOCUS AX131095 19 bp DNA linear PAT 15-MAY-2001
 DEFINITION Sequence 2313 from Patent WO0130362.
 ACCESSION AX131095
 VERSION AX131095.1 GI:14137400
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Robbins,J.M. and Tritz,R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
 JOURNAL Patent: WO 0130362-A 2313 03-MAY-2001;
 IMMUSOL, INC. (US)
 FEATURES
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
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 Query Match 0.4%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2869 GGTACACGGAGGCTG 2885
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 Db 19 GGTACACGGAGCCAG 3
 |||||
 RESULT 1495
 LOCUS AX411903 19 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 3 from Patent WO0226968.
 ACCESSION AX411903
 VERSION AX411903.1 GI:21444368
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE 1
 AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
 TITLE Antisense iap nucleic acids and uses thereof
 JOURNAL Patent: WO 0226968-A 3 04-APR-2002;
 University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
 FEATURES
 Location/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="based on Homo sapiens"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2831 CATATATATATAAACA 2847
Db 1 CAGATATATATGTAACA 17

RESULT 1496
AX472591
LOCUS AX472591 19 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 5 from Patent WO0207757.
ACCESSION AX472591
VERSION AX472591.1 GI:22207494
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Lue,T.F., Lin,C.S. and Kan,Y.W.
TITLE Prevention and treatment of sexual arousal disorders
JOURNAL Patent: WO 0207757-A 5 31-JAN-2002;
Lue, Tom (US)
FEATURES
Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="VEGFR-1b Primer"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1954 ATCGCGGAGTGTGGCA 1970
Db 1 ATGCTGGATTGCTGGCA 17

RESULT 1497
AX643396/c
LOCUS AX643396 19 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 262 from Patent WO02099099.
ACCESSION AX643396
VERSION AX643396.1 GI:28551047
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Penger,A., Sprenger,R. and Brinkmann,U.
TITLE Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02099099-A 262 12-DEC-2002;
Epidaurus Biotechnologie AG (DE)
FEATURES
Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2827 TATACATATATATATAT 2843
Db 1 TATACATATATATATAT 17

source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1222 TTCGGCCAGGTGTGCAT 1238
Db 18 TTCGGCTAGGGGTGCAT 2

RESULT 1500
AX763838
LOCUS AX763838 19 bp RNA linear PAT 25-JUN-2003
DEFINITION Sequence 11 from Patent WO03040294.
ACCESSION AX763838
VERSION AX763838.1 GI:32258200
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Db 18 TATACATATATATATTT 2

RESULT 1498
AX643399
LOCUS AX643399 19 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 265 from Patent WO02099099.
ACCESSION AX643399
VERSION AX643399.1 GI:28551051
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Penger,A., Sprenger,R. and Brinkmann,U.
TITLE Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
and their use in diagnostic and therapeutic applications
JOURNAL Patent: WO 02099099-A 265 12-DEC-2002;
Epidaurus Biotechnologie AG (DE)
FEATURES
Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2827 TATACATATATATATAT 2843
Db 2 TATACATATATATATTT 18

RESULT 1499
AX659444/c
LOCUS AX659444 19 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 46 from Patent WO02102824.
ACCESSION AX659444
VERSION AX659444.1 GI:29161674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Beimfohr,C. and Snaidr,J.
TITLE Method for specific fast detection of relevant bacteria in drinking
water
JOURNAL Patent: WO 02102824-A 46 27-DEC-2002;
Vermicon AG (DE)
FEATURES
Location/Qualifiers
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match
Best Local Similarity 0.4%; Score 13.8; DB 1; Length 19;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1222 TTCGGCCAGGTGTGCAT 1238
Db 18 TTCGGCTAGGGGTGCAT 2

RESULT 1500
AX763838
LOCUS AX763838 19 bp RNA linear PAT 25-JUN-2003
DEFINITION Sequence 11 from Patent WO03040294.
ACCESSION AX763838
VERSION AX763838.1 GI:32258200
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KEYWORDS      .
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1
AUTHORS        de Backer,M.D. and Harris,A.N.
TITLE          Method for the in vitro synthesis of short double stranded RNAs
JOURNAL        Patent: WO 03040294-A 11 15-MAY-2003;
               JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES      Location/Qualifiers
source         1..19
               /organism="synthetic construct"
               /mol_type="unassigned RNA"
               /db_xref="taxon:32630"
               /note="19 nt target sequence within the coding sequence of
               EGFP"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1515 CACCTGCAAGCCGCGC 1531
Db      2 CACCGCAAGCTGCCCG 18

RESULT 1501
LOCUS      AX776236
DEFINITION Sequence 6 from Patent WO03048362.
ACCESSION  AX776236
VERSION     AX776236.1 GI:32693892
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE    1
AUTHORS      Farrar,G.J., Humphries,P., Millington-Ward,S. and Kenna,P.F.
TITLE        Suppression of polymeric alleles
JOURNAL      Patent: WO 03048362-A 6 12-JUN-2003;
               College of the Holy and Undivided Trinity of Queen Elizabeth (IE)
FEATURES      Location/Qualifiers
source       1..19
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="5' human collagen 1A2 primer"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1354 GAGATGATGAAGATGAT 1370
Db      3 GAGATGATGAAGATGAT 19

RESULT 1502
LOCUS      AX804504
DEFINITION Sequence 672 from Patent WO03060160.
ACCESSION  AX804504
VERSION     AX804504.1 GI:38521645
KEYWORDS    Oreochromis niloticus
SOURCE      Oreochromis niloticus
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
               Labroidae; Cichlidae; Oreochromis.
REFERENCE    1
AUTHORS      Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE        Verification of food origin based on nucleic acid pattern

KEYWORDS      recognition
SOURCE         Patent: WO 03060160-A 672 24-JUL-2003;
               Genomar ASA (NO)
FEATURES      Location/Qualifiers
source         1..19
               /organism="Oreochromis niloticus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:8128"

Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3399 AGACGGTTTCCAGGGAG 3415
Db      1 AGCCGGTTTCCAGTGAG 17

RESULT 1503
LOCUS      BD070496
DEFINITION Methods for detecting mitochondrial mutations diagnostic for
               Alzheimer's disease and methods for determining heteroplasmy of
               mitochondrial nucleic acid.
ACCESSION  BD070496
VERSION     BD070496.1 GI:22616099
KEYWORDS    unidentifed
SOURCE      unidentifed
ORGANISM    unclassified.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Parker,W.D., Herrnstadt,C., Ghosh,S. and Fahy,E.D.
TITLE        Methods for detecting mitochondrial mutations diagnostic for
               Alzheimer's disease and methods for determining heteroplasmy of
               mitochondrial nucleic acid
JOURNAL      Patent: JP 2001514500-A 53 11-SEP-2001;
               MITOKOR
COMMENT      OS Unidentified
               PN JP 2001514500-A/53
               PD 11-SEP-2001
               PF 27-FEB-1998 JP 1998537738
               PR 28-FEB-1997 US 08/810599
               PI WILLIAM DAVIS PARKER,CORINNA HERRNSTADT,SOUMITRA GHOSH,BOIN D
               FI FAHY
               PC C12Q1/68,C07H21/04
               CC Strandedness: Double;
               CC Topology: Linear;
               CC Methods for detecting mitochondrial mutations diagnostic for
               CC disease and methods for determining heteroplasmy of CC
               CC mitochondrial nucleic
               CC acid
               CC Key Location/Qualifiers
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Query Match      0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1932 CACACGACCTGTACA 1948
Db      3 CACACGACCTGTCCA 19

RESULT 1504
LOCUS      BD084645/C

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DEFINITION RNase L activators and antisense oligonucleotides effective to
treat telomerase-expressing malignancies.
ACCESSION BD084645
VERSION BD084645.1 GI:22630255
KEYWORDS JP 2001524100-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 19)
AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.
TITLE RNase L activators and antisense oligonucleotides effective to
treat telomerase-expressing malignancies
JOURNAL Patent: JP 2001524100-A 9 27-NOV-2001;
COMMENT THE CLEVELAND CLINIC FOUNDATION,NATIONAL INSTITUTES OF HEALTH
OS Artificial Sequence
PN JP 2001524100-A/9
PD 27-NOV-2001
PF 13-APR-1998 JP 1998546125
PR 21-APR-1997 US 60/044507,03-FEB-1998 US 09/018125 PI
ROBERT H SILVERMAN,SEIJI KONDO,JOHN K COWELL,GUYING LI,PAUL F
PT TORRENCE
PC C07H21/00,C07H21/02,C12Q1/68,A61K48/00
CC Description of Artificial Sequence: oligonucleotide FH Key
FT source 1..19
FT Location/Qualifiers
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FT 1..19
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FT /organism="synthetic construct"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32630"

Query Match 0.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2558 TGCCTTTGCACCCGGG 2574
Db 18 TGCATTTGCACCCGGG 2

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Search completed: October 28, 2004, 11:53:31
Job time : 111 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 12:35:44 ; Search time 118 Seconds
(without alignments)
3.649 Million cell updates/sec

Title: US-10-630-401-10

Perfect score: 3799

Sequence: 1 aaggatggcacaggctggt.....gacacctggtgctaacctg 3799

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 2175 seqs, 56666 residues

Total number of hits satisfying chosen parameters: 4350

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 447 summaries

Database : rst10.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38.2	1.0	47	1	AZ656611
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C 4	35.8	0.9	48	1	AZ312965
5	35.6	0.9	43	1	AZ786511
6	35.6	0.9	46	1	AZ819086
C 7	35.6	0.9	50	1	CR217570
C 8	35.4	0.9	47	1	CA970070
9	35.4	0.9	47	1	AZ659442
10	35.2	0.9	40	1	AZ319970
11	35.2	0.9	41	1	AZ837595
12	35.2	0.9	46	1	AZ352709
13	35.2	0.9	49	1	AZ837815
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15	34.8	0.9	39	1	AZ947712
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20	34.6	0.9	46	1	AZ451066
21	34.6	0.9	48	1	AZ875739
22	34.4	0.9	39	1	AZ781129
23	34.4	0.9	39	1	AZ824420
24	34.4	0.9	39	1	AZ826855
C 25	34.4	0.9	39	1	AZ339974
26	34.2	0.9	39	1	AZ389462
27	34.2	0.9	39	1	AZ765740
28	34.2	0.9	40	1	AZ338857
29	34.2	0.9	40	1	AZ513473
C 30	34.2	0.9	42	1	AZ336373
31	34.2	0.9	43	1	AZ982787
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33	34.2	0.9	47	1	AZ430498

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35	34.2	0.9	47	1	AZ595746
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39	34.2	0.9	47	1	AZ471416
40	33.8	0.9	37	1	AZ441623
41	33.8	0.9	37	1	AZ653918
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44	33.8	0.9	38	1	AZ433034
45	33.8	0.9	38	1	AZ586159
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47	33.8	0.9	38	1	AZ968714
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51	33.8	0.9	39	1	AZ837376
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53	33.8	0.9	40	1	AZ387867
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77	33.6	0.9	46	1	AZ951498
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80	33	0.9	47	1	AL040422
C 81	33	0.9	47	1	AZ437179
82	33	0.9	47	1	DR23D13T
83	32.8	0.9	36	1	AZ514497
84	32.8	0.9	36	1	AZ766984
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87	32.8	0.9	37	1	AZ308741
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102	32.4	0.9	36	1	AZ422282
103	32.4	0.9	36	1	AZ579564
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ACCESSION:AZ514610
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ACCESSION:AZ603138
ACCESSION:AZ838755

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0532 row: H column: 16
Seq primer: CGTTGTAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 47.

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FEATURES
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
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            /db_xref="taxon:10090"
            /clone="YUGCLIM0532H16"
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            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGCLM library"
            /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (GII4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

	Query Match	1.0%;	Score 38.2;	DB 1;	Length 47;
	Best Local Similarity	93.0%;	Fred. No.3.9;		
	Matches	40;	Conservative	3;	Indels
					Gaps
QY	2309	GCATTGGTCATGTGTGTGTGTGCGGTGTGTGTGTGTGTG	2351		
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RESULT 2	AZ760053/c
LOCUS	AZ760053
DEFINITION	mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
ACCESSION	AZ760053
VERSION	AZ760053.1
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 48) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokess,K., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	

C 399	17.8	0.5	23	1	TA300F12P	ACCESSION:AL490817
C 400	17.8	0.5	25	1	AC644875	ACCESSION:AZ644875
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C 402	17.8	0.5	38	1	BG920906	ACCESSION:BG920906
C 403	17.6	0.5	24	1	AZ811237	ACCESSION:AZ811237
C 404	17.6	0.5	25	1	AZ976143	ACCESSION:AZ976143
C 405	17.6	0.5	45	1	AL037866	ACCESSION:AL037866
C 406	17.4	0.5	19	1	AZ401252	ACCESSION:AZ401252
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C 408	17.4	0.5	19	1	AZ431700	ACCESSION:AZ431700
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C 420	17.2	0.5	24	1	AL038913	ACCESSION:CF299772
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C 423	17	0.4	20	1	AW250841	ACCESSION:CF299772
C 424	17	0.4	32	1	TA379A06P	ACCESSION:CF299772
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C 438	16.4	0.4	21	1	BJ054011	ACCESSION:CF298071
C 439	16.4	0.4	37	1	BX564796	ACCESSION:CF298071
C 440	16.4	0.4	40	1	CN546803	ACCESSION:CF298071
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ALIGNMENTS

RESULT 1	
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LOCUS	47 bp DNA linear GSS 14-DEC-2000
DEFINITION	IM032H16F Mouse 10kb plasmid UUGCM library Mus musculus genomic clone UUGCM0532H16 F, genomic survey sequence.
ACCESSION	AZ656611
VERSION	AZ656611.1 GI:11793757
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 47) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.F., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.:Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0032 row: L column: 01
Seq primer: CTTGTAAACGACGCCGCTG
Class: plasmid ends
High quality sequence stop: 43.

FEATURES

Source

Query Match	0.9%;	Score 35.6;	DB 1;	Length 43;
Best Local Similarity	90.5%;	Pred. No. 7.3;		

RESULT	6	AZ819086	46 bp	DNA	linear	GSS 20-FEB-2001					
LOCUS	AZ819086										
DEFINITION	2M0089G01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0089G01 R, genomic survey sequence.										
ACCESSION	AZ819086										
VERSION	AZ819086.1										
KEYWORDS	GSS.										
SOURCE	Mus musculus (house mouse)										
ORGANISM	Mus musculus										
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.										
AUTHORS	1 (bases 1 to 46) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.										
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts										
JOURNAL	Unpublished (2000)										
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT										

University of Utah
200 Biomedical Research Bldg., 20 S. 2030 E., SLC, UT

VERSION AZ837595.1 GI:13007503
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 41)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0132 row: N column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
FEATURES Location/Qualifiers
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0132N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 35.2; DB 1; Length 41;
Best Local Similarity 92.5%; Pred. No. 7.7;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2313 TGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGC 2352
||| ||||||||||||||||||||||||||||||||
Db 1 TGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGC 40

RESULT 12
AZ352709
LOCUS AZ352709 46 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0091J18F Mouse 10kb plasmid UUGClM library Mus musculus genomic
clone UUGC1M0091J18 F, genomic survey sequence.
ACCESSION AZ352709
VERSION AZ352709.1 GI:10431946

KEYWORDS GSS.

[illegible]

[illegible]

[illegible]


```

REFERENCE      Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Musineae; Mus
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausen,A. and Wright,D. Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               Plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
               84112, USA
               Tel.: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0347 row: F column: 09
               Seq primer: CACGACAGAAACACTATGCAC
               Class: plasmid ends
               High quality sequence stop: 41.
FEATURES       Location/Qualifiers
source         1..41
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUCGM0347F09"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUCGM library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57Bl/6J (male); was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adapted range DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PMW42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
Query Match    0.9%; Score 33.8; DB 1; Length 41;
Best Local Similarity 94.6%; Pred. No. 11;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy             2315 GTCTGTGTGTGTGTGTGGCGTGTGTGTGTGTGTGTC
                |||||
Db             41 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTC 5

RESULT_58     41 bp DNA linear GSS 16-FEB-2001
A2795539      2M0049N1R Mouse 10kb plasmid UUCGM library Mus musculus genomic
LOCUS         clone UUCGM049N1R 1, genomic survey sequence.
DEFINITION
VERSION       A2795539
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Musineae; Mus.
```


TITLE	JOURNAL	COMMENT
Moose, whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	
Contact: Robert B. Weiss		

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Sfd Error: 0.00
Plate: 0055 row: I column: 01
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence, stop: 42.

FEATURES
SOURCE

location/Qualifiers

1. 42

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGGCM0059101"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_id="Mouse 10kb plasmid UGGCM library"

/note="Vector: PWD42nv. Purified genomic DNA from M. musculus C57BL/6J (male). was obtained from the Jackson Laboratory Mouse Resource (<http://www.jax.org/resources/documents/dnars/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD2 (G114732114[g]/AF123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.9%	Score	33.8	DB	1	Length	42
Best Local Similarity	94.6%	Pred.	No. 12				
Matches	35	Conservative	0	Mismatches	2	Indels	0
						Gaps	0

Dy 2315 GTCTGTGTCGTGTCGTGCCTGTGTCGTGTCGTG 2351
 |||||
Db 5 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 41

RESULT 61	
AZ593813	
LOCUS	AZE93813
DEFINITION	42 bp DNA linear
	100405K02 Mouse 10kb plasmid UUCG1M library Mms musculus genomic
	clone UUCG1M0405K02 R, genomic survey sequence.

VERSION	AZ593813.1	GI:11716003
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,

TITLE
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
rbw@wustl.edu

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0405 row: K Column: 02
Seq primer: CACACAGGAACGCGATGACAC
Class: plasmid ends
High quality sequence stop: 42.

FEATURES

SOURCE

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0405K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lid="Mouse 10kb plasmid UGGCM library"
/note="Vector: pMD4adv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative of
pMD42 (gll4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.9%	Score 33.8;	DB 1;	Length 42;
Best Local Similarity	94.6%	Pred. NO. 12;		
Matches 35; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

[illegible]

RESULT	62
AZ851228	
LOCUS	42 bp DNA linear GSS 21-PEB-2000
DEFINITION	ZM0153E22F Mouse 10kb plasmid UOCCIM library Mus musculus genomic clone UOCC2M0153E22 F, genomic survey sequence.

VERSION	AZ851228.1	GI:13037016
KEYWORDS	GSS.	
SOURCE	Mus musculus	(house mouse)
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

1 (baes 1 to 42)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus


```

Query Match      0.9%; Score 33.8; DB 1; Length 45;
Best Local Similarity 94.6%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0298L16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGGCM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMDA2 (g14732114[gB]AP129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

```

/db xref="taxon:10090"
/clone="UGICM0547P02"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UGICM library"
/notes="Vector: PWD42nv: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g1473114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

DY 2315 GTCTGTCGTGTCGTGTCGCGTGTGTCGTGTCGTGTCG 2351

Dd 8 GTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCG 44

[illegible]

RESULT 73	
AZ665896	
LOCUS	45 bp DNA linear
DEFINITION	GM0547P02 Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION	Clone U06C1M0547P02 R, genomic survey sequence.
VERSION	AZ665896
KEYWORDS	AZ665896.1 GI:11803042
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

LOCUS	BX548613	46 bp	mRNA	linear	EST 10-OCT-2003
DEFINITION	BX548613 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse102a05_p1c, mRNA sequence.				
ACCESSION	BX548613				
VERSION	BX548613.1	GI:33298846			
KEYWORDS	EST.				
SOURCE	Glossina morsitans morsitans				
ORGANISM	Glossina morsitans morsitans				
	Eukaryota; Metacoa; Arthropoda; Hexapoda; Insecta; Pterygota;				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 45)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellay, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
	Unpublished (2000)			Contact: Robert B. Weiss

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PubMed
1 (bases 1 to 46)	Lehane, M. J., Akcay, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M. B., Ronaldo, M. F., Lehane, S. and Hall, N.	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune response genes	Genome Biol. 4 (10), R63 (2003)	22881942	14519198

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0547 row: P column: 02
Seq primer: CACACGGAACACGCTATGAC
Class: plasmid ends
High quality sequence stop: 45.

The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.U. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cdna all p1c reads are from the 3' end.

```
FEATURES
    source          Location/Qualifiers
    1..45
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
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FEATURES
source
location/Qualifiers
1..46
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/mol_type="mRNA"
/sub_species="morsitans"
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[illegible][illegible]

RESULT 107
AZ857946
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ857946 37 bp DNA linear GSS 21-FEB-2001
2M0162M19P Mouse 10kb plasmid UUCGIM library Mus musculus genomic
clone UUCG2M0162M19 R, genomic survey sequence.
AZ857946
AZ857946.1 GI:13050609
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weise, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genomic Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0162 row: M column: 19
Seq primer: CACACAGGAACAGCTATGACG
Class: plasmid ends
High quality sequence stop: 37.
1. .37
location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"

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RESULT 108
AZ875282/c

LOCUS      AZ875282              37 bp    DNA          linear    GSS 21-FEB-2001
DEFINITION  ZMO189A2OR Mouse 10kb plasmid UOCCIM library Mus musculus genomic
            clone UOCCZMO189A20 R, genomic survey sequence.
ACCESSION  AZ875282
VERSION    AZ875282.1  GI:13085139
KEYWORDS   GSS.

SOURCE      Mus musculus (house mouse)
            Mus musculus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.

REFERENCE  1 (bases 1 to 37)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
JOURNAL    Contact: Robert B. Weiss
            University of Utah Genome Center
COMMENT    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel.: 801 585 5506
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0189 row: 4 column: 20
            Seq primer: CACACAGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 37.
            Location/Qualifiers
                1..37
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /extra="CS7BL/6J"
                /db_xref="taxon:10090"
FEATURES
SOURCE

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```

/clone="UUGC2M0189A20"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 32.2; DB 1; Length 37;
Best Local Similarity 91.9%; Pred. No. 16;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
Db      37 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 37

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RESULT 109
LOCUS      AZ808181      40 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0071A18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  AZ808181
VERSION     AZ808181.1 GI:12973460
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: A column: 18
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1. 40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0071A18"

```

```

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 32.2; DB 1; Length 40;
Best Local Similarity 91.9%; Pred. No. 17;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
Db      1 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 37

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RESULT 110
LOCUS      AZ387857      41 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION 1M0147122R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  AZ387857
VERSION     AZ387857.1 GI:10501565
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 row: L column: 22
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
1. 41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0147L22"
/sex="Male"

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FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0071A18"

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```

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone.lib="Mouse 10kb plasmid UUCGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [g1|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 32.2; DB 1; Length 41;
Best Local Similarity 91.9%; Pred. No. 17;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2315 GTCTGTGTGTGTGTGTGTGCCTGTGTGTGTGTGTGTG 2351
        |||||||||
Db       41 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5

RESULT 111
A2462065      41 bp   DNA      linear    GSS 04-OCT-2000
LOCUS         1M0269L1F Mouse 10kb plasmid UUCGCM library Mus musculus genomic
DEFINITION    clone UUCGCM0265L1 F, genomic survey sequence.
ACCESSION     A2462065
VERSION       A2462065
KEYWORDS      A2462065.1 GI:10620190
SOURCE        GSS.
ORGANISM      Mus musculus (house mouse)
MUS MUSCULUS
Mus musculus
Bukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: L column: 11
Seq primer: CGTTGAACAAGACGCGCACAT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
1..41
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0265L1"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"

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/clone_1lb="Mouse10kb plasmid UGCGIM library"
/note=Vector: pMD247n; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (gll4732114|gb|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 32.2; DB 1; Length 41;
Best Local Similarity 91.9%; Pred. No. 17;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Dy 2315 GTCTGTGTGTGTGTGTGTGCCTGTGTGTGTGTGTGTG 2351
 |||||||||
Db 4 GTGTGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTG 40

RESULT 112
LOCUS A2346889/c
DEFINITION 1M0082A20F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
VERSION c clone UGCGIM0082A20 F, genomic survey sequence.
KEYWORDS A2346889
ORGANISM A2346889.1 GI:10426126
GSS.

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: A column: 20
Seq primer: CGTTGTAAACAGCAGCCACAT
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers

FEATURES
SOURCE
1..42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0082A20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 32.2; DB 1; Length 42;
Best Local Similarity 91.9%; Pred. No. 18;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
DB 42 GTATGATGTCGTGTCGTGTCGTGTCGTGTCGTG 6

RESULT 113
AZ355175 42 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0094D20R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0094D20 R, genomic survey sequence.

ACCESSION AZ355175.1 GI:10467323

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 42)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0094 row: D column: 20

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 42.

Location/Qualifiers

1..42

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCM0094D20"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 32.2; DB 1; Length 42;
Best Local Similarity 91.9%; Pred. No. 18;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 2351
DB 2 GTGTGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTG 38

RESULT 114
AZ371099 44 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0122G02P Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0122G02 F, genomic survey sequence.

ACCESSION AZ371099.1 GI:10484799

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 44)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0122 row: G column: 02

Seq primer: CGTGTAAACGACGCCACGT

Class: plasmid ends

High quality sequence stop: 44.

Location/Qualifiers

1..44

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCM0122G02"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

RESULT 135	
LOCUS	A2370273
DEFINITION	A2370273 35 bp DNA linear GSS 02-OCT-2000
ACCESSION	U01012BI1F Mouse 10kb plasmid U00C1M library Mus musculus genomic
VERSION	clone U01012BI1 F, genomic survey sequence.
KEYWORDS	A2370273
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus. 1 (bases 1 to 35)
TITLE	Dunn, D., Aoyagi, A., Barber, M., Baecorn, T., Duval, B., Hamill, C., Iellam, H., Longacre, S., Mahmond, M., Meenen, E., Pedersen, T., Rellay, W., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weiss, R.
JOURNAL	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0121 row: B column: 13 Seq primer: CGTTGTAAACGACGCGCAGT Class: plasmid end High quality sequence stop: 35. Location/Qualifiers
FEATURES	

LOCUS	A2430974				
DEFINITION	37 bp DNA linear GSS 03-OCT-2000				
ACCESSION	IM0215L08R Mouse 10kb plasmid U06C1M library Mus musculus genomic				
VERSION	clone U06C1M0215L08 R, genomic survey sequence.				
KEYWORDS	A2430974				
SOURCE	A2430974.1 GI:10554987				
ORGANISM	GSS.				
REFERENCE	Mus musculus (house mouse)				
AUTHORS	Bukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 37) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rally,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Nedehausen,A. and Wright,D.Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0215 row: L column: 08 Seq primer: CACACAGAAACAGACTATGACC Class: plasmid ends High quality sequence stop: 37. Location/Qualifiers 1..37				
TITLE					
JOURNAL					
COMMENT					
FEATURES					
SOURCE					

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Query Match          0.8%; Score 31.4; DB 1; Length 35;
Best Local Similarity 97.0%; Pred. No. 18;
Matches      32; Conservative   0; Mismatches    1; Indels     0; Gaps     0;
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QY 2319 GTGTGTTGTTGTCTCCGTGTGTGTGTGTGTG 2351
Db 3 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 35

RESULT 136

	Query Match	0.8%;	Score 31.4;	DB 1;	Length 37;
	Best Local Similarity	97.0%;	Pred. No. 19;		
	Matches 32; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
QY	2319 GTGCTGTGTGTGTGCGTGTGTGTGTGTGTG	2351			
Dd	5 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	37			
	RESULT 137				
	AZ357262				

LOCUS	AZ397262	40 bp	DNA	linear	SSS 03-OCT-2000
DEFINITION	IM0162112.F Mouse 10kb plasmid U08C1M library Mus musculus genomic				
ACCESSION	clone U08C1M0162112 F, genomic survey sequence.				
VERSION	AZ397262				
KEYWORDS					
SOURCE	AZ397262.1	GI:10512334			
ORGANISM	GSS.				
	Mus musculus (house mouse)				
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 40)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0162 row: 1 column: 12 Seq primer: CCGTGTAAACGACGCGCAAG Class: plasmid ends High quality sequence stop: 40.				

location/Qualifiers
1. .40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U961CM0162112"
/sex="male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U961CM library"
/note="Vector: FMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/shares/>). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD2 (g114732114[g]/AF123072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.8;	Score 31;	DB 1;	Length 40;
Best Local Similarity	87.2%;	Pred. NO. 24;		
Matches 34; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

Qy	2315	GTCTGTCATGTCATGTCACCGTATGTCATGTCACA	2353
Db	2	GTGTGTGTGTGTGTGTGTGTGTGAATGATGTCTA	40

RESULT 138			
AZ819018			
LOCUS	40 bp	DNA	linear
AZ819018			GSS 20-FEB-2001

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL COMMENT
2N00689119F Mouse 10kb plasmid UGCLIM library Mus musculus genomic clone UGCC2N00689119 F, genomic survey sequence.	AZ819018								
	AZ819018.1	GI:12988926	GSS.	Mus musculus	(house mouse)	Euarctos; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhasenrn,A. and Wright,D.,Weiss,R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000) Contact: Robert B. Weiss University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: dduwn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0089 row: I column: 19 Seq primer: CGTGTATAACGACGGCAGAT Class: plasmid ends High quality sequence. stop: 40.

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location/Qualifiers
1..40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TUGC2M0089119"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="mouse 10kb plasmid UGCGM library"
/notes="Vector: PMD42uv1 Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative of
pMD42 (gll473211\[g\]Afl23072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	0.8%	Score 31;	DB 1;	Length 40;
Best Local Similarity	87.2%;	Pred. No. 24;		
Matches 34;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

```

Oy      2313 TGGTCGTCGTCTGTCGCAGTGTCTGTCTGTG   2351
        ||| | | | | | | | | | | | | | | |
Db       1  TTGATTAAGTGATGACGATGCTGTCTGTGTG   39

```

RESULT	139		
AZ509672			
LOCUS	AZ509672	34 bp	DNA linear
DEFINITION	1M035A18R Mouse 10kb plasmid UUC1M library Mus musculus genomic		

[illegible]

```

ACCESSION   A2489673
VERSION     A2489673.1
KEYWORDS    GI:10659652
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriongnath; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 36)
AUTHORS     Dunn,D., Loyagiri,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Nollacre,S., Mahmoud,W., Meenen,E., Pedersen,T., Riedel,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert length: 10000 Std Error: 0.00
            Plate: 0322 row: E column: 18
            Seq primer: CATTGTAAACGACGGCCAGT
            Class: plasmid ends
FEATURES             location/Qualifiers
     source           1..36
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UFGICM0322B18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                     /clone_id="Mouse 10kb plasmid UFGICM library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4tj3114[gb|AF129072.1], a copy-number inducible derivative of plasmid Rt. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor-vectored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match          0.8%; Score 30.8; DB 1; Length 36;
Best Local Similarity 94.1%; Pred. No. 22;
Matches              32; Conservativity 0; Mismatched 2; Indels 0; Gaps 0;
QY                  2318 TGATGATGATGATGCATGATGATGATGATGATG 2351
                |||||
Db                   2  TGTGTGTTGGTGATGATGATGATGATGATG 35
                |||||
RESULT_141         AZ447539               38 bp        DNA          linear      GSS 04-OCT-2000
LOCUS              A2447539
DEFINITION         JM0244E1R Mouse 10kb plasmid UFGICM library Mus musculus genomic
Clone UFGICM0244E1 R, genomic survey sequence.
ACCESSION          A2447539

```


[illegible]

```
GSS . Mus musculus (house mouse)
SOURCE      Mus musculus
ORGANISM    Mammalia; Eutheria; Rodentia; Scurionachti; Muridae; Murinae; Mus.
REFERENCE   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS     Irlam,H., Longcore,S., Mahmoud,M., Meenen,E., Pedersen,T.,
             Nedderhaussen,A., and Wright,D.,Weiss,R., Tingay,A., von
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0231 row: F column: 18
            Seg primer: CACKAGCAAAACAGCTATGACC
            Class: plasmid ends
FEATURES
source      High quality sequence stop: 44.
            Location/Qualifiers
                1..44
                    /organism="Mus musculus"
                    /mol_type="genomic DNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="UUC2M0231P18"
                    /sex="Female"
                    /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
                    /cdate_1ib="Mouse 10kb plasmid UUGCCM library"
                    /note=Vector: PMD42nv; Purified genomic DNA from M.
musculus C57Bl/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMDA2 [gil473114[gb|AF129072.1], a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match          0.8%; Score 30.8; DB_1; Length 44;
Best Local Similarity 83.3%; Pred. No. 27;
Matches              35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```


SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 38) Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tinger,A., von Niederhauern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0311 row: B column: 02 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 38. Location/Qualifiers 1..38
FEATURES	
SOURCE	

	Query Match	0.8%;	Score 30.6;	DB 1;	Length 38;
	Best Local Similarity	89.2%;	Pred. No. 25;		
Matches	33;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0;
OY	2319	GTCGTGCTGTCGTGCCTGTCGTGTCGTGTCGACA	2355		
Dd	2	GTCGTGCTGTCGTGTCGTGTCGTGTCGTATATAA	38		
RESULT 144	AZ346424				
LOCUS	AZ346424	39 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	IM008INI2R Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCGM008INI2 R, genomic survey sequence.				
ACCESSION	AZ346424				
VERSION	AZ346424.1	GI:10425661			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				

ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 39)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rally,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished. (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0081 row: N column: 12 Seq primer: CACACAGAAACAGCATATGACC Class: plasmid ends High quality sequence stop: 39. Location/Qualifiers 1..39
FEATURES	
SOURCE	

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 32)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0010 row: A column: 03 Seq primer: CACACAGCAACACACTATGACC Class: plasmid ends High quality sequence stop: 32.
FEATURES	SOURCE	location/Qualifiers		
1..32	/organism="Mus musculus"			
	/mol_type="genomic DNA"			
	/strain="C57BL/6J"			
	/db_xref="taxon:10090"			
	/clone="UUC1M0010A03"			
	/sex="Male"			
	/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"			
	/clone_lib="Mouse 10kb plasmid UUC1M library"			
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
Query Match	Best Local Similarity	0.8%; Score 30.4; DB 1; Length 32;		
Matches	31; Conservative	0; Mismatches	1; Indels	0; Gaps
Qy	2318 TGTGTGTGTGTGTGTGCGGTGTGTGTGTGTG	2349		
Db	1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	32		
RESULT 148	LOCUS	ACCESSION	VERSION	KEYWORDS
AZ311840	32 bp DNA linear GSS 29-SEP-2000			
DEFINITION	1M0027M21F Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0027M21 F, genomic survey sequence.			
AZ311840				
AZ311840.1	GI:10355201			
SOURCE	ORGANISM			
Mus musculus (house mouse)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
1 (bases 1 to 32)				

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SVC, UT
84112, USA

Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0027 row: M column: 21
Seq primer: CGTTGTAACAGCAGCGCACGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES

source	1..32 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="MUGCIM0027M21" /sex="Male" /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /clove_lib="Mouse 10kb plasmid UMGCM library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 [gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E.coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
--------	--

Query Match

Best Local Similarity 96.9%; Pred. No. 22;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2318 TGTCGTGTGTGTGCCTGGTGTGTGTGTGTG 2349
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 32

RESULT 149

AZ495235

LOCUS

1M0331B05F Mouse 10kb plasmid UMGCM library Mus musculus genomic clone UMGCM0331B05 F, genomic survey sequence.

DEFINITION

AZ495235

ACCESION VERSION

AZ495235.1 GI:10670567

KEYWORDS SOURCE ORGANISM

GSS.
Mus musculus (house mouse)
Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euarchontomi;
Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

TITLE
JOURNAL
COMMENT

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: E column: 05
Seq primer: CATTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES
source

1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0331R05"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|9b|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match
Best Local Similarity 96.9%; Pred. No. 22;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGGTGTGTGTGTG 2349
|||||
1 TGTGTGTGTGTGTGTGTGTGTGTGTGTG 32

RESULT 150
BX559884 33 bp mRNA linear EST 10-OCT-2003
BX559884 Glosina morsitans morsitans adult infected gut Glosina
morsitans morsitans cDNA clone Tse46c02_plc, mRNA sequence.
ACCESSION BX559884
VERSION BX559884.1 GI:33367775
KEYWORDS EST.
SOURCE Glosina morsitans morsitans
ORGANISM Glosina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glosina.
1 (bases 1 to 33)
REFERENCE Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glosina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix plc are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
Location/Qualifiers

FEATURES
source

1..33
/organism="Glosina morsitans morsitans"
/mol_type="mRNA"
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/db_xref="taxon:37546"
/clone="Tse46c02_plc"
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/clone_lib="Glosina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 93.9%; Pred. No. 27;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGCGGTGTGTGTGTG 2351
|||||
1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTG 33

RESULT 151
AZ638769 33 bp DNA linear GSS 13-DEC-2000
LOCUS IM0498820R Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION clone UGGCM0498820 R, genomic survey sequence.
ACCESSION AZ638769
VERSION AZ638769.1 GI:11760959
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: B column: 20
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends

TITLE
JOURNAL
COMMENT

Location/Qualifiers
1. .33

location/Qualifiers

1. 35

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0441C17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_id="Mouse 10kb plasmid UUGCIM library"

/note="Vector: pMD29env. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The digested DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD24 [GII4723114|bp|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.8%	Score 29.8	DB 1	Length 35
Best Local Similarity	93.9%	Pred. No. 25		
Matches 31; Conservative	0	Mismatches 2	Indels 0	Gaps 0

[illegible]

RESULT 153					
AZ968276					
LOCUS	AZ968276	36 bp	DNA	linear	GSS 27-APR-2007
DEFINITION	2M0240K02R Mouse 10kb plasmid U0GC2M library Mus musculus genomic				
ACCESSION	clone U0GC2M0240K02 R, genomic survey sequence.				
	AZ968276				

VERSION	AZ9688276.1	GI:13839503
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata	

REFERENCE
AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mamoud, M., Neenan, E., Petersen, T.,
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
1 (bases 1 to 36)

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT
84112, USA
Tel: 801 585 5606

```

FEATURES
Email: ddmg@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0240 Row: K Column: 02
Seq primer: CACACGAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence atop: 36.
Location/Qualifiers

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Location/Qualifiers

QY 2315 GTCGTGTCGTGTCGTGTCGTGTCGTGTCGT 2346
 Db 1 GTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 32

RESULT 170 32 bp DNA linear GSS 13-DEC-2000
 AZ606329 1M0428K07F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 LOCUS clone UGCGIM0428K07 F, genomic survey sequence.

ACCESSION AZ606329
 VERSION AZ606329.1 GI:11728519
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

REFERENCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 32)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0428 row: K column: 07
 Seq primer: CATTGTAAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES

source

1. 32
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGIM0428K07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.8%; Score 28.8; DB 1; Length 32;
 Best Local Similarity 93.8%; Pred. No. 34;
 Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2313 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 32

RESULT 171 35 bp DNA linear GSS 20-FEB-2001
 AZ832583 2M0113N06F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 LOCUS clone UGCGIM0113N06 F, genomic survey sequence.

ACCESSION AZ832583
 VERSION AZ832583.1 GI:13002491
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

REFERENCE Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 35)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0113 row: N column: 06
 Seq primer: CATTGTAAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 35.
 Location/Qualifiers

FEATURES

source

1. 35
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0113N06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.8%; Score 28.8; DB 1; Length 35;
 Best Local Similarity 93.8%; Pred. No. 37;
 Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2322 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2353

RESULT	174
AZ989744	
LOCUS	
DEFINITION	AZ989744 30 bp DNA linear GSS 27-APR-2001
ACCESSION	2M027JN10F Mouse 10kb plasmid UUCG2M library Mus musculus genomic
VERSION	clone UUCG2M027JN10 F, genomic survey sequence.
KEYWORDS	AZ989744
SOURCE	AZ989744.1 GI:13860971
ORGANISM	GSS.
	Mus musculus (house mouse)
	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
REFERENCE	
AUTHORS	1 (bases 1 to 30) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedenhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid insets Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	

FEATURES	Location/Qualifiers
SOURCE	1. .30

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGC2M0273N10"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGC2M library"
 /note="Vector: pMD24nv1. Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD24 (g11473111[g1Afl23072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.7%;	Score 28.4;	DB 1;	Length 30;
Best Local Similarity	96.7%;	Pred. No. 35;		
Matches 29;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 2319 GTGTGCTGTGTGTGCCTGTGTGTGTGT 2348
|||
Db 1 GTGTGCTGTGTGTGTGTGTGTGTGTGT 30

RESULT	175
AZ432709/c	
LOCUS	
DEFINITION	AZ432709 31 bp DNA linear GSS 03-OCT-2000 M0218C1F Mouse 10kb plasmid tUGCIM library Mus musculus genomic clone tUCGCM0218C1 F, genomic survey sequence.
ACCESSION	AZ432709
VERSION	AZ432709
KEYWORDS	AZ432709.1 GI:10556722
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathii; Muridae; Murinae; Mus-
AUTHORS	1 (bases 1 to 31) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,W., Meenen,B., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright D.Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
JOURNAL COMMENT	Contact: Robert B. Weiss rweiss@ucdavis.edu

FEATURES	Location/Qualifiers
source	1. .31

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0218C16"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG library"
 /note="Vector: pMD24ny, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse Resource
<http://www.jax.org/resources/documents/dnares/>. The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (g[1473211[gbl]A129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.7%;	Score 28.4;	DB 1;	Length 31;
Best Local Similarity	96.7%;	Pred. No. 36;		
Matches 29;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

```

QY      2322 TGTGTGTCGTCCGTATGATGTCGTCTG 2351
          |||||
DB      31 TGTGTGTCGAGCGTGTGTGTGTGTG 2

```



```

RESULT 176
LOCUS AZ628068 31 bp DNA linear GSS 13-DEC-2000
DEFINITION IN0476P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION UUGC1M0476P22 F, genomic survey sequence.
VERSION AZ628068
KEYWORDS
SOURCE GSS.
ORGANISM GI:11750258
Mus musculus (house mouse)
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0476 row: P column: 22
Seq primer: CGTGTAAACAGACGCCACAT
Class: plasmid ends
High quality sequence stop: 31.
FEATURES
source
1..31
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0476P22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/vector="PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114[gB]AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.7%; Score 28.4; DB 1; Length 31;
Best Local Similarity 96.7%; Pred. No. 36;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 2323 GTGTGTGTGTCGCGTGTGTGTGTGTGTGTC 2352
DB 31 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTC 2
RESULT 177

```

CD744339	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CD744339	34 bp	mRNA	linear	EST 25-JUN-2004			
IR64_F06_4_048	Infected Rat Blood-fed (IRB) An.gam.	30 hr Abdomen					
CD744339		Library Anopheles gambiae cDNA 5', mRNA sequence.					
CD744339							
CD744339.1	GI:49248276						
EST							
Anopheles gambiae	(African malaria mosquito)						
Anopheles gambiae							
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.							
1 (bases 1 to 34)							
Dana,A.N., Lobo,N.F., Hillemeier,M.E. and Collins,F.H.							
Hematophagy-associated gene expression patterns in adult female Anopheles gambiae mosquitoes							
Unpublished (2003)							
Contact: Dana A.N.							
Frank H. Collins Laboratory							
University of Notre Dame							
Center for Tropical Disease Research and Training, Dept. of Biol. Sci., Notre Dame, IN 46556, USA							
Tel: 574 - 631 - 3241							
Fax: 574 - 631 - 3996							
Email: adana@nd.edu							
PCR Primers							
FORWARD: ctcggaagcgcgcacatgtgtgtg							
BACKWARD: atacgactacataaggcgcaatggc							
Seq primer: ctcggaagcgcgcacatgtgtg.							
Location/Qualifiers							
1..34							
/organism="Anopheles gambiae"							
/mol_type="mRNA"							
/strain="4Atr"							
/db_xref="taxon:7165"							
/sex="female"							
/issue_type="Abdomens"							
/dex_stage="Female adult 5-7 days post eclosion"							
/lab_host="E. coli XLI-Blue"							
/clone_id="Infected Rat Blood-fed (IRB) An.gam. 30 hr Abdomen Library"							
/note="Vector: lambdaTriplex2 (Clontech) ; Site 1: Sfi IA; Site 2: Sfi IB; Plasmid mod beyhei-infected rat blood-fed adult female An. gambiae mosquitoes were flash frozen after a 30 hour incubation of adult mosquitoes at 19 degrees Celsius. Total RNA extracted from abdomens separated from remaining carcasses. CDNA inserts >500 bp cloned directionally into Triplex2; Sfi IA site is 5'. Non-normalized and Non-amplified phagemid library. Single pass sequencing reactions from 5' end."							
Query Match	0.7%	Score 28.4;	DB 1;	Length 34;			
Best Local Similarity	90.6%;	Pred. No. 40;					
Matches	29;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;		
Qy	2319	GTGCTGTGTGTGTGCGCTGTGTGTGTGTGT	2350				
Db	3	GTGCTGTGTGTGTGTGTGTGTGTGTGTGT	34				
RESULT 178							
AZ514079/c							
LOCUS	AZ514079	33 bp	DNA	linear	GSS 05-OCT-2000		
DEFINITION	1M0360F07R Mouse 10kb plamid UGCLM library Mus musculus genomic clone UGCLM0360F07 R, genomic survey sequence.						
ACCESSION	AZ514079						
VERSION	AZ514079.1	GI:10695395					
KEYWORDS	GSS.						
SOURCE	Mus musculus (house mouse)						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
REFERENCE	1 (bases 1 to 33)						

TITLE Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
JOURNAL Direct Submission
Submitted (07-Jan-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@kribb.kribb.re.kr, URL: http://pns.grc.kribb.re.kr/
Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS

Sequencing: T7
LIBRARY
Vector : PBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI

FEATURES
source Location/Qualifiers

1..29
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-063J22.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.7%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 44;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2346
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 29

RESULT 185
AZ497897 30 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0334K20R Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0334K20 R, genomic survey sequence.
ACCESSION AZ497897
VERSION AZ497897.1 GI:10675242
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0334 row: K column: 20
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.

FEATURES
source Location/Qualifiers

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="UGCLM0334K20"

/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"

/note="Vector: pMD22nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 27.4; DB 1; Length 30;
Best Local Similarity 96.6%; Pred. No. 46;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2347
Db 2 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30

RESULT 186
AZ635862 30 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0493004F Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0493004 F, genomic survey sequence.
ACCESSION AZ635862
VERSION AZ635862.1 GI:11758052
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: O column: 04
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 30.

FEATURES
source Location/Qualifiers

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

/clone="UGCLM0493004"
 /sex="Male"
 /la_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: PMD429. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gll4732114|gb|AF12072.1), a copy-number
 inducible derivative of plasmid RL. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

[illegible]

RESULT	187
AZ4A0652	
LOCUS	
DEFINITION	
<p>AZ4A0652 31 bp DNA linear GSS 03-OCT-2000 10023J1N14R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M023J1N14 R, genomic survey sequence.</p>	

VERSION AZ44065Z.1 GL:10364663
KEYWORDS GSS.

SOURCE ORGANISM	REFERENCE
Mus musculus (house mouse)	Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Mus musculus	1 (bases 1 to 31)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	

Niederhausern, A. and Wright, D., Weiss, K.

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0231 row: N column: 14
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

```
FEATURES
source
location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cname="U06C1M0231N14"
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Query Match      0.7%; Score 27.4; DB 1; Length 31;
Best Local Similarity 96.6%; Pred. No. 48;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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[illegible]

RESULT	188		
AZ335085/c			
LOCUS	AZ335085	32 bp	DNA linear GSS 29-SEP-2000
DEFINITION	NM0064F17 Mouse 10kb plasmid UUCGM library Mus musculus genomic clone UUCGM0064F17 R, genomic survey sequence.		

VERSION A2335085.1 GT:10403040
KEYWORDS GSS.

SOURCE ORGANISM	REFERENCE
<i>Mus musculus</i> (house mouse)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
<i>Mus musculus</i>	1 (bases 1 to 32)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0064 row: F column: 17
Seq primer: CACGACGAAACAGCTTACAC
Class: plasmid ends
High quality sequence: stop: 32.

```

FEATURES
source
1..32
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/stRAIN="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0064F17"
/sex="Male"

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DB 30 GGTGTGTGAGGTGTGTGTGTGTGTGT 1

RESULT 195
A2626646 33 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0467E06F Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0467E06 F, genomic survey sequence.
ACCESSION A2626646
VERSION A2626646
KEYWORDS A2626646.1 GI:11748836
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 33)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0537 row: C column: 17
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers

FEATURES
source 1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0537C17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 26.8; DB 1; Length 31;
Best Local Similarity 93.3%; Pred. No. 56;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2316 TCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2345
DB 2 TATGTGTGTGTGTGTGTGTGTGTGTGTGT 31

RESULT 196
A2626646 33 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0467E06F Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0467E06 F, genomic survey sequence.
ACCESSION A2626646
VERSION A2626646
KEYWORDS A2626646.1 GI:11748836
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
REFERENCE Mus musculus
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 33)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0467 row: E column: 06
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers

FEATURES
source 1..33
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0467E06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 26.8; DB 1; Length 33;
Best Local Similarity 93.3%; Pred. No. 60;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
2319 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2348
DB 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 30

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RESULT 197
A2642584
LOCUS A2642584 33 bp DNA linear GSS 14-DEC-2000
DEFINITION U0505K12R Mouse 10kb plasmid U05C1M library Mus musculus genomic
clone U05C1M0505K12 R, genomic survey sequence.
ACCESSION A2642584
VERSION A2642584.1 GI:11769336
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 33)
AUTHORS Dunn,P., Aoyagi,A., Barber,M., Beacon,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,S., Pedersen,T.,
Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)
JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., UHC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0505 row: K column: 12
Seq primer: CACACAGGAAACAGTAGACC
Class: plasmid ends
High quality sequence stop: 33.
FEATURES
source
1..33
Location/Qualifiers
1..33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U05C1M0505K12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TM-resistant, F-"
/clone_lib="Mouse 10kb plasmid U05C1M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.7%; Score 26.6; DB 1; Length 33;
Best Local Similarity 87.9%; Pred. No. 63;
Matches 29; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
2315 GTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 2347
1 GTGTGTGTGTCATGTGTGTCATGTGTGTGTG 33

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[illegible]

[illegible]

1. 38
/locatidn/Vectors
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0264105"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb Plasmid UGCG2M library"
/note="Vector: PMD429; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse Genome Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repeated with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD2 (g1473211[gb|AF123072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

	Query Match	0.7%	Score 26.6;	DB 1,	length 38;
	Best Local Similarity	87.9%;	Pred. No. 73;		
	Matches	29; Conservative	0; Mismatches	4; Indels	0; Gaps
QY	2311	TTTGATCTGTCGTCTGTCTGCACGTGGTGG	2343		
b	6	TGTGATGGTCTGTCTGTCTGTCTGTCTGG	38		

RESULT 200
BX553058

LOCUS BX553058 28 bp mRNA linear EST 10-OCT-2003
DEFINITION BX553058 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Isel27a09_plc, mRNA sequence.
ACCESSION BX553058
VERSION BX553058.1 GI:33377257
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippodrosocidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane, M., Aksoy, S., Gibson, W., Kethrou, A., Berriman, M.,
Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PubMed 14519198
COMMENT Contact: Hall N

Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.

```

1: 28
2: /organism="Glossina morsitans morsitans"
3: /mol_type="mRNA"
4: /sub_species="morsitans"
5: /db_xref="taxon:37346"
6: /clone="seiz7a09_pic"
7: /tissue_type="adult infected gut"
8: /clone_lib="Glossina morsitans morsitans adult infected
9: gut"
10: /note="country: Zimbabwe; EST from adult gut infected with
11: m.brucei"

```

Query Match	0.7%	Score 26.4	DB 1	Length 28
Best Local Similarity	96.4%	Pred. No. 56		
Matches 27; Conservative	0	Mismatches	1	Indels 0; Gaps 0

Oy	2319	G T G T G T G T G T G T G C C G T G T G T G T G T	2346
Db	1	G T G T G T G T G T G T G T G T G T G T G T	28

RESULT 201

[illegible]

KEYWORDS

ORGANISM

REFERENCE

TITLE

JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N

Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all pic reads are from
 the 3' end.

FEATURES location/Qualifiers

1. 28
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse46d02_p1c"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"

Query Match 0.7%; Score 26.4; DB 1; Length 28;
 Best Local Similarity 96.4%; Pred. No. 56;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2319 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2346
 Db 1 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 28

RESULT 202

AZ330730 28 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0056C1F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 DEFINITION clone UUGCLM0056C1F, genomic survey sequence.

ACCESSION AZ330730
 VERSION AZ330730.1 GI:10392723
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0056 row: C column: 11
 Seg primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES location/Qualifiers
 source 1. 28
 /organism="Mus musculus"

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0056C1F"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.7%; Score 26.4; DB 1; Length 28;
 Best Local Similarity 96.4%; Pred. No. 56;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2319 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2346
 Db 1 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 28

RESULT 203

AZ366137 28 bp DNA linear GSS 02-OCT-2000
 LOCUS 1M0115B21F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 DEFINITION clone UUGCLM0115B21F, genomic survey sequence.

ACCESSION AZ366137
 VERSION AZ366137.1 GI:10479837
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 28)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weis,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0115 row: B column: 21
 Seg primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES location/Qualifiers
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 /mol_type="genomic DNA"

/strain="CS7BL/6J"
/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344

DB 1 CTGTGTGTGTGTGTGTGTGTGTGTGTGT 28

RESULT 204
AZ467078 28 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0278C15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0278C15 F, genomic survey sequence.
ACCESSION AZ467078 GI:10625203
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0278 row: C column: 15
Seq primer: CCGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers

FEATURES
source
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"

/db_xref="taxon:10090"
/clone="UUGC1M0278C15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 56;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2345

DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 28

RESULT 205
AZ514383 28 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0361G05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0361G05 F, genomic survey sequence.
ACCESSION AZ514383 GI:10695699
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: G column: 05
Seq primer: CCGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers

FEATURES
source
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"

musculus C57BL/6J (male) was obtained from the Jackson Laboratory mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 [G114732114|G9|AF12072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      0.7% Score 26.4; DB 1; Length 30;  
Best Local Similarity    96.4%; Pred. No. 60;  
Matches   27; Conservative    0; Mismatches  
  
QY          2317 CTGTGTCGTCTGTCGCATGGTCTGTT 2344  
            |||||  
Dd          3     CTGTGTCGTCTGTCGTCTGTCGTCT 30
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Accession	Definition	Locust	Result 211
AZ961995	30 bp DNA linear		
AZ961995	2M023G12R Mouse 10kb plasmid UGC2M library Mus musculus genomic		
AZ961995	clone UGC2M023G12 R, genomic survey sequence.		
AZ961995			

VERSION	AZ961995.1	GI:13833222
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Petersen, T.,
1 (bases 1 to 30)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus

TITLE	Mouse whole genome scaffolding with paired end reads from 10xK
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss
	University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.000
 Plate: 0230 Row: G Column: 12
 Seq primer: CACGACGAAACACGATCACC
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

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/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-
/clone_lib="Mouse 10kb plasmid UGGCM library"
/nucleo="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson

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RESULT 220
LOCUS      A2425112
DEFINITION 30 bp DNA linear GSS 03-OCT-2000
            1M0205101F Mouse 10kb plasmid UUCGM1 library Mus musculus genomic
            clone UUCGM1M0205101 F, genomic survey sequence.
ACCESSION  A2425112
VERSION     A2425112.1
KEYWORDS    GI:10549125
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0205 row: 1 column: 01
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            Class: plasmid ends
            High quality sequence stop: 30.

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            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUCGM1 library"
            /note="Vector: pMD42HV, Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid RL. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

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[illegible]

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FEATURES
source
1..34
Location/Qualifiers

TITLE
JOURNAL
COMMENT
34 bp DNA linear GSS 20-FEB-2001

DEFINITION
2M0070B06R Mouse 10kb plasmid U00C1M library Mus musculus genomic
clone U00C2M0070B06 R, genomic survey sequence.

ACCESSION
A2807557

VERSION
A2807557

KEYWORDS
A2807557.1 GI:12972024
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Euarctota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Baccaro,T., Duval,B., Hamll,C.,
Jellam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 row: B column: 06
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid end
High quality sequence stop: 34.

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Best Local Similarity	93.14	Pred. No. 81		
Matches 27	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	2325	GTGTGTGTCCTGTGTGTGTGTGTCA	2353	
Ob	1	GTGTGTGTGTGTGTGTGTGTGTGAA	29	

RESULT 223
AZ491991

LOCUS	AZ491991	35 bp	DNA	linear	GENS 05-OCT-2000
DEFINITION	1M0325C24R Mouse 10kb plasmid UNGCM library Mus musculus genomic				
ACCESSION	clone UNGCM0325C24 R, genomic survey sequence.				
VERSION	AZ491991				
KEYWORDS	GSS.				
SOURCE	AZ491991.1	GI:10664237			
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Mus musculus				
AUTHORS	Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
	1 (bases 1 to 35)				
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D. Weis,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weis University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0325 row: C column: 24 Seq primer: CACACAGAAACAGCATATGACC Class: plasmid ends High quality sequence stop: 35. Location/Qualifiers 1..35				
FEATURES					
Source	1..35				

	Query Match	0.78;	Score 25.8;	DB 1;	Length 35;
	Best Local Similarity	93.1%;	Pred. No. 83;	Matches 27; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	2319	GTCGTGCTGCATGCCATGTCGTGCGTGG	2347		
D6	7	GCCTGTCGTGCTGTCGTGCTGTCGTG	35		

RESULT 224		
AZ661921		
LOCUS		
AZ661921	32 bp	DNA linear
		GSS 14-DEC-2000

DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT								
IM0540B17R Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0540B17 R, genomic survey sequence.	A2661921			Mus musculus (house mouse)	1 (bases 1 to 32)	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Rolly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niedernhausen,A. and Wright,D.,Weise,R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Published (2000)	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0540 row: B column: 17 Seq primer: CACACAGGAACACGCTTACGACC Class: plasmid ends High quality sequence stop: 32.								
FEATURES	location/qualifiers	1..32	/organism="Mus musculus"	/mol_type="genomic DNA"	/strain="C57BL/6J"	/db_xref="taxon:10090"	/clone="U06C1M0540B17"	/sex="male"	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	/clone_id="Mouse 10kb plasmid U06C1M library"	/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi14732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."						
Query Match	0.7%	Score 25.6	DB 1	Length 32	Best Local Similarity	87.5%	Prod. No. 80	Matches	28	Conservative	0	Mismatches	4	Indels	0	Gaps	0
Db	2318	TGTGNGTGTGTGACGTGTGTGTGTGTG	2349														
1	TGTTGCTGTGTGTGTGTGTGTGTGTG	32															
RESULT 225	AZ814562	34 bp	DNA	linear	GSS 20-FEB-2001	LOCUS	2M0082A222P	Mouse 10kb plasmid U06C1M library Mus musculus genomic	DEFINITION								

```

ACCESSION   clone UUGC2M0082A22 F, genomic survey sequence.
VERSION     A2814562
KEYWORDS    A2814562.1 GI:12984470
SOURCE      GSS.
ORGANISM    Mus musculus (house mouse)
MUS musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE   1 (bases 1 to 34)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
            Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhassen,A. and Wright D. Weiser,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
TITLE       unpublished (2000)
JOURNAL     Contact: Robert B. Weiser
COMMENT     University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
            84112, USA
            Tel.: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert length: 10000 Std Error: 0.00
            Plate: 0082 row: A column: 22
            Seq primer: CGTTGTAAACGACGCGCAGC
            Class: plasmid ends
            High quality sequence stop: 34.
            Location/Qualifiers
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                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (g14732114[gblAF129072.1]), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
FEATURES
SOURCE
Query Match      0.7%; Score 25.6; DB 1; Length 34;
Best Local Similarity 87.5%; Pred. No. 85;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      2319  GTGATGTGTGTGTCGCTGTGTGTGTGTGTGT 2350
DB      3  GGGTGTGTGTGAGTGAGTGTGTGTGTGTGTGT 34
RESULT 226
A2342492      27 bp DNA linear GSS 29-SEP-2000
LOCUS      1M0075004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION  clone UUGC1M0075004 R, genomic survey sequence.

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ACCESSION	AZ42492
VERSION	AZ42492.1
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eumalota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 27) Dunn,D., Loyagaci,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islami,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts unpublished (2000)
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: dduumgenetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0075 row: O column: 04 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 27.
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COMMENT	Query Match 0.7% Score 25.4; DB 1; Length 27; Best Local Similarity 96.3%; Pred. No. 71; Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	2319 GTGTGTGTGTGTGCCTGTGTGTGTG 2345
Dn	1 GTGTGTGTGTGTGTGTGTGTGTGTGTG 27
RESULT 227	AZ435344 27 bp DNA linear GSS 03-OCT-2000 LOCUS 1M0222K17 Mouse 10kb plasmid UUCGIM library Mus musculus genomic DEFINITION Clone UUCGIM0222K17 F, genomic survey sequence.
ACCESSION	AZ435344

VERSION	AZ635344.1	GI:10559357
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27) Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Ross,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
TITLE	Unpublished (2000)	
JOURNAL	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112 USA Tel.: 801 585 5606 Fax: 801 585 .7177 Email: ddunne@genetics.utah.edu Insert length: 1000 Std Error: 0.00 Plate: 0222 row: K column: 17 Seq primer: CGTGTAAACAGCAGCCACAT Class: plasmid ends High quality sequence stop: 27. Location/Qualifiers	
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Query Match	0.7%; Score 25.4; DB 1; Length 27;	
Best Local Similarity	96.3% ; Pred.No. 71;	
Matches	26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Dn	1 TGTTGGTGCTGTCGTGCGTCGTGTGT	2344
Oy	TGTTGGTGCTGTCGTGCGTCGTGTGT	2344
RESULT 228		
LOCUS	AZ583081	
DEFINITION	mouse 10kb plasmid UUCGM library Mus musculus genomic clone UTGCIM0376L6 R, genomic survey sequence.	
ACCESION	AZ583081	
VERSION	AZ583081.1 GI:11702607	

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0550 row: G column: 18
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 27.

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/strain="C57BL/6J"
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/clone="UUGCIM0550G18"
/sex="Male"
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/clone_1lb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD22nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 71;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGCGTGTGTGTG 2345
DB 1 GTGTGTGTGTGTGTGTGTGTGTG 27

RESULT 231
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DEFINITION 2M0262D3F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
ACCESSION AZ981811
VERSION AZ981811.1 GI:13853038
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: D column: 23
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0550G18"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pMD22nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G114732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 71;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGCGTGTGTGTG 2344
DB 27 TGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 232
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DEFINITION 1M0173N21R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
ACCESSION AZ405219
VERSION AZ405219.1 GI:10529232
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Thu Oct 28 12:48:27 2004

vivi1emore401-10.rst

Page 116

REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS	1 (bases 1 to 28) Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C., Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: dduan@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0173 row: N column: 21 Seq primer: CACACAGGAACACTATGACC Class: plasmid ends High quality sequence stop: 28. Location/Qualifiers 1..28 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UTGCIM0173N21" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_id="Mouse 10kb plasmid UTEGCM library" /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gil14732114[gb][AF129072.1)], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
QUERY MATCH	0.7%; Score 25.4; DB 1; Length 28; Best Local Similarity 96.3%; Pred. No. 74;
Matches	26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 233	
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DEFINITION	JM0238NO3R Mouse 10kb plasmid UTEGCM library Mus musculus genomic
ACCESSION	U00238NM0238NO3 R, genomic survey sequence.
VERSION	AZ443611 GI:10591759
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 28)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	
	Contact: Robert B. Weis			
	University of Utah			
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA			
	Tel.: 801 585 5606			
	Fax: 801 585 7177			
	Email: dunn@genetics.utah.edu			
	Insert length: 10000	Std Error: 0.00		
	Plate: 0238	row: N	column: 03	
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	Class: plasmid ends			
	High quality sequence stop: 28.			
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	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource			
	(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (gi 4732114 gb AF12972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
Query Match	0.74; Score 25.4; DB 1; Length 28;			
Best Local Similarity	96.3%; Pred. No. 74;			
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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Db 2	TGTCGTGTCGTGTCGTGTCGTGTCGT	28		
RESULT 234				
LOCUS	AZ782113	28 bp	DNA	linear
DEFINITION	2M0022N03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0022N03 F, genomic survey sequence.			
ACCESSION	AZ782113			
VERSION	AZ782113			
KEYWORDS	GS. GI:12915480			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 89;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
DB 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 249
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LOCUS 1M0343F01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0343F01 R, genomic survey sequence.
ACCESSION AZ503652
VERSION AZ503652.1 GI:10684968
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0343 row: F column: 01
Seq primer: CACACAGAAACGCTATACCC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

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1. 26
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/clone="UGCGIM0343F01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 89;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
DB 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 250
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LOCUS 2M0051P11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0051P11 F, genomic survey sequence.
ACCESSION AZ795803
VERSION AZ795803.1 GI:12943205
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0051 row: F column: 11
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Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 96.2%; Score 24.4; DB 1; Length 27;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 2 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 255
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LOCUS 2M0059P03R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGM0059P03 R, genomic survey sequence.

ACCESSION A2801217 GI:12935340
VERSION A2801217.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends
High quality sequence stop: 27.

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/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 96.2%; Score 24.4; DB 1; Length 27;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
DB 2 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 256
A2807584 29 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0070H04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGM0070H04 R, genomic survey sequence.

ACCESSION A2807584 GI:12972078
VERSION A2807584.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Placer: 0070 row: H column: 04
Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends
High quality sequence stop: 29.

FEATURES
source Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 25.
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Query Match 0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2342
DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 266
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LOCUS 1M0172D10F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0172D10 F, genomic survey sequence.
ACCESSION AZ404057
VERSION AZ404057.1 GI:10528070
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 row: D column: 10
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
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/sex="Male"
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2343
DB 25 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 267
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LOCUS 1M0570D12R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0570D12 R, genomic survey sequence.
ACCESSION AZ769673
VERSION AZ769673.1 GI:12890050
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 25)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0570 row: D column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES
Source

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/clove_lib="mouse 10kb plasmid UUCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1[4732114]gb[AP129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.6%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGCCTGTGTGTG 2343
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Db 1 GTGTGTGTGTGTGTGTGTGTGTG 25
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RESULT 268
A2771881
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE

A2771881 25 bp DNA linear GSS 16-FEB-2001
IM057AF23F Mouse 10kb plasmid UUCIM library Mus musculus genomic
clone UUCIM057AF23 F, genomic survey sequence.
A2771881
A2771881.1 GI:12894610
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)

AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Irlam, H., Longcore, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D. Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid insets
 Unpublished (2000)
JOURNAL
 COMMENT
 Contact: Robert B. Weis
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0574 row: F column: 23
 Seq primer: CGTGTGAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
FEATURES
 Location/Qualifiers
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 /strain="C57BL/6J"
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 /clone="U08C1M0574F23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid U08C1M library"
 /note="Vector: PMD42ny, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114[gb|AF12972.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 92.3%; Score 22.8; DB 1; Length 26;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTCGTGTCGTGTCGTGTCGTG 2343
DB 26 TGTGTCGTGTCGTGTCGTGTCGTGAG 1

RESULT 274
AZ494629 26 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0330F01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0330F01 F, genomic survey sequence.
ACCESSION AZ494629
VERSION AZ494629.1 GI:10669392
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0330 row: F column: 01
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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/clone="UUGC1M0330F01"
/sex="Male"

FEATURES

source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0330F01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 92.3%; Score 22.8; DB 1; Length 26;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2312 TTGGTCTGTGTCGTGTCGTGTCGTG 2337
DB 1 TTGGTCTGTGTCGTGTCGTGTCGTG 26

RESULT 275
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LOCUS 1M0564D08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0564D08 F, genomic survey sequence.
ACCESSION AZ766495
VERSION AZ766495.1 GI:12883629
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: D column: 08
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564D08"
/sex="Male"

FEATURES

source

1..26
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M0564D08"
/sex="Male"

/clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 22.8; DB 1; Length 26;
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2319 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2344
 Db 1 GGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 276
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 DEFINITION 2M0019A07F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 accession AZ781130
 version AZ781130.1 GI:12913513
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0019 row: A column: 07
 Seq primer: CAGTGTAAACGACGCGCAT
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1. 26
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
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 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"

/note="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 22.8; DB 1; Length 26;
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2343
 Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 26

RESULT 277
 AZ404479 27 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0172F18R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 accession AZ404479
 version AZ404479.1 GI:10528408
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0172 row: F column: 18
 Seq primer: CACACAGAAACAGCTATGACC
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 High quality sequence stop: 27.
 Location/Qualifiers
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 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PWD42nv, Purified genomic DNA from M.


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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

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/clone_idb="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe, EST from adult gut infected with
T.brucei"

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query match	0.6%;	Score 22.4;	DB 1;	Length 24;
-------------	-------	-------------	-------	------------

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0464 row: J column: 22
Seq primer: CATTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES

source

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.2; DB 1; Length 28;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2318 TTGTCGTGTCGTGTCGTGTCGTGTCGT 2344
DB 1 TTGTCGTGTCGTGTCGTGTCGTGTCGT 27

RESULT 293
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LOCUS 1M0145M04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0145M04 F, genomic survey sequence.
ACCESSION AZ386218
VERSION AZ386218.1 GI:104999218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: M column: 04
Seq primer: CATTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 30.

FEATURES

source

1. 30
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 22.2; DB 1; Length 30;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2312 TTGTCGTGTCGTGTCGTGTCGTGTCGT 2338
DB 4 TTGTCGTGTCGTGTCGTGTCGTGTCGT 30

RESULT 294
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DEFINITION clone UUGC1M0502H10 F, genomic survey sequence.
ACCESSION AZ640238
VERSION AZ640238.1 GI:11763638
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The digested DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 [g114731114[SP]A123072.1], a copy-number of pMDA2 [g114731114[SP]A123072.1], the vector was ligated to the blunt end derivative of plasmid RI. The copy was purified. The sheared, adaptor-complementary to the insert adaptors and adapted vector DNA, and transformed mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

clone_jib="Mouse 10kb plasmid U06GM library"
/note="Vector: PMD429; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD23 (gil14732114[gb|AF128072.1]), a copy-number
inducible derivative of plasmid RL1, the copy-number was
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Place: 0147 row: F column: 22

/strain="C57BL/6J"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 21.6; DB 1; Length 29;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2322 TGTGTGTGTGTCGTCGTGTGTGTGTG 2349
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 Db 2 TATATGTGTGTGTGTGTGTGTGTGTG 29

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 LOCUS 1M0367BE06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0367BE06 F, genomic survey sequence.

ACCESSION AZ579506
 VERSION AZ579506.1 GI:11693935
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 30)
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C., Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: B column: 06
 Seq primer: CGTGTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"

/db xref="taxon:10090"
 /clone="UUGC1M0367E06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 21.6; DB 1; Length 30;
 Best Local Similarity 85.7%; Pred. No. 2.2e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2311 TTTGTGTGTGTGTGTGTGTGTGTGTGTGT 2338
 |||||
 Db 30 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3

RESULT 302
 AL943661 30 bp DNA linear GSS 31-MAR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-276A12-015154,
 DEFINITION genomic survey sequence.

ACCESSION AL943661
 VERSION AL943661.1 GI:24400267
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.

TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 MEDLINE 22755829
 PUBMED 12874060

REFERENCE
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
 TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 MEDLINE 23117147
 PUBMED 14756321

REFERENCE
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.
 TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050

REFERENCE
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G. and Weishaar, B.
 TITLE Direct Submission
 4 (bases 1 to 30)
 Direct Submission

JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. Details on the protocols used for generation of the source are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
1. .30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-276A12-015154"
/db_xref="taxon:3702"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

Query Match 0.6%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2817 ATATGGATATATACATATATATATATAT 2844
Db 1 ATACTATATATATATATATATATATATATA 28

RESULT 303
AL943661 30 bp DNA linear GSS 31-MAR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-276A12-015154,
DEFINITION genomic survey sequence.
ACCESSION AL943661
VERSION AL943661.1 GI:24400267
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060

REFERENCE
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
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JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050
REFERENCE 4 (bases 1 to 30)
AUTHORS Strizhov, N., Li, Y., Rosso, M.G. and Weishaar, B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
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FEATURES
source
1. .30
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-276A12-015154"
/db_xref="taxon:3702"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

Query Match 0.6%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2823 TATATATACATATATATATATATATATAT 2850
Db 28 TATATATATATATATATATATATATATAT 1

RESULT 304
BX557786 23 bp mRNA linear EST 10-OCT-2003
LOCUS BX557786
DEFINITION moritans moritans adult infected gut Glossina morsitans moritans CDNA clone Tse34f11_p1c, mRNA sequence.
ACCESSION BX557786
VERSION BX557786.1 GI:33428961
KEYWORDS EST.
SOURCE Glossina morsitans moritans
ORGANISM Glossina morsitans moritans

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
TITLE 1 (bases 1 to 23)
JOURNAL Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berrian, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
MEDLINE 22881942
PUBMED 14519198

REFERENCE
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berrian, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans moritans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2DW

ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
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 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 1.8e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2340
 Db 23 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 309
 AZ824638 23 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0099A22F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGM0099A22 F, genomic survey sequence.

ACCESSION AZ824638
 VERSION AZ824638.1 GI:12994546
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: A column: 22
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0099A22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: pMD22nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to
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 electrophoresis. Vector DNA was prepared from a derivative
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 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 1.8e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2317 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2339
 Db 1 CTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 23

RESULT 310
 AZ828969 23 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0106013F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCGM0106013 F, genomic survey sequence.

ACCESSION AZ828969
 VERSION AZ828969.1 GI:12998877
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
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 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0106 row: O column: 13
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0106013"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: pMD22nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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 0.005 inch orifice at constant velocity. The sheared DNA
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 polynucleotide kinase. Adaptor oligonucleotides were
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adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
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 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

REFERENCE 1 (bases 1 to 30)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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 COMMENT Contact: Robert B. Weiss
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 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: D column: 03
 Seq primer: CATTGTAACGACGCGCACT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers
 1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIM0367D03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 21.2; DB 1; Length 30;
 Best Local Similarity 88.5%; Pred. No. 2.4e+02;
 Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3461 TTTATATATATATATATATATTT 3486
 Db 29 TTTATATATATATATATATATAT 4

RESULT 320
 LOCUS AZ780500/c 25 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0017J19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0017J19 R, genomic survey sequence.
 ACCESSION AZ780500
 VERSION AZ780500.1 GI:12912224
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 25)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0017 row: J column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0017J19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2316 TCTGTGTGTGTGTGTGTGTGTGTG 2339
 Db 24 TTTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 321
 LOCUS AZ589684 27 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0398017R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0398017 R, genomic survey sequence.
 ACCESSION AZ589684
 VERSION AZ589684.1 GI:11711874
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: 0 column: 17
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

Location/Qualifiers

1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0398017"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
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Query Match 0.5%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2821 GGTATATATACATATATATATA 2844
Db 1 GATATATATATATATATATATA 24

RESULT 322
AZ589684/c 27 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0398017R Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION clone UGGCM0398017 R, genomic survey sequence.
ACCESSION AZ589684
VERSION AZ589684
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: 0 column: 17
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

Location/Qualifiers

1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0398017"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 20.8; DB 1; Length 27;
Best Local Similarity 91.7%; Pred. No. 2.4e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2823 TATATATATATATATATATATAC 2846
Db 24 TATATATATATATATATATATATC 1

RESULT 323
AZ823699 27 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0097G23R Mouse 10kb plasmid UGGCM library Mus musculus genomic
DEFINITION clone UGGCM0097G23 R, genomic survey sequence.
ACCESSION AZ823699
VERSION AZ823699
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

TITLE
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhuesern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0097 row: G column: 23
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
FEATURES
source
1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0097G23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[9b]/AF129072.1), a copy-number
inducible derivative of the insert adapsors and
with adapsors complementary to the insert adapsors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptors vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

TITLE	Niederhausern,A. and Wright,D.,Weiss,R.
JOURNAL	Muscle whole genome scaffolding with paired end reads from 10kb Plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0513 row: C column: 13 Seq primer: CGTTGTAAACGAGCGCCACT Class: plasmid ends High quality sequence stop: 27. Location/Qualifiers
FEATURES	
source	1. 27 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGGCIM0513C13" /sex="male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /c_lone_lib="Mouse.10kb plasmid UGGCIM library" /note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource http://www.jax.org/resources/documents/dnares/ . The DNA was hydromatically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with T4 DNA polymerase and T4 ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 [gil473114[gb AF129072.1)], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match	0.5%; Score 20.6; DB 1; Length 27;
Best Local Similarity	85.2%; Pred. No.2.6e+02;
Matches	23; Conservative : 0; Mismatches 4; Indels 0; Gaps 0;
CY	2319 GTGTGTGTGTGTGTGCCGTGTGTGTGTG 2345
Dbl	1 GTGTGTGTGTGTGTGTATGTATGTATGTG 27
RESTRT 325	
AZ484090	
LOCUS	22 bp DNA linear GSS 05-OCT-2000
DEFINITION	1M031011SF Mouse 10kb plasmid UGGCIM library Mus musculus genomic clone UGGCIM031011F, genomic survey sequence.
ACCESSION	AZ484090 GI:10648679
VERSION	GSS.
KEYWORDS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

JOURNAL COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0045 row: H column: 20
 Seq primer: CACACAGAAACAGCATATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

source

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0045H20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUCG2M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 95.5%; Score 20.4; DB 1; Length 22;
 Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2323 GTGTGTGTGTGTGTGTGTGTGT 2344

Db 1 GTGTGTGTGTGTGTGTGTGTGT 22

RESULT 328

AZ985497

LOCUS 22 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0267D23P Mouse 10kb plasmid UUCG2M library Mus musculus genomic

clone UUCG2M0267D23 F, genomic survey sequence.

ACCESSION AZ985497

VERSION AZ985497.1 GI:13856724

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Mus.

REFERENCE 1 (bases 1 to 22) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0267 row: D column: 23
 Seq primer: CTTCTTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES

source

Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0267D23"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUCG2M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 95.5%; Score 20.4; DB 1; Length 22;
 Pred. No. 2.2e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGTGT 2340

Db 1 GTGTGTGTGTGTGTGTGTGTGT 22

RESULT 329

TA324H01P

LOCUS 22 bp DNA linear GSS 13-DEC-2000

DEFINITION T. Brucei sheared genomic DNA clone 324h01, forward sequence,

genomic survey sequence.

ACCESSION AL493407

VERSION AL493407.1 GI:11867772

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 22) Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submision

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Center, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh1@sanger.ac.uk

JOURNAL

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES
source
1. 22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="324h01"

Query Match 0.5%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
|||||
1 TATATATATATATATATATATA 22

Db 1 TATATATATATATATATATATA 22

RESULT 330
LOCUS TA324H01P/C 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 324h01, forward sequence,
genomic survey sequence.
ACCESSION AL493407 GI:11867772
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 22)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES
source
1. 22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="324h01"

Query Match 0.5%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATACATATATATATATA 2844
|||||
22 TATATATATATATATATATA 1

Db 22 TATATATATATATATATATA 1

RESULT 331
LOCUS AZ371475 23 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0122K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0122K19 R, genomic survey sequence.
ACCESSION AZ371475 GI:10485175
VERSION AZ371475.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0122 Row: K Column: 19
Seq primer: CACACAGAAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source
1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0122K19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PWD42ny. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGT 2338
 Db 2 CTGTGTGTGTGTGTGTGT 23

RESULT 332

AZ584665

LOCUS 24 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0389423F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0389423 F, genomic survey sequence.

AZ584665

VERSION 1 GI:11705779
 KEYWORDS GSS.

SOURCE

Mus musculus (house mouse)
 Mus musculus

ORGANISM

REFERENCE
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0389 row: A column: 23
 Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends
 High quality sequence stop: 24.

Location/Qualifiers

FEATURES

source

1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0389423"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 2.4e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATATATATATATATA 2844

Db 1 TATATATATATATATATATA 22

RESULT 333

AZ584665/c

LOCUS

DEFINITION 24 bp DNA linear GSS 13-DEC-2000
 1M0389423F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0389423 F, genomic survey sequence.

AZ584665

VERSION 1 GI:11705779
 KEYWORDS GSS.

SOURCE

Mus musculus (house mouse)
 Mus musculus

ORGANISM

REFERENCE
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0389 row: A column: 23
 Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends
 High quality sequence stop: 24.

Location/Qualifiers

FEATURES

source

1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0389423"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 2.4e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATATATATATATATA 2844

Db 24 TATATATATATATATATATA 3

RESULT 334
TA280H02Q 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 280h02, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL485433 GI:11851540
VERSION AL485433.1 GI:11851540
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS 1 (bases 1 to 24)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submision
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="280h02"

Query Match 0.5%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 2 TATATATATATATATATATATA 23

RESULT 335
TA280H02Q/C 24 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 280h02, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL485433
VERSION AL485433.1 GI:11851540
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS 1 (bases 1 to 24)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submision
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and

COMMENT
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 CUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="280h02"

Query Match 0.5%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
Db 23 TATATATATATATATATATATA 2

RESULT 336
AZ585116 25 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0389124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0389124 R, genomic survey sequence.
ACCESSION AZ585116
VERSION AZ585116.1 GI:11706514
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meener, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0389 row: L column: 24
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0389124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G114732114[9b]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 2.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
DB 1 TATATATATATATATATATATA 22

RESULT 337 25 bp DNA linear GSS 13-DEC-2000
AZ585116
LOCUS IM0369L24R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0369L24 R, genomic survey sequence.

ACCESSION AZ585116
VERSION AZ585116.1 GI:11706514

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
AUTHORS Isalam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0389 row: L column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers

FEATURES

source 1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0369L24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G114732114[9b]/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 2.5e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
DB 24 TATATATATATATATATATA 3

RESULT 338 27 bp DNA linear GSS 13-DEC-2000
TA319C02P
LOCUS T. brucei sheared genomic DNA clone 319c02, forward sequence,
DEFINITION genomic survey sequence.

ACCESSION AL482452.1 GI:11867396

KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE Trypanosoma.
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrett, B.G.
Direct Submision
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nh@sanger.ac.uk
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES

source 1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="319c02"

Query Match 0.5%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 2.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
 Db 1 TATATATATATATATATATATA 22

RESULT 339
 TAJ19C02P/C 27 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 319C02, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL492452
 VERSION AL492452.1 GI:11867396
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
 AUTHORS 1 (bases 1 to 27)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Acklin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
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 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source
 1..27
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="319C02"

Query Match 0.5%; Score 20.4; DB 1; Length 27;
 Best Local Similarity 95.5%; Pred. No. 2.7e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
 Db 26 TATATATATATATATATATATA 5

RESULT 340
 AZ387831 28 bp DNA linear GSS 02-OCT-2000
 LOCUS IM0147F22R Mouse 10kb plasmid UGCM library Mus musculus genomic
 DEFINITION clone UGCM0147F22 R, genomic survey sequence.
 ACCESSION AZ387831
 VERSION AZ387831.1 GI:10501539
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0147 row: F column: 22
 Seq primer: CACACAGAAACGCTATGACC
 Class: Plasmid ends
 High quality sequence stop: 28.

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0147F22"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI|473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 28;
 Best Local Similarity 95.5%; Pred. No. 2.8e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATA 2844
 Db 27 TATATATATATATATATATATA 6

RESULT 341
 AZ648796 28 bp DNA linear GSS 14-DEC-2000
 LOCUS IM0518A05F Mouse 10kb plasmid UGCM library Mus musculus genomic
 DEFINITION clone UGCM0518A05 F, genomic survey sequence.
 ACCESSION AZ648796
 VERSION AZ648796.1 GI:11781618
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0518 row: A column: 05
Seq primer: CATTCTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source

Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0518A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.4; DB 1; Length 28;
Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2823 TATATACATATATATATA 2844
DB 1 TATATATATATATATATA 22

RESULT 342
AZ459694 25 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0264P10R Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0264P10 R, genomic survey sequence.
ACCESSION AZ459694
VERSION AZ459694.1 GI:10617819
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
AUTHORS Dunn, D., Ayagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: P column: 10
Seq primer: CACACAGAAAACGATGAC
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
source

Location/Qualifiers
1..25
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGM0264P10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCGM library"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2319 GTGTGTGTGTGTGTGTGTGTG 2343
DB 1 GTGTGTGTGTGTGTGTGTGTG 25

RESULT 343
AZ766498 25 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0564E08F Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION clone UUCGM0564E08 F, genomic survey sequence.
ACCESSION AZ766498
VERSION AZ766498.1 GI:12883635
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
AUTHORS Dunn, D., Ayagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0564 row: B column: 08
 Seq primer: CGTTGTAACGACGCGCCACT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0564E08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_11b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g9|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 88.0%; Score 20.2; DB 1; Length 25;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2342

Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 344
 TAL94F01Q 26 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 194f01, reverse sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL477302
 VERSION AL477302.1 GI:11841328
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 26)

REFERENCE

AUTHORS

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh1@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v+ i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. .26
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="194f01"

Query Match 0.5%; Score 20.2; DB 1; Length 26;
 Best Local Similarity 88.0%; Pred. No. 2.7e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2342

Db 1 TGTTCGCTGTGTGCGCGCTGTGTGT 25

RESULT 345
 AZ579497 30 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0367D03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0367D03 F, genomic survey sequence.
 ACCESSION AZ579497
 VERSION AZ579497.1 GI:11693926
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 30)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Ismail, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
 Niederhuesern, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

Unpublished (2000)
 Contract: Robert B. Weiss

COMMENT

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: D column: 03
 Seq primer: CGTTGTAACGACGCGCCACT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

source

1. .30

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0367D03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_11b="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 3.2e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3455 TACAAGTTATATATCTATATATA 3480
DB 1 TATATTTTATATATTTTATATATA 26

RESULT 350
AZ781477 28 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION 2M0019H24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0019H24 R, genomic survey sequence.

ACCESSION
AZ781477
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0019 row: H column: 24
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source
Location/Qualifiers

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0019H24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.6; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2313 TGGTCTGTGTGTGTGTGTGTGTGTGT 2338
DB 3 TGGTGGGTTGTGTGTGTGTGTGTGT 28

RESULT 351
AZ310642 21 bp DNA linear GSS 29-SEP-2000
LOCUS
DEFINITION 1M0025N09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0025N09 R, genomic survey sequence.

ACCESSION
AZ310642
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: N column: 09
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
Location/Qualifiers

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0025N09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGT 2338
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 352
AZ333309 21 bp DNA linear GSS 29-SEP-2000
LOCUS IM0062P13F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0062P13 F, genomic survey sequence.

ACCESSION AZ333309
VERSION AZ333309.1 GI:10397798
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: P column: 13
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Location/Qualifiers
1..21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0062P13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD29v, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTGTGT 2338
DB 1 TGTGTGTGTGTGTGTGTGTGT 21

RESULT 353
AZ513902 21 bp DNA linear GSS 05-OCT-2000
LOCUS IM0360A13F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0360A13 F, genomic survey sequence.

ACCESSION AZ513902
VERSION AZ513902.1 GI:10695218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0360 row: A column: 13
Seq primer: CGTTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
Location/Qualifiers
1..21

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0360A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/note="Vector: pMD29v, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATA 2844
Db 21 ATATATATATATATATATATA 1

RESULT 356
AZ621072/c 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0454M05F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0454M05 F, genomic survey sequence.
ACCESSION AZ621072
VERSION AZ621072.1 GI:11743262
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0454 row: M column: 05
Seq primer: CGTGTAAACGACGCGCAGCT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source Location/Qualifiers

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0454M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGM library"
/note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2325 GTGTGTGTGCGTGTGTGTG 2345
Db 21 GTGTGTGTGCGTGTGTGTG 1

RESULT 357
AZ635627 21 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0493D06F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0493D06 F, genomic survey sequence.
ACCESSION AZ635627
VERSION AZ635627.1 GI:11757817
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: D column: 06
Seq primer: CGTGTAAACGACGCGCAGCT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source Location/Qualifiers

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0493D06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGM library"
/note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGT 2338
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 360
AZ854856 21 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0158109R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM2M0158109 R, genomic survey sequence.

ACCESSION AZ854856
VERSION AZ854856.1 GI:13044389
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0158 row: 1 column: 09

Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCM2M0158109"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/notes="Vector: PMD2nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGT 2338
Db 1 TGTGTGTGTGTGTGTGTGT 21

RESULT 361
AZ780002 22 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0016J20R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM2M0016J20 R, genomic survey sequence.

ACCESSION AZ780002
VERSION AZ780002.1 GI:12911227
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: J column: 20

Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. 22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCM2M0016J20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/notes="Vector: PMD2nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PMD2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATA 2844
 |||||
 22 ATATATATATATATATATA 2

RESULT 366
 A2822069 24 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0095D03F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG2M0095D03 F, genomic survey sequence.
 ACCESSION A2822069
 VERSION A2822069.1 GI:12891977
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0095 row: D column: 03
 Seg primer: CCGTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0095D03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (gl[4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid RI. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 24;
 Best Local Similarity 95.2%; Pred. No. 3.1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2326 TGTGTGTGCGTGTGTGTGTGT 2346
 |||||
 4 TGTGTGTGCGTGTGTGTGTGT 24

RESULT 367
 TAI70G05P 27 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 170g05, forward sequence.
 DEFINITION genomic survey sequence.
 ACCESSION AL473335
 VERSION AL473335.1 GI:11838934
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 27)
 Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 Direct Submision
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TRSU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1..27
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TRSU927"
 /db_xref="taxon:5691"
 /clone="170g05"

Query Match 0.5%; Score 19.4; DB 1; Length 27;
 Best Local Similarity 95.2%; Pred. No. 3.5e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3462 TTATATATCTATATATATA 3482
 |||||
 7 TTATATATATATATATATA 27

RESULT 368
 A2650121 27 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0520C09F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 DEFINITION clone UGCG1M0520C09 F, genomic survey sequence.
 ACCESSION A2650121
 VERSION A2650121.1 GI:11784286
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Query Match 0.5%; Score 19.4; DB 1; Length 24;
 Best Local Similarity 95.2%; Pred. No. 3.1e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source Location/Qualifiers

1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM0520C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 27;
Best Local Similarity 95.2%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATAT 2843
DB 7 TATATATATATATATATATAT 27

RESULT 369
AZ650121/c 27 bp DNA linear GSS 14-DEC-2000
LOCUS IM0520C09F Mouse 10kb plasmid UGCIM library Mus musculus genomic
DEFINITION clone UGCIM0520C09 F, genomic survey sequence.
ACCESSION AZ650121
VERSION AZ650121.1 GI:11784286
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, W., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source Location/Qualifiers

1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM0520C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19.4; DB 1; Length 27;
Best Local Similarity 95.2%; Pred. No. 3.5e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATACATATATATATATATA 2844
DB 27 ATATATATATATATATATATA 7

RESULT 370
AA995094/c 19 bp mRNA linear EST 27-AUG-1998
LOCUS ou89909.s1 NCI_CGAP Kid3 Homo sapiens cDNA clone IMAGE:1635040 3
DEFINITION similar to TR_069566 Q69566; contains TAR1.2 MER35 repetitive
element ;, mRNA sequence.
ACCESSION AA995094
VERSION AA995094.1 GI:3181583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaabbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbtp/image/image.html

Trace considered overall poor quality
 Insert Length: 1087 Std Error: 0.00
 Seq primer: -40m3 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES
 source

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1635040"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid3"
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.5%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2333 GCCTGTGTGTGTGTGTG 2351
 Db 19 GCCTGTGTGTGTGTGTG 1

RESULT 371
 AZ579516 22 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0367G01F Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM0367G01 F, genomic survey sequence.

ACCESSION AZ579516
 VERSION AZ579516.1 GI:11693945
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (baes 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: G column: 01
 Seg primer: CATTGTAAACGACGCGCAGT
 Class: plasmid ends

FEATURES
 source
 High quality sequence stop: 22.
 Location/Qualifiers

1.22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM0367G01"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 19; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2336 TGTGTGTGTGTGTGTGCAC 2354
 Db 22 TGTGTGTGTGTGTGTGCAC 4

RESULT 372
 AZ314354 22 bp DNA linear GSS 29-SEP-2000
 LOCUS 1M0031R07F Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM0031R07 F, genomic survey sequence.

ACCESSION AZ314354
 VERSION AZ314354.1 GI:10360159
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (baes 1 to 22)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islem, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0031 row: B column: 07
 Seg primer: CATTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGGCM0259H17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGGCM library"
 /note="Vector: pMD29v, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.8; DB 1; Length 23;
 Best Local Similarity 90.9%; Pred. No. 3.5e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2312 TTGGTCTGTGTGTGTGTGTG 2333

Db 1 TAGGTGTGTGTGTGTGTGTG 22

RESULT 377

AZ456517

LOCUS

DEFINITION 23 bp DNA linear GSS 04-OCT-2000

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNIVERSITY

BLDG.

ST.

UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0259 row: H column: 17

Seq primer: CGTTGTAAACGACGCGCAGCT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. 23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UGGCM0259H17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGGCM library"
 /note="Vector: pMD29v, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.8; DB 1; Length 23;
 Best Local Similarity 90.9%; Pred. No. 3.5e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2823 TATATATACATATATATATATA 2844

Db 1 TACATATACATATATATATA 22

RESULT 378

AZ792245

LOCUS

DEFINITION 26 bp DNA linear GSS 16-FEB-2001

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNIVERSITY

BLDG.

ST.

UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0043 row: N column: 01

Seq primer: CACACAGAAACAGCATATGACC

Class: plasmid ends

High quality sequence stop: 26.

Location/Qualifiers

1. 26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0043N01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.8; DB 1; Length 26;
 Best Local Similarity 90.9%; Pred. No. 4e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2823 TATATTACATATATATATATA 2844
 |||||
 26 TATATATAATATATATATAATA 5

RESULT 379
 AZ498814 25 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M0336H14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0336H14 F, genomic survey sequence.
 ACCESSION AZ498814
 VERSION AZ498814.1 GI:10677018
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0336 row: H column: 14
 Seq primer: CATTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0336H14"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.6; DB 1; Length 25;
 Best Local Similarity 84.0%; Pred. No. 4e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2327 GGTGTGCGTGTGTGTGTGTGTG 2351
 |||||
 1 GTGCACACGTGTGTGTGTGTGTGTG 25

RESULT 380
 AZ760251 25 bp DNA linear GSS 16-FEB-2001
 LOCUS 1M0553E20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0553E20 R, genomic survey sequence.
 ACCESSION AZ760251
 VERSION AZ760251.1 GI:12867877
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0553 row: E column: 20
 Seq primer: CACACAGAAACGCGTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES
 source Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0553E20"
 /sex="Male"

lac host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone.lib="Mouse 10kb plasmid UNGCM library"
/note="Vector: pMD24ny, Purified genomic DNA from M.
labradorius C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrolyzed/analytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
ligated DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD24 (gill473111[gb|AI23072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.5%	Score 18.6	DB 1	Length 25
Best Local Similarity	84.0%	Pred. No. 4e+02		
Matches	21	Conservative	0	Mismatches 4
				Indels 0
				Gaps 0
Qy	2311	TTTGGCTGTGTGTGTGTGTGCG	2335	
Db	1	TTTCTACGTGTGTGTGTGTGTG	25	

RESULT	381				
AZ368875					
LOCUS					
DEFINITION					
	AZ368875	20 bp	DNA	linear	GSS 02-OCT-2000
	U0013112	Mouse 10kb	plasmid	U00C1M library	Mus musculus genomic
	clone U00C1M011912	F, genomic	survey	sequence.	

/clone_11="Mouse 10kb plasmid UNGCJM library"
"note="Vector: PMD29v1. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 [g1-473214]gd/AF12072.11", a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

	Query Match	0.5%;	Score 18.4;	DB 1;	Length 20;
	Best Local Similarity	95.0%;	Pred. No. 3.4e+02;		
	Matches 19; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Oy	2319 GTCGCTGTCTGTCGCTGT	2338			
D6	1 GTCGCTGTCTGTCGCTGT	20			

RESULT	382
AZ465453	
LOCUS	
DEFINITION	AZ465453. 20 bp DNA linear GSS 04-OCT-2000
	U00275F22F Mouse 10kb plasmid U00C1M library Mus musculus genomic
	clone U00C1M0275F24 F, genomic survey sequence.

FEATURES

SOURCE

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/organism="Mus musculus"
/mol_type="Genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0119112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

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FEATURES
Source

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1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1CM0275F24"
/sex="Male"
/lab_note="B. Coli strain XL10-Gold, T1-resistant, F-"  

/clone_lib="Mouse 10kb plasmid UUC1CM library"

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2319 GTGTGTGTGTGTGTGTGTGTGT 2338
Db 1 GTGTGTGTGTGTGTGTGTGTGT 20

RESULT 383

AZ470768

LOCUS AZ470768 20 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0285109F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0285H09 F, genomic survey sequence.

ACCESSION AZ470768
VERSION AZ470768.1 GI:10628893
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: H column: 09
Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source Location/Qualifiers
1..20

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0285H09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTGTGTGT 2337
Db 1 TGTGTGTGTGTGTGTGTGTGTGT 20

RESULT 384

AZ580200

LOCUS AZ580200 20 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0368420F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0368A20 F, genomic survey sequence.

ACCESSION AZ580200
VERSION AZ580200.1 GI:11694625
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0368 row: A column: 20
Seq primer: CGTTGTAAACGACGCGCCAGT

Class: plasmid ends
High quality sequence stop: 20.

FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 95.0%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2317 CTGTGTGTGTGTGTGTGTGT 2336
DB 2 CTGTGTGTGTGTGTGTGTGT 21

RESULT 389
AZ991225 21 bp DNA linear GSS 27-APR-2001
LOCUS 2M0275K17F Mouse 10kb plasmid UGCG2M library Mus musculus genomic
DEFINITION clone UGCG2M0275K17 F, genomic survey sequence.

ACCESSION AZ991225
VERSION AZ991225.1 GI:13862452
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: K column: 17

Seq primer: CATTGTAAACGACGCGCACT
Class: plasmid ends

High quality sequence stop: 21.

FEATURES
Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0275K17"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG2M library"
/note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 95.0%; Score 18.4; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2319 GTGTGTGTGTGTGTGTGTGT 2338
DB 21 GTGTGTGTGTGTGTGTGTGT 2

RESULT 390
AZ645446 24 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0510H22R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0510H22 R, genomic survey sequence.

ACCESSION AZ645446
VERSION AZ645446.1 GI:11774942
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

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JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: H column: 22

Seq primer: CACACAGAAACGATGACG
Class: plasmid ends

High quality sequence stop: 24.

FEATURES
Location/Qualifiers

1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0510H22"
/sex="Male"

/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi4732114|db|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 18.4; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2334 CCGTGTGTGTGTGTGTGCA 2353
Db 1 CTTGTGTGTGTGTGTGCA 20

RESULT 393
TA197D12P/c 25 bp DNA linear GSS 13-DEC-2000
LOCUS TA197D12P
DEFINITION T. Brucei sheared genomic DNA clone 197d12, forward sequence,
ACCESSION AL475774
VERSION AL475774.1 GI:11842542
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 25)

REFERENCE Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
AUTHORS Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajadream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="197d12"

Query Match 0.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2330 TGTGCGTGTGTGTGTGTGCG 2352
Db 25 TATGTGTGTGTGTGTGTTC 3

RESULT 394
AG200915 26 bp DNA linear GSS 06-MAR-2004
LOCUS AG200915
DEFINITION Pan troglodytes DNA, clone: RP43-083C08.TU, genomic survey

sequence.
ACCESSION AG200915
VERSION AG200915.1 GI:45233090
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
TITLE Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
JOURNAL BAC end sequences of library RP-43
REFERENCE
AUTHORS 2 (bases 1 to 26)
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

TITLE Direct Submission
JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail: redstone@kribb.re.kr, URL: <http://pbs.grc.kribb.re.kr/>,
Tel: 82-42-866-7181, Fax: 82-42-860-4403)

Clones are derived from the chimpanzee BAC library RP-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TU

LIBRARY
Vector 1: pBACE3.6
R.site 1: EcoRI
R.site 2: EcoRI.
Location/Qualifiers
1..26

/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-083C08.TU"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.5%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATTA 2845
Db 2 TACACATATATATATATATTA 24

RESULT 395
AG200915/c 26 bp DNA linear GSS 06-MAR-2004
LOCUS AG200915
DEFINITION Pan troglodytes DNA, clone: RP43-083C08.TU, genomic survey
sequence.

ACCESSION AG200915
VERSION AG200915.1 GI:45233090
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE
AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
TITLE Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
JOURNAL BAC end sequences of library RP-43
REFERENCE
AUTHORS 2 (bases 1 to 26)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.

Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);

52, Oun-dong, Yusong-Gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
Tel: 82-42-866-7181, Fax: 82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

PRIMERS

Sequencing: TV

LIBRARY

Vector : pBac3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. 26

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-083C08.TU"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.5%; Score 18.2; DB 1; Length 26;
Best Local Similarity 87.0%; Pred. No. 4.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2823 TATATATACATATATATATATTA 2845

Db 23 TATATATATATATATATATATATTA 1

RESULT 396

AZ415089

LOCUS AZ415089 21 bp DNA linear GSS 03-OCT-2000

DEFINITION IM0189G17R Mouse 10kb plasmid UGCLM library Mus musculus genomic

clone UGCLM0189G17 R, genomic survey sequence.

ACCESSION AZ415089

VERSION AZ415089.1 GI:10539102

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0189 row: G column: 17

Seq primer: CACACAGAAACAGCATGAC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCLM0189G17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCLM library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrolytically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

QY 2319 GTGTGTGTGTGTGTGTGTGTGTG 2339

Db 1 GTGTGTGTGTGTGTGTGTGTGTG 21

RESULT 397

AZ665302

LOCUS AZ665302/c 21 bp DNA linear GSS 14-DEC-2000

DEFINITION IM0546J09R Mouse 10kb plasmid UGCLM library Mus musculus genomic

clone UGCLM0546J09 R, genomic survey sequence.

ACCESSION AZ665302

VERSION AZ665302.1 GI:11802448

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0546 row: J column: 08

Seq primer: CACACAGAAACAGCATGAC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCLM0546J09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

QY 2830 ACATATATATATATATAT 2850
 Db 22 AAATATATATATATATATAT 2

RESULT 400
 AZ644875 25 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0510E03F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 DEFINITION clone UGCGM0510E03 F, genomic survey sequence.
 ACCESSION AZ644875
 VERSION AZ644875.1 GI:11773823
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 25)
 Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0510 row: E column: 03
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES
 source

1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0510E03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 4.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2327 GTGTGTGCGTGTGTGTGTG 2347

Db 5 GTGTGCGCATGTGTGTGTG 25

RESULT 401
 AZ775159 25 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0007F13F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 DEFINITION clone UGCG2M0007F13 F, genomic survey sequence.
 ACCESSION AZ775159
 VERSION AZ775159.1 GI:12901359
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 25)
 Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0007 row: F column: 13
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES
 source

1..25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0007F13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (GI4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.5%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 4.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2311 TTGTGTGTGTGTGTGTGTG 2331

Db 5 TTTAGTGTGTGTGTGTGTG 25

RESULT 402

LOCUS BG920906/c

DEFINITION BG920906 38 bp mRNA linear EST 05-JUN-2001
602822814F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4951803 5',
mRNA sequence.

ACCESSION BG920906

VERSION BG920906.1 GI:14301382

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straube, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
Plate: LLAM10908 row: k column: 04
High quality sequence stop: 38.

FEATURES

source

Location/Qualifiers
1..38
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4951803"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/lab_host="NCI CGAP Mam6"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Query Match

Best Local Similarity 0.5%; Score 17.8; DB 1; Length 38;
Pred. No. 7.1e+02;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3262 TATTTATTTGCTTGTCTTTCAGGAGATTAGA 3298

Db 37 TTTTATTTTATTTTATTTTGTGAGATTATCAAA 1

RESULT 403

LOCUS AZ811237

DEFINITION AZ811237 24 bp DNA linear GSS 20-FEB-2001
2M0077K19P Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0077K19 F, genomic survey sequence.

ACCESSION AZ811237

VERSION AZ811237.1 GI:12979487

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0077 row: K column: 19
Seq primer: CGTTGTAACACGACGCGCAGT
Clase: plasmid ends
High quality sequence stop: 24.

FEATURES

source

Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0077K19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
<http://www.jax.org/resources/documents/dnares/>. The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

Best Local Similarity 0.5%; Score 17.6; DB 1; Length 24;
Pred. No. 5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2328 TGTGCGCGTGTGTGTGTGTG 2351

Db 1 TATTTGGGTGTGTGTGTGTG 24

RESULT 404

LOCUS AZ976143

DEFINITION AZ976143 25 bp DNA linear GSS 27-APR-2001
2M0251P21F Mouse 10kb plasmid UGCG2M library Mus musculus genomic
clone UGCG2M0251P21 F, genomic survey sequence.

ACCESSION AZ976143

VERSION AZ976143.1 GI:13847370

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2824 ATATATCATATATATAT 2842
DB 1 ATATATATATATATATAT 19

RESULT 407
AZ401252 19 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0167E20R Mouse 10kb plasmid UGCI1M library Mus musculus genomic
DEFINITION clone UGCI1M0167E20 R. genomic survey sequence.
ACCESSION AZ401252
VERSION AZ401252.1 GI:10516326
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D. Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0167 row: E column: 20
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCI1M0167E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid UGCI1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2823 TATATATCATATATATAT 2841
DB 19 TATATATATATATATAT 1

RESULT 408
AZ431700 19 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0216G18R Mouse 10kb plasmid UGCI1M library Mus musculus genomic
DEFINITION clone UGCI1M0216G18 R. genomic survey sequence.
ACCESSION AZ431700
VERSION AZ431700.1 GI:10555713
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D. Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0216 row: G column: 18
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCI1M0216G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid UGCI1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2824 ATATATACATATATATATATA 2842
Db 1 ATATATATATATATATATA 19

RESULT 411
AZ630416 19 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0484B03F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0484B03 F, genomic survey sequence.

ACCESSION AZ630416
VERSION AZ630416.1 GI:11752606
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0484 row: B column: 03
Seq primer: CATTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0484B03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2823 TATATATACATATATATATAT 2841
Db 19 TATATATATATATATATAT 1

RESULT 412
AZ649147 19 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0518B17R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0518B17 R, genomic survey sequence.

ACCESSION AZ649147
VERSION AZ649147.1 GI:11782334
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0518 row: B column: 17
Seq primer: CACACAGAAACAGCTATGACCC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0518B17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

adaptoed vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTGTG 2333
|||
Db 1 GTCTGTGTGTGTGTGTGTG 19

RESULT 415

AZ822936 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0096E08R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG2M0096E08 R, genomic survey sequence.

ACCESSION AZ822936
VERSION AZ822936.1 GI:12992844
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: B column: 08
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0096E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2315 GTCTGTGTGTGTGTGTGTG 2333
|||
Db 1 GTCTGTGTGTGTGTGTGTG 19

RESULT 416

AZ827177 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0103A05R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCG2M0103A05 R, genomic survey sequence.

ACCESSION AZ827177
VERSION AZ827177.1 GI:12997085
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: A column: 05
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0103A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2318 TGTGTGTGTGTGTGTGTGTGT 2336
DB 1 TGTGTGTGTGTGTGTGTGT 19

RESULT 417
AZ514387/c 22 bp DNA linear GSS 05-OCT-2000
LOCUS 1M0361H03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0361H03 F, genomic survey sequence.
ACCESSION AZ514387
VERSION AZ514387.1 GI:10695703
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: H column: 03
Seq primer: CGTTGTAAACGACGCGCAAT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361H03"
/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42ny. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.5%; Score 17.4; DB 1; Length 22;
Best Local Similarity 94.7%; Pred. No. 4.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2318 TGTGTGTGTGTGTGTGTGTGT 2336
DB 22 TGTGTGTGTGTGTGTGTGT 4

RESULT 418
CF299772/c 23 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-017.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-017, mRNA
sequence.
ACCESSION CF299772.1 GI:33671533
VERSION CF299772
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim, J.S., Jun, K.M., Cheong, P.D., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-017"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI, mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.5%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2823 TATATATACATATATATATATAT 2844
DB 23 TACATATACATATATACATATAT 2

RESULT 419
AZ442547 23 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0336B15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0336B15 R, genomic survey sequence.
ACCESSION AZ442547
VERSION AZ442547.1 GI:10589665
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)

REFERENCE
1 (bases 1 to 23)

TITLE EST (Osterweider, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

FEATURES
source MIPS
Ingelstaedter Landstr.1, D-85764 Neuberg, Germany.
Location/Qualifiers
1. .31

/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="DKFZ566J2347"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_1ib="566 (synonym: hfxd2)"
/note="vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.5%; Score 17.2; DB 1; Length 31;
Best Local Similarity 73.3%; Pred. No. 7e+02;
Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3266 TTATTTGCTTGTCTTTTCAGAGAAAT 3295
Db 31 TTTT TTTT TTTT TTTT TTTT CAGAGAAAT 2

RESULT 422
AZ491644 19 bp DNA linear GSS 05-OCT-2000
LOCUS IM0325A20F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0325A20 F, genomic survey sequence.
ACCESSION AZ491644
VERSION AZ491644.1 GI:10663543
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0325 row: A column: 20
Seq primer: CATTGTAAAACGACGGCAGCT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

FEATURES
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0325A20"
/sex="Male"

/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGIM library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

Query Match 0.4%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2333 GCGTGTGTGTGTGTGTG 2349
Db 3 GCGTGTGTGTGTGTGTG 19

RESULT 423
AZ785549 20 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0029F01R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCG2M0029F01 R, genomic survey sequence.
ACCESSION AZ785549
VERSION AZ785549.1 GI:12922419
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: F column: 01
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0029F01"
/sex="Male"

/lab_host="E. Coli strain X110-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UGCGIM library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|g14732072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli X110-Gold (Stratagene) cells
and selected for ampicillin resistance."

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 100.0%; Score 17; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GTGTGTCGTGTGTGTG 2351
Db 4 GTGTGTCGTGTGTGTG 20

RESULT 424
AM250841 32 bp mRNA linear EST 07-JAN-2000
LOCUS 2821274.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821274 3',
DEFINITION mRNA sequence.

ACCESSION AM250841
VERSION AM250841.1 GI:6593834
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 32)
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT Other ESTs: 2821274.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnll.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross_match from University of Washington Genome Center PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 32 contiguous PHRED high quality bases following trace sequence. Very low Quality Sequence: Trace file contained 32 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

FEATURES
source
High quality sequence stop: 32.
Location/Qualifiers
1..32

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821274"
/cissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NIH_MGC 7"
/note="Organ: lung; Vector: POTB; site_1: XhoI; site_2:

ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcorI/XhoI sites using the following 5' adaptor: GGCAAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match
Best Local Similarity 80.0%; Score 17; DB 1; Length 32;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3310 TTTTCTTTCAGAGATTATTTT 3334
Db 1 TTTTCTTTCAGAGATTATTTT 25

RESULT 425
TA379A06P/C 42 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 379a06, forward sequence,
DEFINITION genomic survey sequence.

ACCESSION AL497629
VERSION AL497629.1 GI:11873351
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei

REFERENCE Eukaryota; Elenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma. 1 (bases 1 to 42)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrett,B.G.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Cambridge CB10 1SA, E-mail: barrett@anger.ac.uk and nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..42
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="379a06"

Query Match
Best Local Similarity 63.4%; Score 17; DB 1; Length 42;
Matches 26; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3294 TTAGATTCTATAGAGATTTCCTTAGAGAGATTATTTT 3334
Db 42 TTTTCTTTCAGAGATTATTTT 25

RESULT 426
AZ482421 20 bp DNA linear GSS 04-OCT-2000
LOCUS IM0307P01R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM0307P01 R, genomic survey sequence.
ACCESSION AZ482421

VERSION AZ482421.1 GI:10643486
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0307 row: P column: 01
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0307P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTG 2337
DB 1 TGTGTGTGTGTGTGTGTG 20

RESULT 427
AZ654458 20 bp DNA linear GSS 14-DEC-2000
LOCUS AZ654458
DEFINITION 1M0528610R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0528610 R, genomic survey sequence.
ACCESSION AZ654458
VERSION AZ654458.1 GI:11791604

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0528 row: G column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0528610"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2318 TGTGTGTGTGTGTGTGTG 2337
DB 1 TGTGTGTGTGTGTGTGTG 20

RESULT 428
AZ958303 20 bp DNA linear GSS 27-APR-2001
LOCUS AZ958303/C
DEFINITION 2M0225106R Mouse 10kb plasmid UUCG2M library Mus musculus genomic
clone UUCG2M0225106 R, genomic survey sequence.
ACCESSION AZ958303
VERSION AZ958303.1 GI:13829530
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0225 row: I column: 06
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0225106"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3465 TATATCTATATATATAT 3484
 Db 20 TATATCTATATCTATAGT 1

RESULT 429
 AZ635078/c
 LOCUS 23 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M041C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 AZ635078
 accession UUGC1M041C14 F, genomic survey sequence.
 VERSION AZ635078.1 GI:11757268
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0491 row: C column: 14
 Seq primer: CATTGTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0491C14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.8; DB 1; Length 23;
 Best Local Similarity 90.0%; Pred. No. 5.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2318 TGTGTGTGTGTGTGTGTG 2337
 Db 22 TGTGTGTGTGTGTGTGCGTG 3

RESULT 430
 CF333289
 LOCUS 30 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--02-C01.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--02-C01, mRNA sequence.
 accession CF333289
 version CF333289.1 GI:33814856
 keywords EST.
 source Oryza sativa (japonica cultivar-group)

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristaceae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-C01"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="pJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis thaliana Col-0 methylation
methyltransferase overexpression line."

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 30;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3264 TTTTATGCTGCTGCTTTTTCAGGAG 3291
Db 2 TTTTATGCTGCTGCTTTTTCAGGAG 29

RESULT 431
CP298071/c
LOCUS
DEFINITION
34 bp mRNA linear EST 15-AUG-2003
7LEAF--01-E22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-E22, mRNA
sequence.
ACCESSION
CP298071
VERSION
CP298071.1 GI:33669832
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristaceae; Oryzaceae; Oryza.
1 (bases 1 to 34)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

Query Match
Best Local Similarity 0.4%; Score 16.8; DB 1; Length 34;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3310 TTTTCTTGAAGAGATTATTTTGA 3337
Db 29 TTTTCTTGAAGAGATTATTTTGA 2

RESULT 432
AJ658745
LOCUS
AJ658745 KN277 Sus scrofa cDNA clone C0005213_I02, mRNA sequence.
DEFINITION
ACCESSION
AJ658745.1 GI:49342814
VERSION
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
Oryzaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 23)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match and the -mnscore 20
and -mismatch 12 options. Vector:phuescriptII(SK+) R. Site1: EcoRI
R. Site2: NotI 5' Seg Primer M13F Normalised library constructed
from pooled early embryos, from 8-cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.airgenomics.org.

FEATURES
source
1..23
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005213_I02"
/issue_type="embryo"
/clone_lib="KN277"
/note="Vector: phuescriptII(SK+); Site_1: EcoRI; Site_2:
NotI. Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."

Query Match
Best Local Similarity 0.4%; Score 16.6; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2924 GGGGCGTGGGGGGCGTGAAGG 2946
Db 1 GGGGCGTGGGGGGCGGCGGCG 23

RESULT 433
AZ411764
LOCUS
DEFINITION
23 bp DNA linear GSS 03-OCT-2000
IM0184022R Mouse 10kb plasmid UDGCM library Mus musculus genomic

accession AZ411764.1 GI:10535777
 version AZ411764.1
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 authors 1 (bases 1 to 23)
 title Dunm, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
 journal Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 comment Unpublished (2000)
 contact: Robert B. Weiss
 university of Utah Genome Center
 rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 tel: 801 585 5606
 fax: 801 585 7177
 email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0184 row: 0 column: 22
 seq primer: CACACAGAAACAGCATATGACC
 class: plasmid ends
 high quality sequence stop: 23.
 location/qualifiers
 1. 23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0184O22"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 6.2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2920 GGGCGGGCGCTGGGGGGCGCTGG 2942
 DB 1 GGGGGGGGGCGGGGGGGGGGGGG 23

RESULT 434
 AZ618720/c 23 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0450019F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0450019 F, genomic survey sequence.

accession AZ618720.1 GI:11740826
 version AZ618720.1
 keywords GSS.
 source Mus musculus (house mouse)
 organism Mus musculus
 reference Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 authors 1 (bases 1 to 23)
 title Dunm, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.
 journal Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 comment Unpublished (2000)
 contact: Robert B. Weiss
 university of Utah Genome Center
 rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 tel: 801 585 5606
 fax: 801 585 7177
 email: ddunn@genetics.utah.edu
 insert length: 10000 Std Error: 0.00
 plate: 0450 row: 0 column: 19
 seq primer: CGTTGTAACAGACGCGCAGT
 class: plasmid ends
 high quality sequence stop: 23.
 location/qualifiers
 1. 23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0450019"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 6.2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2924 GGGCGGGCGGGGGGGCGTGGAGGG 2946
 DB 23 GGGGGGGGGGGGGGGGGGGGGGGG 1

RESULT 435
 AZ764518 23 bp DNA linear GSS 16-FEB-2001
 LOCUS 1M056011R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M056011R, genomic survey sequence.

VERSION AZ764518.1 GI:12879563
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0560 row: L column: 11
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 23.
 FEATURES
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid TUGC1M library"
 /note="Vector: PMD42ny. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114gb/AP12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 6.2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2924 GGGGCGTGGGGGGCGTGAAGG 2946
 Db 23 GGGGGGGGGGGGGGGGGGGGGG 1

RESULT 436
 CDS77045/c 38 bp mRNA linear EST 15-JUN-2004
 LOCUS
 DEFINITION
 Igot1_c12_03_088 ESTs from wild-caught Anopheles funestus populations Anopheles funestus cDNA 5', mRNA sequence.
 CDS77045
 CDS77045.1 GI:48718060

KEYWORDS EST.
 SOURCE Anopheles funestus
 ORGANISM Anopheles funestus
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 REFERENCE 1 (bases 1 to 38)
 AUTHORS Beanesky, N.J., Serazin, A.C. and Dana, A.
 TITLE Towards the transcriptome of Anopheles funestus: a molecular snapshot
 JOURNAL Unpublished (2003)
 COMMENT Contact: Andrew Serazin
 Collins/Beanesky Lab
 Center for Tropical Disease Research and Training, University of Notre Dame
 317 Galvin Life Science, Notre Dame, IN 46556, USA
 Tel: 5746319321
 Email: nbeanesk@nd.edu
 These sequences may be of either nuclear or mitochondrial origin.
 FEATURES
 Location/Qualifiers
 1..38
 /organism="Anopheles funestus"
 /mol_type="mRNA"
 /strain="West African"
 /db_xref="taxon:62324"
 /sex="male and female"
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 /note="Vector: LambdaTriplEx2"

Query Match 0.4%; Score 16.6; DB 1; Length 38;
 Best Local Similarity 71.0%; Pred. No. 9.4e+02;
 Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3310 TTTTCTTGAAGATTATTTTGGACTT 3340
 Db 34 TTTTCTTGAAGATTATTTTGGAAAT 4

RESULT 437
 AZ786779 19 bp DNA linear GSS 16-FEB-2001
 LOCUS
 DEFINITION
 2M0032C01R Mouse 10kb plasmid TUGC1M library Mus musculus genomic clone UGCGM0032C01 R, genomic survey sequence.
 AZ786779
 AZ786779.1 GI:12924882
 VERSION
 SOURCE
 KEYWORDS
 ORGANISM Mus musculus (house mouse)
 GSS.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0032 row: C column: 01
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_1lb="Mouse 10kb plasmid UGCLM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 94.4%; Score 16.4; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2313 TGGTGTGTGTGTGTGTGT 2330

Db 1 TGGTGTGTGTGTGTGTGT 18

RESULT 438
LOCUS AZ626965 21 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0467E15R Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0467E15 R, genomic survey sequence.
ACCESSION AZ626965
VERSION AZ626965.1 GI:11749155
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0467 row: E column: 15
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

source

1. .21
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCLM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 94.4%; Score 16.4; DB 1; Length 21;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2320 TGTGTGTGTGTGTGTGTGT 2337

Db 4 TGTGTGTGTGTGTGTGTGT 21

RESULT 439
LOCUS BU054011 37 bp mRNA linear EST 29-SEP-2003
DEFINITION BU054011 N1BB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL048p20 3', mRNA sequence.
ACCESSION BU054011
VERSION BU054011.1 GI:117499017
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus. 1 (bases 1 to 37)
AUTHORS Kohara,Y.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.
Location/Qualifiers

FEATURES
source
1. .37
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL048p20"
/tissue_type="whole embryo"

/dev_stage="stage 15"
/clone_lib="NIBB Mochi normalized Xenopus neurula
library"

Query Match 0.4%; Score 16.4; DB 1; Length 37;
Best Local Similarity 67.6%; Pred. No. 9.6e+02;
Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3310 TTTTCTTTAGAGATTATTTTGGACTTCA 3343
|||||
36 TTTTCTTTGGTTTCTTTTCTTTTCTTTTCA 3

RESULT 440 40 bp mRNA linear EST 10-OCT-2003
BX564796
LOCUS BX564796 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse73g04_p1c, mRNA sequence.
ACCESSION BX564796
VERSION BX564796.1 GI:33431939
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossiniidae; Glossina.
1 (bases 1 to 40)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Ronaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
genome Biol. 4 (10), R63 (2003)
2281942
14519198

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix gic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..40
/organism="Glossina morsitans morsitans"
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/clone="Tse73g04_p1c"
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/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.4%; Score 16.4; DB 1; Length 40;
Best Local Similarity 67.6%; Pred. No. 1e+03;
Matches 23; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 3301 TCTATAGATTCTTCTTAGAGATTATTTT 3334
|||||
2 TCTAGAGTTTCTTTTCTTTTCTTTTCTTTT 35

RESULT 441 43 bp mRNA linear EST 30-APR-2004
CNS46803
LOCUS CNS46803
DEFINITION EST 18574 Turning Grape Berry Lambda Triplex2 Library Vitis

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source
Location/Qualifiers
1..43
/organism="Vitis vinifera"
/mol_type="mRNA"
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/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: lambda
Triplex2; Site_1: SfilA; Site_2: SfilB; Oriented library"

Query Match 0.4%; Score 16.4; DB 1; Length 43;
Best Local Similarity 61.9%; Pred. No. 1.1e+03;
Matches 26; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 3456 ACAAGTTATATATCTATATATATATATATGAGTTT 3497
|||||
2 ACGTCTTTTCTTTTCTTTTCTTTTCTTTTGGGGTTT 43

RESULT 442 21 bp DNA linear GSS 04-OCT-2000
AZ476580
LOCUS AZ476580
DEFINITION 1M0295G04R Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM0295G04 R, genomic survey sequence.
ACCESSION AZ476580
VERSION AZ476580.1 GI:10634705
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0295 row: G column: 04
 Seq primer: CACACAGGAACAGCATGAC
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES

source

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/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/
/clone_lib="mouse 10kb plasmid UUCGIM library"
/notes="Vector: FMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g14732072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match

Best Local Similarity 85.7%; Score 16.2; DB 1; Length 21;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2329 GTGTGCGTGTGTGTGTGTG 2349

Db 1 GTGTGAGTGTGTGTGTGTGTG 21

RESULT 443
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 DEFINITION cu27h03.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
 IMAGE:1627541.3 similar to TR:069566 Q69566 ;, mRNA sequence.
 ACCESSION A1016967
 VERSION A1016967.1 GI:3231303
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 22)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/cgi/gap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 This clone is available royalty-free through INL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 961 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 1;
 Location/Qualifiers

FEATURES

source

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1. 22
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Query Match
 Best Local Similarity 85.7%; Score 16.2; DB 1; Length 22;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2319 GTGTGCGTGTGTGTGTGTG 2339

Db 21 GTCTGTGTGTGTGTGTGTG 1

RESULT 444
 LOCUS PCH303886 22 bp DNA linear GSS 03-APR-2001
 DEFINITION Plasmodium chabaudi genome survey sequence, clone PC4d10.p1c,
 genomic survey sequence.
 ACCESSION AJ303886
 VERSION AJ303886.1 GI:11141349
 KEYWORDS GSS; genome survey sequence.
 SOURCE Plasmodium chabaudi
 ORGANISM Plasmodium chabaudi
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 22)
 Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
 Bowman,S., Phillips,R.S. and Turner,C.M.
 Gene discovery in Plasmodium chabaudi by genome survey sequencing
 Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
 PUBLISHED 11295179
 REFERENCE 2 (bases 1 to 22)
 Janssen,C.S.
 Direct Submission
 Submitted (06-NOV-2000) Division of Infection & Immunity,
 University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
 bases 477 to 498 (Q1 to Q3).
 Location/Qualifiers

FEATURES

source

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QY 2823 TATATATACATATATATATAT 2843

Db 2 TATATATGATATGTGTATAT 22

RESULT 445
 LOCUS PCH303886 22 bp DNA linear GSS 03-APR-2001
 DEFINITION Plasmodium chabaudi genome survey sequence, clone PC4d10.p1c,
 genomic survey sequence.

ACCESSION AJ303886
 VERSION AJ303886.1 GI:11141349
 KEYWORDS GSS; genome survey sequence.
 SOURCE Plasmodium chabaudi
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 REFERENCE 1 (bases 1 to 22)
 Janssen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D., Bowman, S., Phillips, R.S. and Turner, C.M. Gene discovery in Plasmodium chabaudi by genome survey sequencing Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
 JOURNAL MEDLINE 21192558
 PUBMED 11295179
 REFERENCE 2 (bases 1 to 22)
 Janssen, C.S. Direct Submision Submitted (06-NOV-2000) Division of Infection & Immunity, University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
 COMMENT bases 477 to 498 (OL to OR).
 FEATURES Location/Qualifiers
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 /organism="Plasmodium chabaudi"
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 Query Match 0.4%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2824 ATATATACATATATATATATA 2844
 DB 22 ATATACATATATATATATA 2
 RESULT 446
 TA300F12P 23 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 300F12, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL490817
 VERSION AL490817.1 GI:11865290
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 23)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G. Direct Submision Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRU927/4 GOTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.
 Location/Qualifiers
 source 1..23
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TRU927"

/db_xref="taxon:5691"
 /clone="300F12"
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 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2817 ATATGATATATATATATATAT 2837
 DB 2 ATATGATATATATATATATTT 22
 RESULT 447
 AZ615581
 LOCUS 23 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0445F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0445F09 F, genomic survey sequence.
 ACCESSION AZ615581
 VERSION AZ615581.1 GI:11737867
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 JOURNAL Contract: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std. Error: 0.00
 Plate: 0445 Row: F Column: 09
 Seq primer: CGTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0445F09"
 /sex="Male"
 /lab_host="E. Coli: strain X110-Gold, T1-resistant, F-"
 /note="Vector: PMD42uv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into (Stratagene) cells chemically-competent E. coli X110-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2309 GCTTGGCTGCTGCTGCTGCTG 2329
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 Db 3 GCTATGCTGCTGCTGCTGCTG 23

Search completed: October 28, 2004, 12:38:04
 Job time : 122 secs

